8.1 Appendix A: Recommendations for Statistics

The following recommendations have been drawn from a review of literature, NATA guidelines, advice from senior quality staff at Forensic and Scientific Services and from National Forensic Statisticians.

For definitions of accuracy (trueness), precision, repeatability, reproducibility (within laboratory and between laboratory), blank. linearity, limit of detection (LOD), limit of (LOR), sensitivity, uncertainty and verification refer to QIS 10662 and QIS 23849, and NATA guidelines (https://nata.com.au/).

Please also refer to the FSS Guidelines for Method Validation QIS 10662.

Considerations in the design and approach to a validation study or research project:

Are statistics necessary given the experiment or analysis being considered:

- For strong statements "significant difference", "linear trend" etc. a statistic will be required to support the statement. For comparative statements it may not always be informative, or operationally appropriate to complete a statistic i.e. "differences were seen", or "appears to be a trend" statements do not require a statistic.
- Where a statistical test is not informative, and/or particularly where the difference between the experimental groups will not have an operational meaning - use of box plots are recommended. Box plots display the variation present in a system. Generally if the box plots overlap the difference between the groups is functionally non-significant.

Sample numbers:

When deciding how many samples are require for an individual experiment the following should be evaluated:

- Consider the amount of variation you are expecting to see. Where little variation is expected (e.g. number of alleles obtained from blood samples) small experimental sample numbers are needed. Where variation is higher (e.g. peak heights from low DNA quantification samples) sample numbers should be much higher. Where the amount of expected variation is unknown it is possible to run one set of samples, assess the results and then run additional samples if required.
- The experimental design is always aiming to include enough samples to model the expected variation in the relevant experiment (given the experimental factors under consideration). Thereby producing sufficient information (via sample numbers) for the development of methods/thresholds to cover "most situations". It is not possible for a study/validation to cover all possible situations.
- In cases were a project/validation is assessing locus amplification efficiency, and inter-locus peak height balance larger sample sizes may be required (suggest use of population samples ~200-250); this is particularly relevant for Y kits where a linear relationship may not be seen.

Which statistics might be most appropriate:

- ANOVA – to compare independent groups of samples
  Example: Dziak, R, Peneder, A, Buetter, A & Hageman, C. 2018 'Trace DNA Sampling Success from Evidence Items Commonly Encountered in Forensic Casework,' *J Forensic Sci*, vol 63, pp 835-841. doi:10.1111/1556-4029.13622

- Kruskal-Wallis – to compare independent groups of samples
  Example: Henry, J & Scandrett, L. 2019 'Assessment of the Yfiler® Plus PCR amplification kit for the detection of male DNA in semen-negative sexual assault cases,' *Science & Justice*, in press 2019.

- Paired T-test – to compare repeated samples i.e. same samples run through two different methods.
  Example: Tsai, L, Lee, C, Chen, C, Lee, J.C, Wang, S, Huang, N, Linacre, A. & Hsieh, H. 2016, 'The Influence of Selected Fingerprint Enhancement Techniques on Forensic DNA Typing of Epithelial Cells Deposited on Porous Surfaces.' *J Forensic Sci*, vol 61: S221-S225
- Chi-square test – may be applied to demonstrate the average peak heights between loci (or dye layer) may differ
  Example: Montpetit, S & O'Donnell, P, 2015, 'An optimized procedure for obtaining DNA from fired and unfired ammunition,' *Forensic Science International: Genetics*, vol 17, pp 70-74,

Tools for statistics:

- Excel – basic statistics
- R software program
- SPSS Software – commercially available software for statistics and graphing

Practical guidelines and suggestions:
It is not possible for a "procedure" to be written that will cover all possible approaches/analysis for studies that may be required within the Forensic DNA Analysis Laboratory. However, some key principles and guidelines are provided below that may assist with the development of an experimental design.

Instrument validations:

- For instruments that perform pipetting tasks, assessment of %inaccuracy and %CV are generally assessed on the Artel MVS instrument, and must meet laboratory guidelines +/- 5% (10% for volumes ≤10µL)
- Contamination checks can be important in many studies, particularly those that involve pipetting or liquid movement steps. This may include soccer-ball plates for 96-well formats.

Software validations

- Ensure the computer on which the software is installed meets the specifications of the software
- The software must have a version number (this must be referenced in the validation)
- Settings/configurations must be consistent with the software specifications, and only able to be accessed by authorised users
- Software should have pre-existing developmental validation (i.e. publication, or manufacturers validation). This validation should ensure that calculations and parameters meet requirements.

Sensitivity and Limit of Detection:

- Sensitivity studies will often be conducted prior to repeatability/reproducibility assessments.
- Concordance assessments may be incorporated with sensitivity studies. Concordance is usually an assessment of ~100 samples.

DNA Extraction

- Serial dilutions of cell suspensions (where a cell count has been done) are useful for DNA extraction sensitivity studies (Refer project #168 final report for further details)
- Dilutions should result in range of cell concentrations~10-500 cells (per extraction), such that the capacity of extraction technology is assessed at ranges suitable for forensic analysis.

DNA Quantification

- Serial dilutions of NIST standards are useful for LOD and sensitivity assessments where DNA quantifications methods are to be evaluated. Percentage change (inaccuracy) may be calculated from the expected and observed results.

- Dilutions should extend both below and above expected functional range as defined by the manufacturer. For example in validating Quant Studio 5 the dilutions utilised were: 0.0001, 0.001, 0.002, 0.003, 0.004, 0.005, 0.006, 0.007, 0.008, 0.009, 0.01, 0.03, 0.05, 0.07, 0.09, 0.1, 0.5, 1.0 and 5.0 ng/µL (Refer project #185 final report for further details)

DNA Amplification

- Optimal PCR cycle number to be evaluated by the laboratory: this should include 7-12 samples, plus controls over at least 3 different PCR cycle numbers.

Capillary Electrophoresis

- Baseline should utilise 20-100 samples, with samples analysed at 1RFU. Stutter, pull-up, carry-over and artefacts should be removed. Average peak height RFU (μ_{Pk}) for each dye channel calculated using the AVERAGE function (Arithmetic mean) in Excel. The standard deviation (σ_{Pk}) will be calculated using the STDEV function in Microsoft Excel (Refer project #196 for further details)
  - Limit of Detection (LOD)= $\mu_{Pk} + 3\ \sigma_{Pk}$
  - Limit of Reporting (LOR)= $\mu_{Pk} + 10\ \sigma_{Pk}$

Repeatability:

- Run a set of samples multiple times on a plate. Ideally each sample should be run at least 7 times.
  - On a standard PCR plate 12 samples can usually be run on a plate 7 times with standards and/or controls – this is considered statistically sound.
  - Scatter plots or box plots can be a way to display the data and evaluate the variability between replicates.

Reproducibility:

- Run a plate over multiple days (as many as is practicable e.g. over 3-5 days), with different operators.
- The "plate" of samples used for reproducibility may include the same samples used for repeatability. It is suggested that ~12 samples (min 7 samples), plus controls are included in the reproducibility plate.
- Scatter plots or box plots can be a way to display the data to evaluate reproducibility within the system.

Performance Study:

For some projects a performance study is worthwhile. This is generally a set of "Typical" samples received within the laboratory. Generally, a larger number of routine samples are processed.

Exemplar publications of forensic validation studies:

Coble, MD, Buckleton, J, Butler, JM, Egeland, T, Fimmers, R, Gill, P, Gusmão, L, Guttman, B, Krawczak, M, Morling, N, Parson, W, Pinto, N, Schneider, PM, Sherry, ST, Willuweit, S & Prinz, M 2016 'DNA Commission of the International Society for Forensic Genetics: Recommendations on the validation of software programs performing biostatistical calculations for forensic genetics applications,' *Forensic Science International: Genetics*, vol 25, pp 191-197

Hollard, C, Ausset, L, Chantrel, Y, Jullien, S, Clot, M, Faivre, M, Suzanne, E, Pène, L & Laurent, F-X. 2019, 'Automation and developmental validation of the ForenSeq™ DNA Signature Preparation kit for high-throughput analysis in forensic laboratories', *Forensic Science International: Genetics,* vol. 40, pp. 37-45

Meuwly, D, Ramos, D & Haraksim, R 2017, 'A guideline for the validation of likelihood ratio methods used for forensic evidence evaluation', *Forensic Science International*, vol. 276, pp. 142-15

8.2 Appendix B: Resources for Statistics

QFAB Biostats Sites Sheet

A list of useful online Biostatistics sites.

Introductory Theory

Discovering Statistics by Andy Field
https://www.discoveringstatistics.com/

Study Design

Phases of Clinical Trials by Australian Clinical Trials
https://www.australianclinicaltrials.gov.au/what-clinical-trial/phases-clinical-trials

Study Designs by The Centre for Evidence-Based Medicine
https://www.cebm.net/2014/04/study-designs/

Choosing the Right Statistical Test

Numerical Methods for Biosciences Students
https://web.anglia.ac.uk/numbers/biostatistics/biostatistics.html

Statistical Decision Tree
https://www.anzmtg.org/stats/

Sample Size and Power

Calculating an optimal samples size or identifying the power of a sample size
https://www.anzmtg.org/stats/Guides/PowerOfSampleSize

Sample Size and Power Calculators

G*Power, MedCalc, EpiTools, StatsToDo, StatsPages

Sample size estimates need to be inflated to take into account estimated drop outs and missing values. QFAB has developed a Study Length Calculator for this.

Randomisation

Directory of randomisation software and services
https://www-users.york.ac.uk/~mb55/guide/randsery.htm

Surveys & Questionnaires

Measurement Tools/Research Instruments
http://guides.lib.uw.edu/c.php?g=99174&p=641942

Prepared by the QFAB Biostatistics Team
https://qfab.org/biostatistics

QFAB recommends using REDcap, especially for longitudinal studies, and provides training in this. Please check if your employer supports this software.

Data Management

Good Data Guidelines
https://qfab.org/good-data-guidelines
Numerical conversion is not required is using the software R.

Online Calculators

MedCalc, Vassar Stats, EpiTools, StatSciCalc

Software

Software support
https://stats.idre.ucla.edu/#

We recommend against using Excel for data analysis. In increasing sophistication but decreasing ease of use: GraphPad Prism, SPSS, STATA, SAS, R. Each software has its own online help documentation. QFAB provides training in R, SPSS, and STATA.

Data Analysis

Choosing the right distribution
https://blog.cloudera.com/blog/2015/12/common-probability-distributions-the-data-scientists-crib-sheet/

Everything you need to complete your data analysis
https://statistics.laerd.com/features-overview.php

Statistical Help
https://www.statsdirect.com/help/default.htm

References

Handbook of Biological Statistics
http://www.biostathandbook.com/analysissteps.html

Biostatistics Resource for Medical, Health and Allied Research
http://www.medicalbiostatistics.com/

Statistics for Biologists
http://www.nature.com/collections/qghhqm/pointsofsignificance

Prepared by the QFAB Biostatistics Team
https://qfab.org/biostatistics

Queensland Health
Forensic and Scientific Services

Initial Request

Stage 1

		Proposal #:	
Proposed by :		**Date:**	
		Due Date:	
Title of Proposal:			
Project type	☐ Administration ☐ IT/LIMS ☐ Laboratory ☐ Data mining/analysis ☐ External Project ☐ Other_____		
Brief Outline of Proposed Change			

Line Manager :		**Recommendation:**
Signature:		☐ Proceed to minor change ☐ Proceed to full project plan ☐ Place on hold or abandon Reason:_____

Proposal restarted by:		**Date:**	
Approved By: **Signature:** **Date:**		**Reason:**	

Please convert to PDF, e-sign and lock document on completion.

Advise quality [redacted] when finalised.

Forensic and Scientific Services

Minor Process Change

Stage 2

		Project #:	
Proposed by :		**Date:**	
Title:			
Comment to be added to SOP:	☐ Yes QIS#_____ ☐ No	**Completed date:**	
Email communication sent:	☐ Yes Team/s_____ ☐ No	**Completed date:**	
Add to minor change register	☐ Yes	**Completed date:**	
Outline of Minor Change:			
Line Manager Signature:		**Comments:**	
Quality & Projects Signature:		**Comments:**	

Please convert to PDF, e-sign and lock document on completion.

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Queensland Health
Forensic and Scientific Services

Methods Template

1 Purpose and scope

↑*6 point space below all headings*
[State any limitations as regards concentration range, matrix etc.]

2 Definitions

2 spaces between major headings ↓

3 Principle

[include reactions, where applicable]

4 Reagents and equipment

4.1 Reagents

1 space between minor headings
[Where possible, list in order of use. Specify grade. Include safety warnings where necessary. Give brief details of standardisation of special reagents, where applicable.] ↓

4.2 Equipment

5 Safety

[Include any relevant items from the risk assessment conducted on the method]

6 Sampling and sample preparation

[Include storage conditions where applicable.]

7 Procedure

1.
2.
3.

8 Calculations

[Give a symbol identification list. State units and number of significant figures for reporting. Where appropriate, use SI (international metric) units for quantitative results]

9 Validation

[Include precision data]
[Include a statement or details of estimation of measurement uncertainty, where applicable]
[Refer to the source of the validation data eg validation file or recognised standard]

10 Quality assurance/acceptance criteria

[Define criteria to be used for deciding whether test results are to be accepted or rejected. Include any specific reporting requirements if necessary]

11 References

Reference sources of information for this document according to "Scientific Style and Format: The CBE Manual for Authors, Editors and Publishers."

Example

Cummins P, Perry SV. Troponin I from human skeletal and cardiac muscles. Biochem J 1978;171:251-9.

12 Associated documents

Include quality system documents closely linked with this document. If there is no associated documentation, insert "Nil" under this heading.

Example

QIS: 10003 – QHPSS Document Management Procedure

QIS: 10001 – QIS Flowchart Manual

Please note: A Macro has been automatically set up in this template. To insert Hyperlinks to other QIS documents, please type QIS: and then document number (e.g. QIS: 19999), then highlight number only and then select 'Ctrl Q'.

13 Amendment history

Insert the history of the document:
Issue Number, Date, Name of person/s writing, amending or reviewing document followed by a description of the amendment.

Example

Revision	Date	Author/s	Amendments
0	4 Jul 2002	S Nilsen	First Issue
1	11 Oct 2002	S Anderson	Introduction of automatic numbering for level 2 headings
2	Oct 2007	N Douglas	
3	Jul 2008	N Douglas/F Stewart	New format. Additional information about some headings.
QIS² Edition			
Version	**Date**	**Updated By**	**Amendments**
5	Mar 2009	N Douglas/F Stewart	Document footer updated from R to V. Document Hyperlink updated to new QIS2 view module site.
6	May 2009	N Douglas	Footer changed to new format. New headings for Amendment History.
7	April 2010	M Paulsen/N Douglas	BDG signed off on renaming Author/s column to Updated By. Added maroon line to header. Added risk assessment summary as mandatory appendix.
8	June 2010	N Douglas	Guidance for content of Appendix A added.
9	Aug 2012	H Gregg	Updated header to HSSA logo
10	May 2013	H Gregg	Included relevant items from 10626 which has been archived
11	Sept 2014	H Gregg	HSQ header
12	Dec 2020	H Gregg	updated header on page 2 onwards to automatically update when title is changed
13	June 2021	H Gregg	Remove HSQ
14	September 2021	D Johnston	Updated Header

14 Appendices

1 Appendix A Summary of Risk Assessment
2 Appendix B (Topic)

14.1

Appendix A

Summary of Risk Assessment

A summary is all that is required here, e.g. "A risk assessment of this method was carried out and the probability was rated as 'A', the exposure was 'B', and the consequences 'C', giving a risk score of 'D' corresponding to a [verbal description] risk. Control measures to reduce the potential risk are given in the method details above. Of these, [cite one or more of the control measures] are the most effective at reducing risk."

14.2

Appendix B

(Topic)

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Queensland Health
Forensic and Scientific Services

FSS Procedure Template

1 Purpose

State the intent of the procedure.

Example

The purpose of this procedure is to describe the preparation of all procedures.

2 Scope

State where, and to whom this procedure applies.

Example

This procedure shall apply to all procedures prepared to control the activities of the Medication Services Queensland Unit.

3 Definitions

Explain a word or action not generally understood, or which may have a specific interpretation in the procedure. If there are no definitions, insert "Nil" under this heading.

Example

Procedure: specified way to perform an action

4 Actions

Describe clearly and concisely the actions required of those personnel involved in the activity.

Example

Answer the telephone after three rings.

5 Records

List all records that will be completed as a result of this procedure. If there are no records, insert "Nil" under this heading.

Example

Audit reports

6 Associated Documentation

Include quality system documents closely linked with this document. If there is no associated documentation, insert "Nil" under this heading.

Example

QIS: 10003 – QHPSS Document Management Procedure

QIS: 10001 – QIS Flowchart Manual

Please note: A Macro has been automatically set up in this template. To insert Hyperlinks to other QIS documents, please type QIS and then document number (QIS: 19999), then highlight number only and then select 'Ctrl Q'.

7 References

Reference sources of information for this document according to "Scientific Style and Format: The CBE Manual for Authors, Editors and Publishers.

Example

Cummins P, Perry SV. Troponin I from human skeletal and cardiac muscles. Biochem J 1978;171:251-9.

8 Amendment History

Insert the history of the document:
Issue Number, Date, Name of person/s writing, amending or reviewing document followed by a description of the amendment.

Example

Revision	Date	Author/s	Amendments
0	3 May 1998	Rob Langdon	First Issue
1	4 Jan 1999	Monica McCulloch	Body of text changed to allow a broader application of the document
2	May 1999	Rob Langdon	Annual review – *List Changes.*
QIS² Edition			
Version	**Date**	**Updated By**	**Amendments**
4	Mar 2009	F Stewart	Template Changes made
5	Nov 2009	P Keleti	BDG signed off on renaming Author/s column to Updated By.
6	Aug 2012	H Gregg	New template header and colours applied.
7	September 2012	F Stewart	Heading 3 updated to black
8	October 2013	F Stewart/A Hardmen	1) Replaced the HSSA graphic in the header of the document. with the blank document size has decreased from 712 KB to 52KB which means it will open a lot faster in QIS. 2) Removed all tabs and changed the default tab length from ½ inch (1.27cm) to 1 cm. 3) Changed the Recommended Options found under Tools -> Options -> Compatibility from Microsoft Word 97 to Microsoft 2002
9	Sept 2014	H Gregg	New HSQ graphic in header
10	Nov 2020	F Stewart	Added auto update to document header. When document title is updated the header on each page will update. To apply update, double click on the header.
11.1	September 2021	D Johnston	Updated the Header

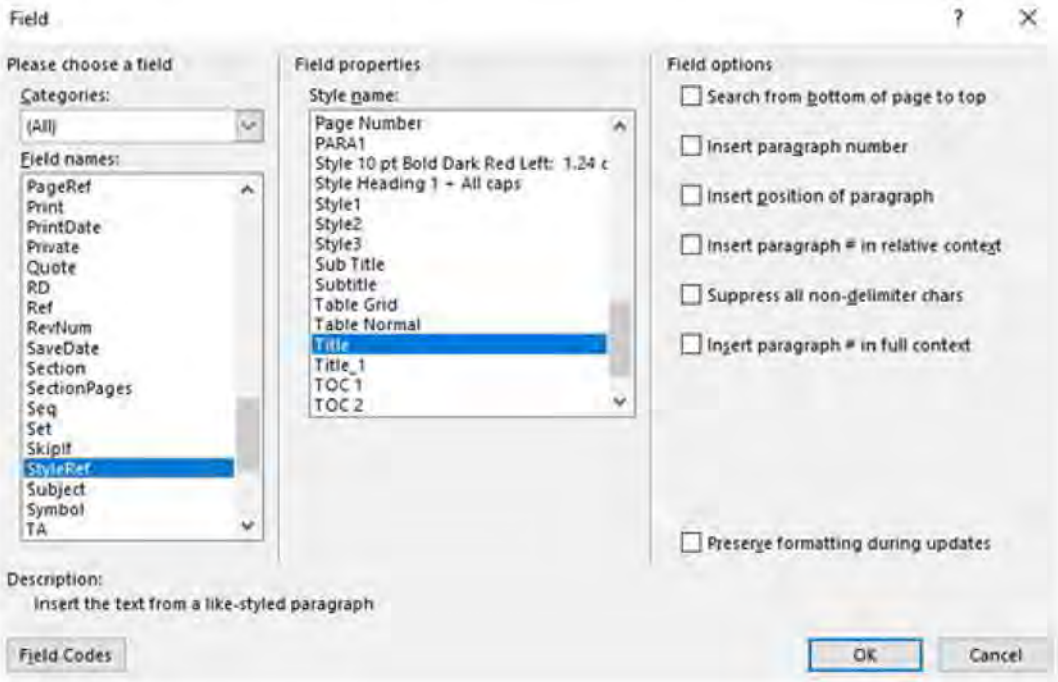
9 Appendices

1 Document Header

9.1 Document Header

Instructions for doing this are

- Highlight the current header wording (FSS Procedure template).
- Click the Insert tab. In the Text group, from the Quick Parts dropdown choose Field.
- Select StyleRef from the Categories list.
- Select Title from the Style Name list
- Untick 'preserve formatting during updates'
- Click OK



- Update Document Title and to apply in document header, double click to open header and the field will update to the new document title.

Queensland Health

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Document Management Procedure

1 Purpose

The control of documentation is an essential part of the Pathology Queensland (PQ), Forensic and Scientific Services (FSS) and Biomedical Technology Services (BTS) quality system and is a requirement of ISO 9001 (clause 7.5), ISO 17025 (clause 8.3) and AS ISO 15189 (clause 4.3) and ISO17034 (clause 8.4). This procedure describes the management of documentation within the Quality Information System (QIS) to ensure only current documentation is in use. Unless made private, all documents on QIS are available for viewing by all staff (see 4.2 below).

2 Scope

This document covers development, control, publication, distribution, review/amendment and archiving of documents on the QIS system. Furthermore, it explains the process for the transfer of participant roles. This procedure will apply to all staff that use QIS2 to control documents.

3 Definitions

Active – The version of a document currently authorised for use.

Approver – The person who has authorised the document for use. This is usually the Director, Chief Scientist, Centre Manager or Supervising Scientist or Team Leader of the laboratory, department or section. The authoriser may also be an acknowledged expert in the field. This person shall be different to the person with update responsibility.

Calibration procedure – A document that is used to describe how a piece of equipment is calibrated or verified. A document must be identified as a calibration procedure on the documents general tab to be able to set up calibration check intervals and tests in the calibration module.

Controlled Document – a document published on QIS. A document needs to be controlled if it is considered that the use of an outdated version will affect the quality of the process. For example, staff contact details may not need to be controlled but a list of test codes would. The decision to control forms in QIS will be at the discretion of the section supervisor and will be based on the criticality of the form and the risk of the incorrect version of the form being used. Forms directly related to casework/testing, that affect test results, or that provide records for traceability must be controlled in QIS (e.g. request forms, report templates, checklists etc).

> *All printed copies are regarded as uncontrolled unless controlled in QIS (see QIS2 User Manual Documents for creation of controlled copies).*

Controlled Copies – A list (usually in QIS) that indicates the physical location of either a printed or electronic copy of the document. Controlled copies (both electronic and printed) require updating to ensure currency.

Distribution – the addition of a user to the QIS Notification List of a document.

Controlled Copy Owner – the person within a site/department/work area with the responsibility for ensuring any hard copies are current

Document Number – this is the unique number issued by QIS2 for each document. It consists of a 5-digit number and is used together with the version number for uniquely identifying a document.

Draft – A document that is still under development, either as a new document or from a previous version of the same. A Draft document is not to be used until it is "published".

Meta Data – information included on the cover sheet of a document which provides a full description of the document.

My QIS2 Events – List on QIS2 that informs a user that an action is required. In the Documents module this may mean that a document requires review, a draft requires approval, an important comment on a document has been submitted, a document has been archived or a new or updated document is on the system.

QIS - Quality Information System

QIS2 - Quality Information System version 2

Resource – A document that can be used for support or help. The document must be division-wide or branch-wide. It includes documents such as templates, QIS2 user manuals and audit checklists. It does not include procedures, methods or work instructions. Documents identified as a resource will have the version number in the footer of a document identified as a T instead of a V.

Reviewer – The person(s) who reviews the document for accuracy and suitability prior to use.

Service – The service that is provided using the document (e.g. Forensic and Scientific Services, Microbiology). Services are useful in Pathology Queensland and Biomedical Technology Services, where many services are provided by one laboratory/work unit (e.g. Mount Isa Laboratory provides blood transfusion, microbiology etc)

Update Responsibility – The person responsible for updating/revising the document – the owner/manager of the document.

Version – a version of a controlled document. The original draft version is designated Version 0.1. Subsequent draft version numbers increment by 0.1. Once published, the original version is designated Version 1, and the version number of each subsequent published version is incremented by 1.

Workplace process – A document used for recording staff training and competencies. Documents must be identified as a workplace process on the documents general tab to be able to 'sign off' an individual as competent against the process in the PD module.

4 Document Control

4.1 Identification

All internal documents will be uniquely identified by a QIS document number and the version number. Numbers are generated once the meta data for the document has been entered onto the system and is automatically added into the footer of the document, providing the 'Force Footer' field on the general tab is selected. If this field is not selected, the document and version number need to be manually added prior to publishing. (see 6.1).

4.2 Access

Access for viewing or printing may be given to all staff or restricted by to a limited number of staff as determined by the approver of the document. Restricted access to documents is via the use of the 'private viewers' functionality in QIS2 (see QIS2 User Manual Documents 26207).

The use of private viewers is not a preferred option because it does not fit with the principles of a state-wide system. Only documents of an extremely sensitive nature should have restricted access (e.g. bioterrorism). Only the Director/Manager of each service has the authority to approve that a document shall be made private. If protection of intellectual property is a concern, a patent should be sought.

5 Developing the document

5.1 Author (often the person with update responsibility)

The Author must:

1 search the QIS database to determine if there are any applicable documents already in existence before proceeding
2 contact the Approver to propose the development of a document

If the Approver agrees to the development (see 5.2):

1 write the document in the appropriate format. (Blank templates, methods and procedures can be found in QIS under the Resources menu tab).
2 publish the document as a draft on QIS and provide the relevant meta data. For initial documents a copy must be emailed to a QIS Document Administrator for publication. (see 6.1).

5.2 Approver

The approver must:

1 if similar documentation exists, decide whether additional documentation is required or whether a review of the existing document should proceed. Consideration should be given to the inclusion of the previous author on the writing team.

2 approve content and decide whether open (all staff) or restricted access is appropriate. If access is to be restricted, private viewers are to be added to the document (see 4.2). Only the Director/Manager of the unit can authorize that the document requires restricted access. This should be indicated by a comment made by them against the draft document

5.3 Reviewer

The role of the reviewer is to review the content of the document for accuracy and suitability. This must occur within a time frame specified by the update responsibility, otherwise QIS records that the document was not reviewed

6 Publication of a document

6.1 Initial document upload to QIS

The initial uploading of a document is performed by the scope QIS2 Document Administrators (see User Manual Documents 26207). Pathology Queensland Document Administrators do not add new documents to QIS. New documents are to be emailed to [redacted] for uploading to QIS, as per QIS 26393.

The QIS Document Administrator is responsible for ensuring that:

- the meta data for the document is completed,
- a QIS number is assigned,
- and the person with update responsibility is notified.

The following meta data options should be ticked when;

- Resource Document: the document is a corporate template or guide
- Workplace Process: the document assesses a competency in a process and is required to be recorded as a competency in QIS
- Calibration Procedure: the document is associated with calibration tests
- Force Footer: the information in the footer is required to be automatically updated from the metadata e.g. page number and pages; document number and version number; valid from date; approver and QH Logo

All documents will be placed on the system in a file format of the application software in which they were created. If a document has been published in pdf, the update responsibility will retain a copy of the formatted Word document.

All documents requiring review must be published in QIS even if they are to be directly accessible through the website. Links may be made via the QIS view-only module to ensure they always remain current. Contact the relevant Web Manager for information on this process.

6.2 Subsequent publications

All subsequent revisions of a document may be performed by the staff member with update responsibility (See 8.1). QIS Document Administrators will help as required.

Active documents may not be altered in any way, except by a document administrator (see section 11). Feedback on documents should be provided by attaching "Comments" to the document on QIS (see QIS2 User Manual Documents for details 26207). These comments can then be considered when documents are reviewed.

Individuals publishing Pathology Queensland documents must ensure all applicable supervisors are included on the notification list. Supervisors are responsible for ensuring all applicable staff in their area are added to the notification list in a timely manner.

6.3 Corporate Documents

Corporate documents must be approved by the appropriate body, e.g. Executive, Pathology Services Advisory Committee (PSAC), Discipline Working Party, BTS Executive, BTS Senior management team (SMT) prior to publication on QIS. See Document Hierarchy. Document Types and Document Authorisation Policy (24756)

6.4 Implementation timeframes

When new or updated documents are published as active, a decision shall be made concerning the criticality of the changes to service delivery (e.g. method change as opposed to editorial change). If deemed critical, a decision shall be made concerning expected implementation timeframes for the document, considering the distribution and whether the document is to be used at a single site or at multiple sites and the nature of the changes made. Sufficient time shall be given to ensure adequate notification and where required updated training before a document is to be implemented.
The implementation timeframe shall be documented in the valid date field of the meta data in QIS.

The 'valid date' field of the general tab currently defaults to the active date. All state-wide documents shall have an implementation time frame of two weeks, thus the valid date shall be two weeks **after** the active date.
Note: For Pathology Queensland documents, the valid date of each document shall be made in consultation with the document authorizer and update responsibility, taking into account the nature of the changes and distribution of the document (refer 23436)

7 Distribution of Documents

Accountability for the distribution of documents in the work area lies with the staff member nominated locally and who appears on the Notification List. The administration of the process may be delegated to another staff member within the work area.

All staff members on the Notification List for a document will receive a QIS Event if a new or revised document has been entered onto the system. Notification lists are usually added by the update responsible officer or Document Administrator, however other staff members can add themselves to the list if they intend to use the document.
Note: Pathology Queensland supervisors and managers must ensure all relevant staff members in their areas are added to the notification list of every document relevant to their role.

On receiving a QIS Event for a new, revised or archived document, the individual is required to:

1 Determine whether the notification is required by the individual (e.g. staff member no longer works in the area, or does not require this information, etc). If not, and notification has not been added as part of a group, and the notification has a status of 'pending', the notification can be deleted.

2 If required, communicate the documents existence, changes or archived status to all staff in the section (unless QIS notifications are used) and record that this has been done.

3 Acknowledge the up-date in the QIS Notification List

If a staff member has a controlled copy of the new, revised or archived document, the individual is required to retrieve, and if necessary, replace any controlled copies with the current version of the document. Controlled copies include both hard and electronic copies.

The QIS2 User Manual Documents (26207) details how to manage notification lists and controlled copies in QIS.

8 Review/Amendments

8.1 Reviewing a document

The recommended review date for all documentation on QIS is 24 months from the Date Issued. Documentation may be reviewed at intervals appropriate to the document. At this time documentation should be reviewed for its current relevance as well as for content. Documents may be reviewed earlier if changes in the context of the document necessitate it. If methods are performed very infrequently, it is suggested that these are archived to avoid the necessity of regular review. Such archived methods must be reviewed before being returned to Active status (see 9).

Document review is the responsibility of the person with update responsibility. This person is the one who will be able to review the document most effectively. However, the writing of the new version may be delegated to another staff member. The person with Update Responsibility will receive notification via the QIS system of any documents due for review. For any given organisational unit or site, the Reports and Documents Modules will indicate all documents due for review during the next month.

Where hard copies of controlled document are available, limited hand-written amendments may be made. The person with update responsibility for the document shall make the changes to all copies of the document and sign and date the changes. All relevant staff shall be informed of the changes and the date implemented; a comment must also be added to QIS. All documents that have manual amendments and or comments must be updated as soon as possible or when the next review falls due.

For Pathology Queensland: Changes to state-wide documents must be authorised by the Chair of the DWP or equivalent. Where documents are distributed to different laboratories, a memo or email detailing the changes shall be sent to the discipline contact and the changes made and authorised by a suitable staff member.

8.2 Review – No change required

When documents are due for their review and no changes are required, the functionality exists in QIS to record that 'no review was required' (see QIS2 User Manual Documents 26207).

8.3 Document revision

1 Revisions to documents need to be made 'off-line' i.e. changes cannot be made directly in QIS. The QIS2 User Manual Documents (26207) provides details of how to review documents in the QIS application. Download the document file, make the necessary amendments and note all changes in the Amendment History.

2 When reviewing a document:

a) Check cross-references to other associated documents, especially corporate policies and procedures. Inserting hyperlinks in documents is available and will

ensure these always "point" to the correct active version. To add a hyperlink in documents, highlight the number and select control Q. Alternatively, talk to a QIS Document Administrator regarding this functionality.

b) Note all changes in the Amendment History. Ensure there is adequate information to clearly identify all changes easily. If there are more changes than are practical to include, note that there has been a complete revision of the document. If the number of entries in the amendment history table is lengthy, the table may be truncated to the last few revisions. The table should refer to the previous versions of the document for the complete amendment history.

c) Note against each comment your response to the comment, the fact that you have considered the comment and have made any changes that may be implied or your reasons for not including the comments implied change at this time

d) Seek comments from the reviewers. These are people who have a vested interest in this document and the list is not limited to the approving officer

e) Seek Approval from the nominated Approver to activate the draft document (Note: review for a document may be sought from several people, however only the Approver's approval is required to publish a document)

f) Publish the document once Approval has been granted.

g) The update responsible person shall ensure that the amendment details are entered into the revision notes of the edit details page.

Note: Once the file has been published on QIS, the file must be deleted from all local computers, or appropriately controlled (see 7).

9 Archiving Documents

The archive option in QIS should be used for documents no longer in use, or for documents used so infrequently as to not require regular review. Reason for archiving the document should be added to the archive notes of the document before archiving (see QIS2 User Manual Documents 26207). Notifiees for the document will be advised through QIS when a document has been archived.

If a revised document has been made active, previous editions of the document will be automatically superseded on the system.

While no changes will be able to be made to archived documents, staff will be able to view them. The QIS number of archived documents will not be used for any future documents. If the process is reintroduced to the work area, the document can be un-archived on the system by the QIS Document Administrators or the individual with update responsibility for the archived document. To ensure suitability of the document, and to allow the notifications to be reset to pending, the document must undergo a full review (ie increment one version number). The Revision notes of the meta data on the General page should state that the document has been reviewed to ensure suitability. Notifications will also need to be re-examined to ensure suitability.

10 Transfer of participant roles

If a staff member with a participant role in a document will be absent for a period of time or has resigned, the 'Transfer Responsibilities' function in the PD module allows the Line Manager to reassign participant roles except document notifications from the current participant to a new staff member. All changes are auditable to prevent misuse.

The QIS2 Admin Team is also able to setup a 'Delegation' from the absent user to another QIS2 User so they can act on the absent users' behalf for a nominated timeframe.

11 Document Administrators

The Document Administrator role is scoped to an organisational unit (OU – e.g. Organic Chemistry) and special privileges only apply within that OU. Document Administrators can add new documents to QIS and can also perform all functions in the documents module (i.e. can take the document through the whole process).

The role of the Document Administrator is

- to assist their Line Manager and others within their organisational unit to manage their document events, and
- to add new documents to QIS for individuals within their OU.

Their responsibilities are

- to comply with the requirements of this document and any other relevant standards, and
- to obtain appropriate authorisation to perform document functions on someone else's behalf.

Note: Pathology Queensland Document Administrators do not add new documents to QIS (see 26393 QIS2 Procedures for Pathology Queensland)

Document Administrators can edit some fields in the metadata without going through another revision cycle. This may be done for minor corrections (e.g. spelling errors), or to add explanatory information (e.g. keywords etc). It is recommended that approval be given by the person with update responsibility, approver, line manager or Quality Manager.

Document Administrators are also able to approve a document on behalf of the nominated approver. This can be done where the approver has requested this to be performed, is on leave, or has limited time or QIS knowledge. It is recommended that direction to perform this task is obtained in writing.

Document Administrators are also able to edit published documents, and re-load the document into QIS without going through the revision process. This can be done for example when a minor error is noted, and none of the notifications have been acknowledged. Changes such as this should be made in consultation with the person with update responsibility, line manager or Quality Manager.

12 Control of External Documents

It is a requirement of ISO 9001, ISO 17025 and AS ISO 15189 that documents of an external origin determined by the organisation to be necessary for the planning and operation of the quality management system are identified and their distribution controlled.

There are various mechanisms for the control of external documents, such as a master list, or registering through your local contact for notification of updated documents via

Standards Watch. It is the responsibility of the individual using the document to ensure that the document represents the current version available before performing any action based on its content.

13 Records

QIS database

14 Associated Documentation

26207 – QIS2 User Manual Documents
24756 –Document Hierarchy. Document Types and Document Authorisation Policy
23436 – Pathology Queensland Quality Manual
26393 – QIS2 Procedures for Pathology Queensland

15 References

Nil

16 Amendment History

Version	Date	Updated by	Amendments
Version 0-14	Various	Various	Various – see previous versions for details
15	Sept 2016	H Gregg	New template. Replaced HSSA with HSQ throughout document. Removed reference to doc 24905 (archived) Added reference to ISO Guide 34 and ISO 17025 to part 1. Amended scope to only apply to HSQ staff using QIS2 for document control Added PQ rules on document notification to 6.2
16	Apr 2019	H Gregg	Updated clauses in section 1 to align with new ISO 17025 and ISO 9001. Added note to section 7 for PQ notifications
17	Jul 2019	H Gregg	Removed reference to ISO 17043 Updated section 6.1 as per comments in V16
18	Apr 2020	H Gregg	Amended definition of controlled copy and section 7.3 to cater for alternate document control lists besides QIS.
19	Sept 2011	H Gregg	Removed reference to HSQ. Added requested statement for PQ regarding manual amendments to documents (section 8.1)

CA-65

HealthSupport Queensland

QUALITY INFORMATION SYSTEM

User Manual

Document Module

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1 Purpose

The purpose of this document is to familiarise users with the Documents module in the Quality Information System (QIS2). This user manual provides step by step instructions and workflow diagrams, to allow for different learning styles.

2 Scope

The scope of this document is to provide a user manual for the Documents module of QIS2. It contains the steps required to perform a specific function (providing you have the scope to perform this function) within the QIS2 application.

3 Definitions

HSQ	Health Support Queensland
QIS2	Quality Information System version 2
OU	Organisational Unit
Participant Role	User name is specified in a particular field for a document
*	Denotes mandatory fields
Resource document	Resource: a document that can be used for support or help. Must be division-wide or branch wide. Includes documents such as templates and QIS2 user manuals. Does not include procedures, methods or work instructions
Workplace Process	A workplace process is a document that describes the requirements that must be met for a staff member to be assessed as competent for a particular skill, method, procedure or role in the workplace.
Calibration Procedure	A document marked as a Calibration procedure defines the scope of 'Calibration Tests' that are performed in the Calibration Module.
Force Footer	This function adds to the footer of Microsoft Word documents, the Page Numbering, Document and Version Number, Valid From and Document Approver based on the Meta-Data of the document. The footer must be in the document for the fields to populate.
DRAFT. Document not yet published.	Initial version published on QIS2 until there is an Active version.
In Review. Document not yet published.	Document submitted to the Reviewers or Approver for review.
DRAFT. Document currently under review.	Active document has been revised
In Review. Document currently under review.	Document submitted to the Reviewers or Approver for review.
Active	Current document in use
Superseded	Previous active version that has been revised
Archived	Document is no longer needed.

4 Document Introduction

The Documents module is used to manage documentation that requires regular review. A document needs to be controlled if it is considered that the use of an outdated version will affect the quality of the process. All controlled internal documents including forms, methods and procedures will be uniquely identified by a QIS2 document number. Numbers are generated once the details for the document have been entered into QIS2. Controlled documents are reviewed at regular intervals. Changes made must be approved by the designated approval officer prior to publishing the updated version on QIS2. All staff impacted by the change must be notified of the new version of the document.

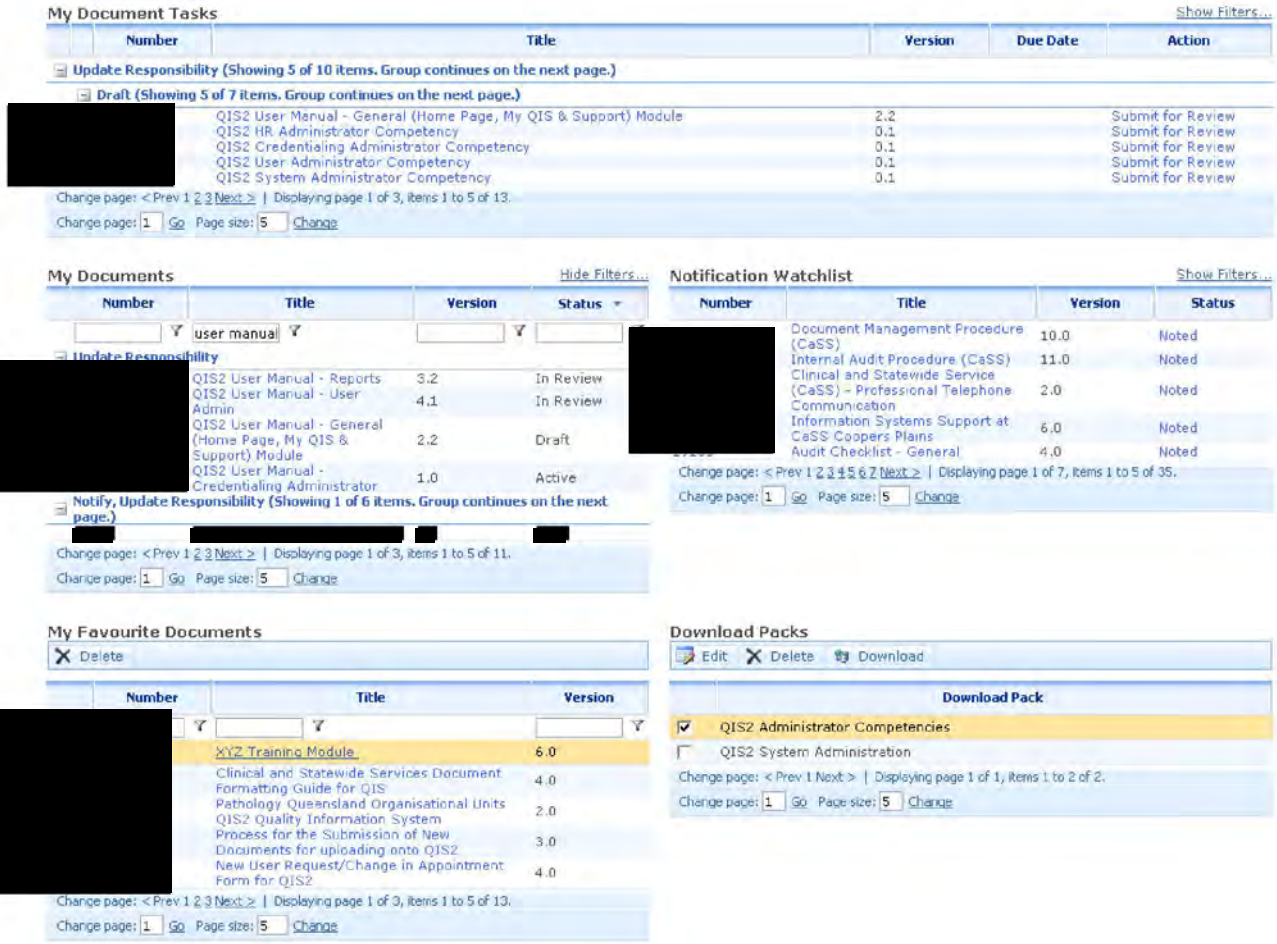
4.1 General Information

Name	Description
QIS2 Home Page	A list of all items that require 'Action' where the user is responsible. Eg: 'Review' document
Documents Homepage	Located by clicking on 'Documents' from the module menu. Module homepages can be customised by using the filters provided in each section. The link to either show or hide the filters is located on the top right hand corner of each section displayed on the module homepage. QIS2 remembers the filters you create on each homepage so each time you log in your customisations will be current. Filters can be changed at any time to reflect your changing needs. Refer to the QIS2 General User Manual for step by step instructions on how to customise your homepage. A list of all items where the user has a participant role.

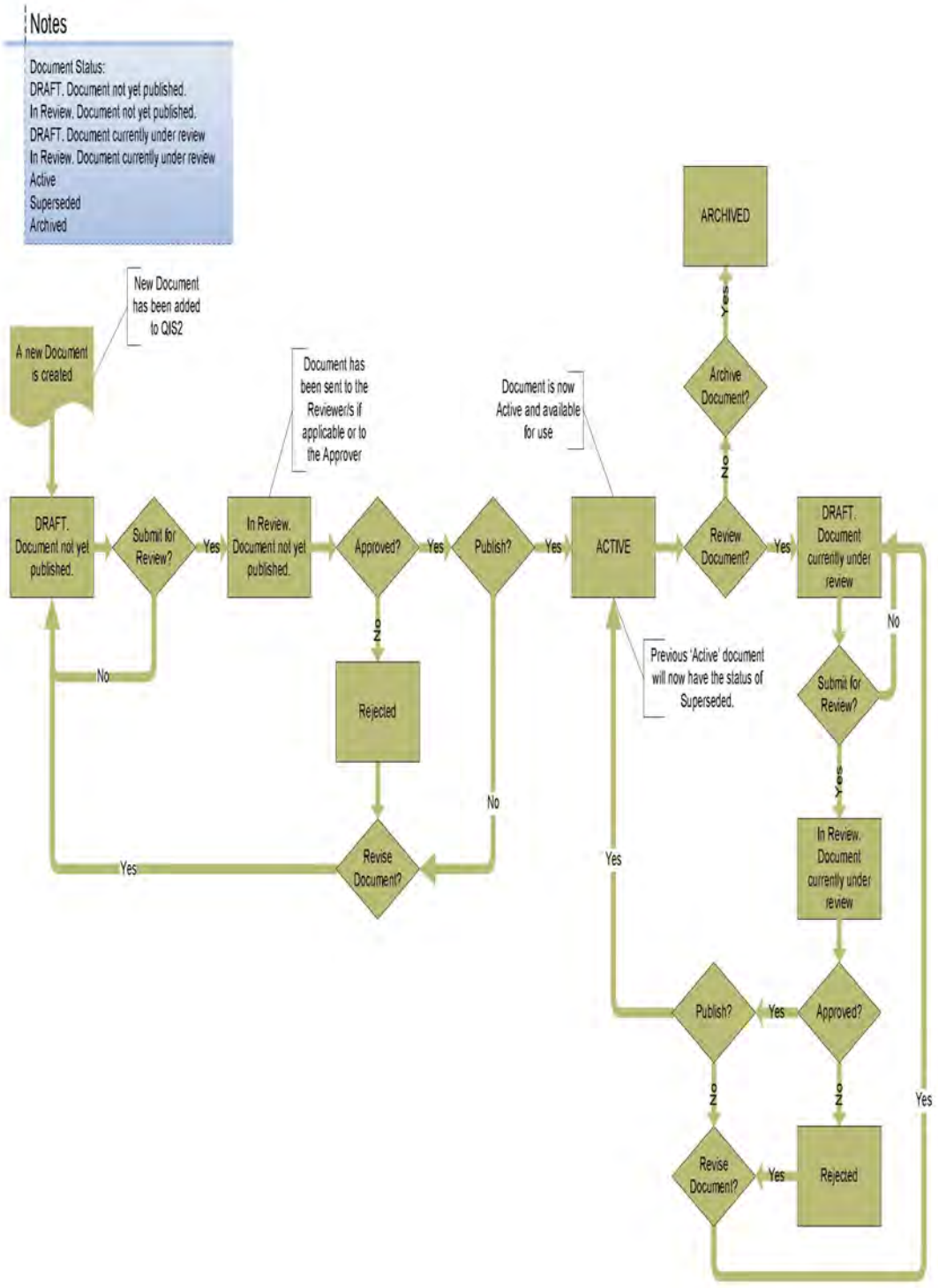
QIS2 Home Page



Document Module Homepage

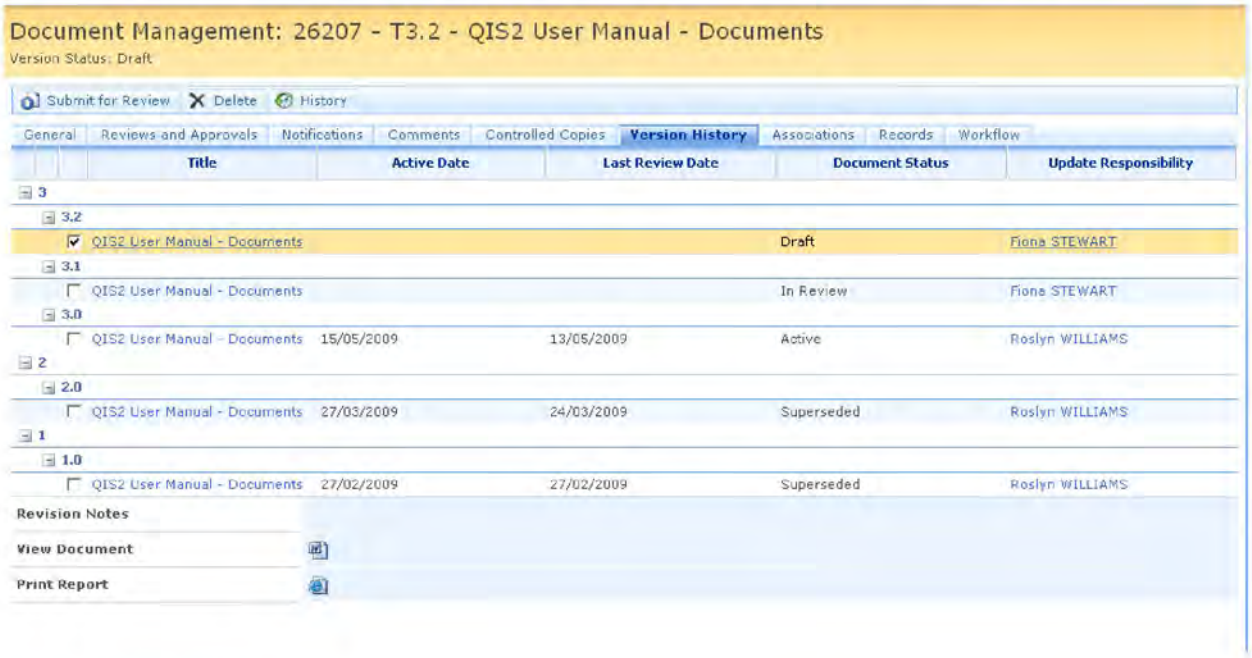


4.2 Document Status Workflow



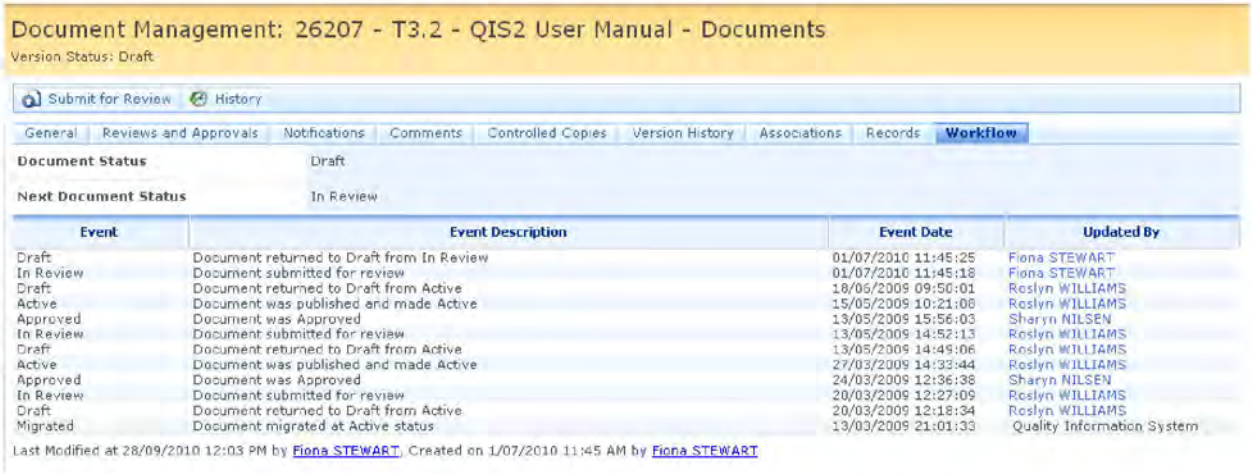
4.3 Version History

The ' Version History ' tab provides an overview of all version instances of a document.



4.4 Workflow Tab

The ' Workflow ' tab provides an overview of the events that have occurred with a document.



4.5 Participant Roles

A person plays a participant role for a document in QIS2 when their name is specified in a particular field for that document. Examples of participant roles are Update Responsibility of a document, Reviewer of a document, Approver of a document, Notifiee of a document and Private Viewer of a document.

When a person has a participant role for a document it usually means that their access to that document is different to that of a standard user with no participant role for that document.

Name	Description
Author	The person who has written the document
Update Responsibility	The person responsible for updating or revising the document
Approver	The person who has authorised the document for use
Reviewer(s)	The person responsible for reviewing the document and advising if changes need to be made prior to the approval process
Private Viewer(s)	A Private Viewer is appointed if there is a security risk if the information is generally available. If a Private Viewer is nominated, only those users nominated can view the Document.
Notifiee/s	A person who should be notified when a change is made to the document.

4.6 Documents Module Matrix

The following matrix describes the functions which can be performed in the Document Module and who is eligible to perform these functions. All roles can perform 'Standard User' functions.

Function	Standard User	Update Responsibility	Document Approver	Document Reviewer	Document Notifiee	Private Viewer	Controlled Copy Owner	Document Administrator
Document Search (No Login)	•							
Document Search (Standard)	•							
Document Search (Advanced)	•							
Add to Favourite Document	•							
Delete Favourite Document	•							
Create a Download Pack	•							
Edit a Download Pack	•							
Add Document to Download Pack	•							
Delete a Download Pack	•							
Delete a Document from a Download Pack	•							
Download your Download Pack	•							
Create New Document								•
Submit Document for Review		•						•
Review Document, No Change (Reviewer)				•				
Review Document, Requires Change (Reviewer)				•				
Review Document, Document Not Reviewed (Reviewer)				•				
Approve a Document			•					•
Reject Approval of a Document			•					•
Revise a DRAFT Document		•						•

Function	Standard User	Update Responsibility	Document Approver	Document Reviewer	Document Notifiee	Private Viewer	Controlled Copy Owner	Document Administrator
Delete DRAFT Document		•						•
Publish a Document		•						•
Edit Document Details		•						•
Active Document – Review, No Change Required		•						•
Active Document – Review		•						•
Add Notification List	•	•						•
Add Self to Notification List	•							
Acknowledge a Notification					•			
Delete User from Notification		•						•
Delete 'User Group' from Notification		•						•
Delete 'OU' from Notification		•						•
Delete Self from Notification List					•			
Add a Comment	•							
Respond to a Comment		•						
Print Controlled Copy Notice	•							
Recall Active/Superseded/Archived Controlled Copy							•	•
Delete Controlled Copies								•
Archive a Document		•						•
Un-archive a Document		•						•
Add an Association		•						•
Edit an Association		•						•
Delete an Association		•						•
Add a Record		•						•
Edit a Record		•						•

Function	Standard User	Update Responsibility	Document Approver	Document Reviewer	Document Notifiee	Private Viewer	Controlled Copy Owner	Document Administrator
Delete a Record		•						•
Notification Search	•							

4.7 Maintenance

4.7.1 Update Responsibility

The Document update responsibility can be changed when the staff member:

- leaves the organisation
- is no longer able / responsible for ensuring the document is updated.

This reassignment can be performed by the Update Responsibility or Document Administrator on a document by document basis. The Line Manager of the employee is able to perform this function via the 'Transfer Responsibilities' tab within the employee's Professional Development module.

4.7.2 Approvers

Reassignment of authorisation: This can be performed at any time the document has the status of 'DRAFT: Document currently under review', the footer of the document will automatically be updated.

This reassignment can be performed by the Update Responsibility or Document Administrator on a document by document basis. The Line Manager of the employee is able to perform this function via the 'Transfer Responsibilities' tab within the employee's Professional Development module. Only appropriate document will be returned in this list.

Approvers cannot be edited at any time the document has the status of Active.

4.7.3 Edit 'General' Details

This detail can be changed when details of the Document have changed when the document has the status of 'Active', 'Active. The document is now overdue for its scheduled review', 'Draft. Document currently under review' 'Draft. Document not yet published.'

The Update Responsibility or Document Administrator is able to perform this function on a document by document basis.

4.7.4 Notifications

Notifications can be deleted:

- If they have not been 'noted' by staff member (status is 'pending')
- When the document has been revised and a new revision is Active

These changes can be performed by the Update Responsibility or Document Administrator on a document by document basis.

4.7.5 DRAFT Approvers and Reviewers

This detail can be changed when the document has the status of 'Draft. Document currently under review' 'Draft. Document not yet published.

The Document Approver and Reviewers can be changed when the staff member:

- leaves the organisation
- is no longer able / responsible for approving or reviewing the document.

These changes can be performed by the Update Responsibility or Document Administrator on a document by document basis, but this should occur only if the activity has not been actioned (response is 'pending').

5 Actions

5.1 Events – For your Information (FYI)

The Document Module Home page displays FYI events along with events that require Actioning.

The events page shows the current status of the Document and if action is required it will be displayed in the Action column.

5.1.1 Document Update Responsibility

This FYI event shows that the document has been 'Revised' from an Active version and is now in DRAFT. This is an FYI event as the Update Responsibility has performed the required action and does not have an action to perform in this participant role in the Document at this point.



5.1.2 Document Approver

This FYI event shows that the document has been 'Submitted for Review' and there are 'Reviewers' that will currently have the action to complete. This is an FYI event as the Approver does not have an action to perform in this participant role in the Document at this point.



5.2 Document Search (No Login)

Only documents with a status of [Active] are returned via the No Login search.

Documents with 'Private Viewers' are displayed with the document and version number and ‹ Private, No View Permission › with no access to view the document.

5.2.1 Access

ALL users	ALL documents where a private viewer has not been nominated

5.2.2 Document Search (Standard) – No Login

From the QIS2 Login Page

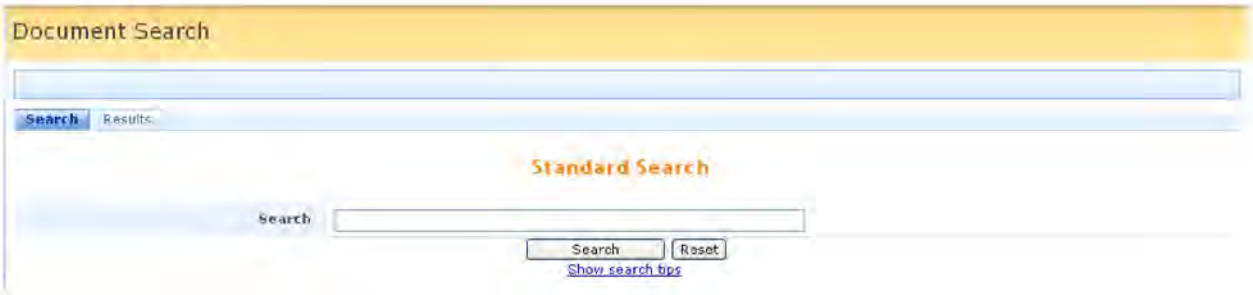
1 Click on the '+' symbol next to the 'Documents' menu

2 Click on 'Search'

3 Enter criteria in the standard search box

4 Click on the 'Search' button underneath or press Enter

For assistance with Standard Search refer to the 'Show search tips' link.



5.2.3 Document Search (Advanced) – No Login

From the QIS2 Login Page

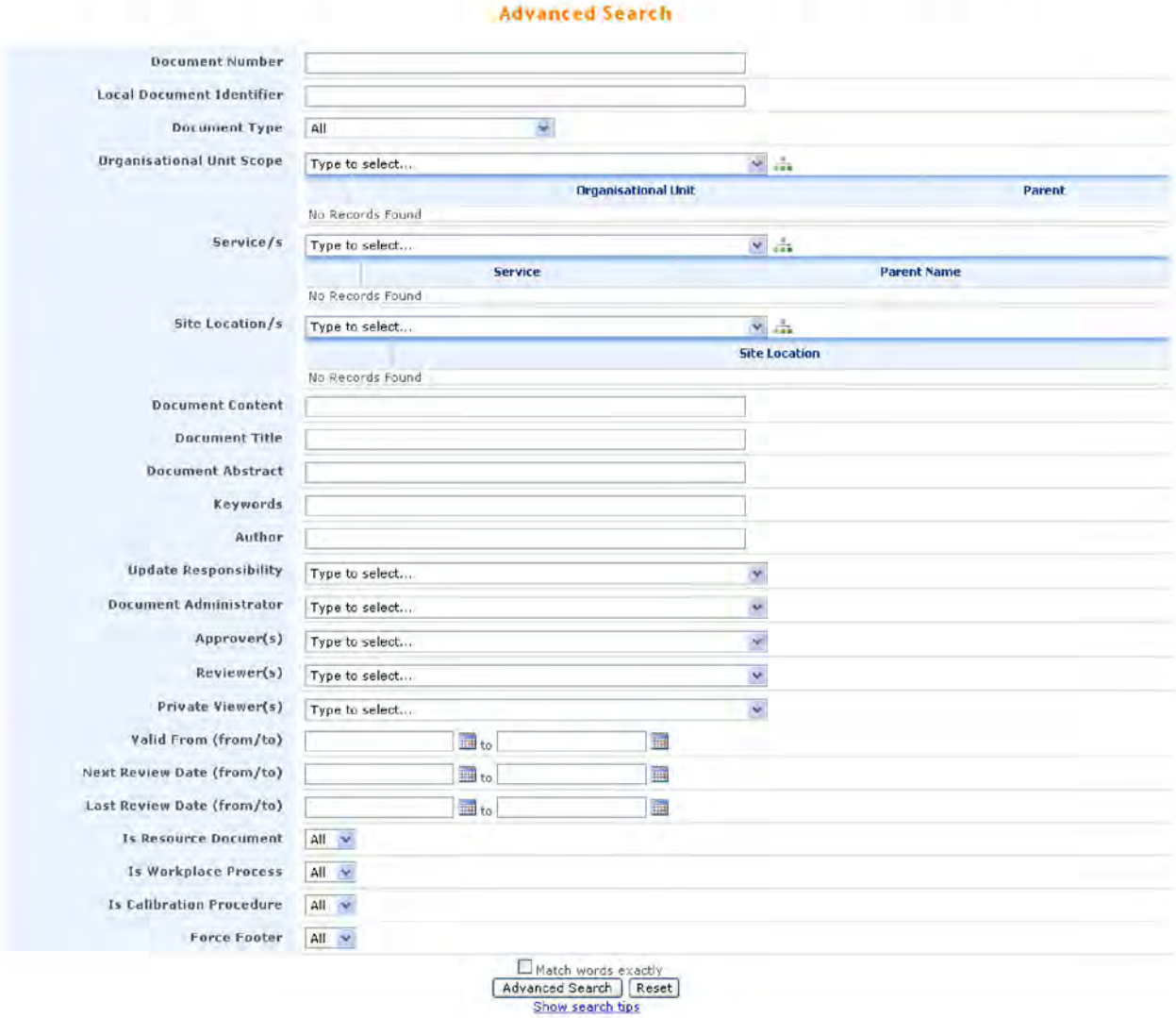
1 Click on the '+' symbol next to the 'Documents' menu

2 Click on 'Search'

3 Enter criteria in the relevant fields under the advanced search

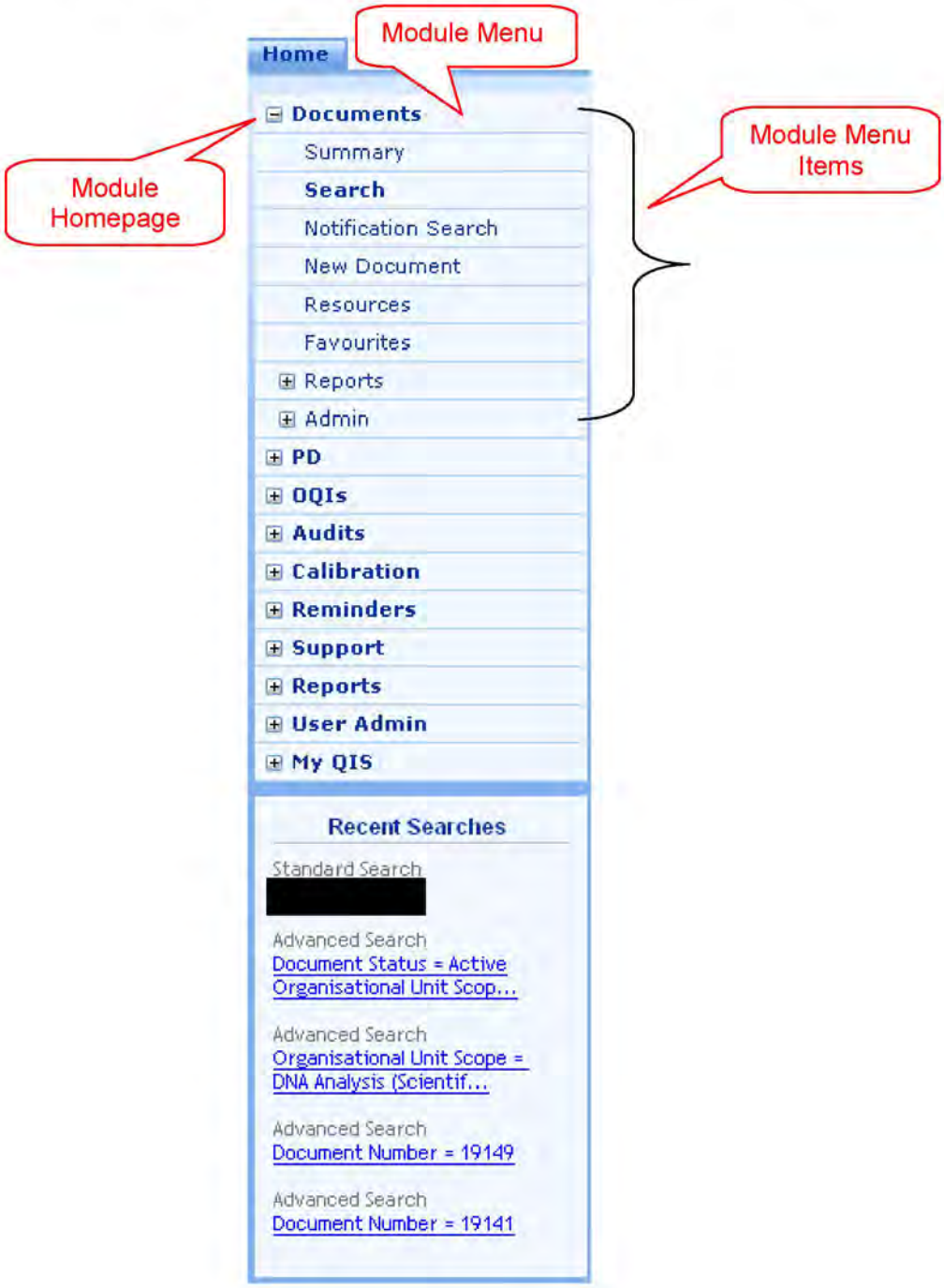
4 Click on the '[Advanced Search]' button at the bottom of the page or press Enter

For assistance with Advanced Search refer to the 'Show search tips' link.



5.3 Document Search

QIS2 keeps a record of the last five searches performed or reports generated. This list appears on the left hand side of the computer screen below the module menu when you click on a search link within any QIS2 module, eg: provides quick access to a record that has been recently searched without the need to re-enter details.



5.3.1 Access

ALL users	ALL documents where a private viewer has not been nominated
Private Viewer	ALL documents including documents where the participant has been nominated as a private viewer

5.3.2 Document Search (Standard)

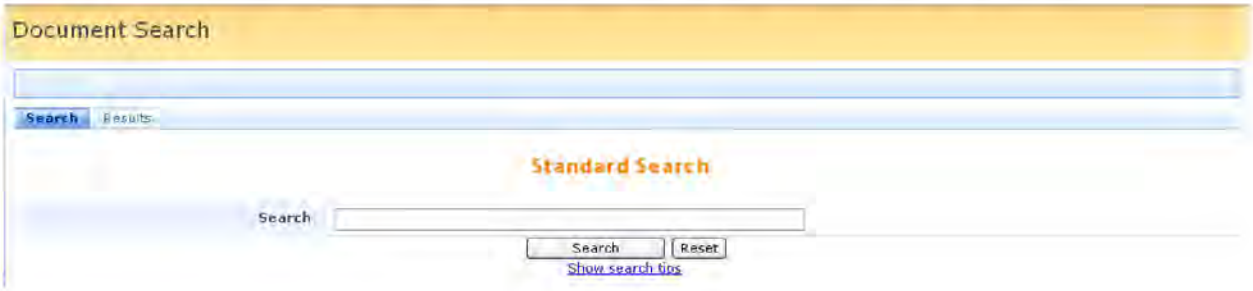
1 Click on the '+' symbol next to the 'Documents' menu

2 Click on 'Search'

3 Enter criteria in the standard search box

4 Click on the '  ' button underneath or press Enter

For assistance with Standard Search refer to the 'Show search tips' link.



5.3.3 Document Search (Advanced)

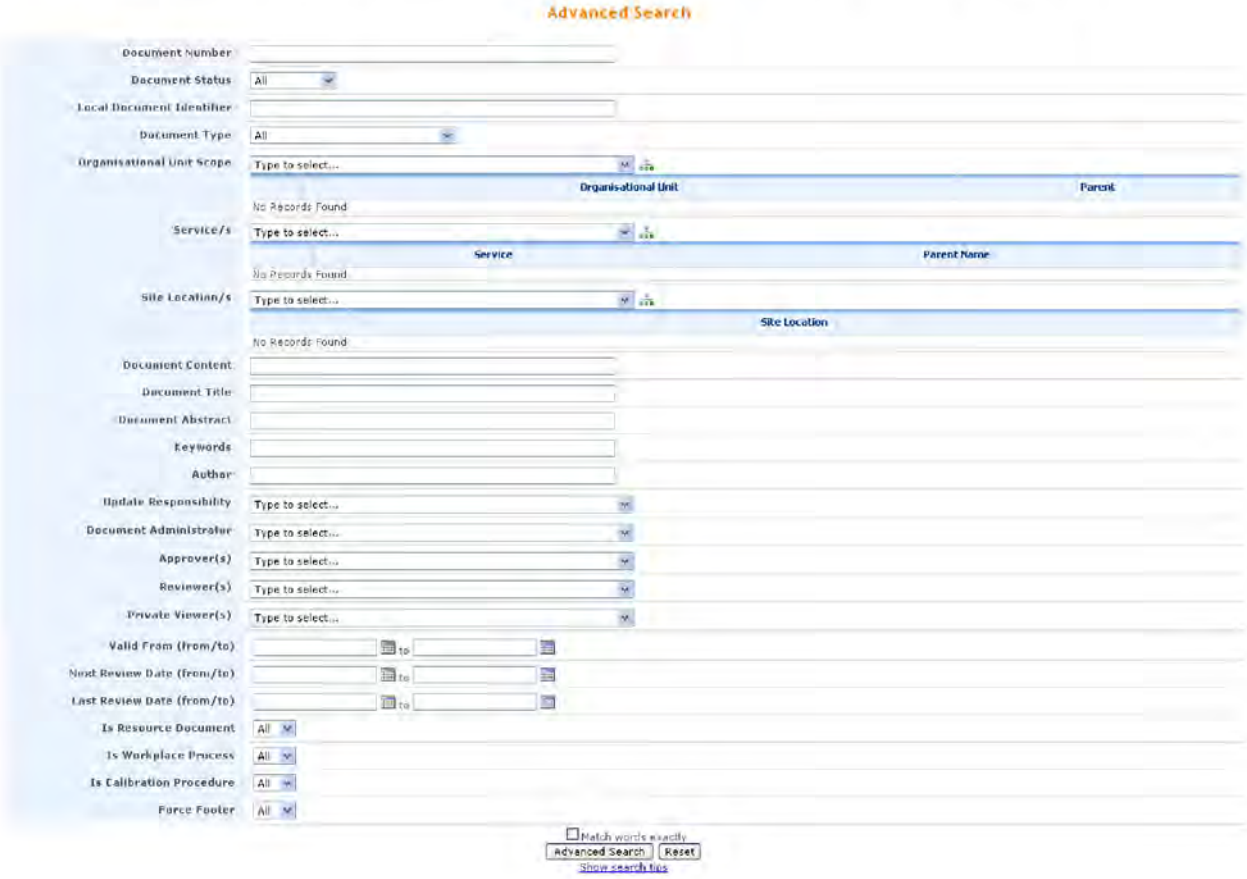
1 Click on the '+' symbol next to the 'Documents' menu

2 Click on 'Search'

3 Enter criteria in the relevant fields under the advanced search

4 Click on the '[Advanced Search]' button at the bottom of the page or press Enter

For assistance with Advanced Search refer to the 'Show search tips' link.



5.4 Add to Favourite Documents

This function is useful if access to the same document/s on a regular basis is required so searching is minimised. The Add Favourite option will not display is the document is already on the favourite list

'My Favourite Documents' via the documents module home page will only display the active version. *Note: Documents that have been archived are still displayed in the 'My Favourite Documents' list and will need to be manually deleted.*



5.4.1 Access

ALL users	ALL documents where a private viewer has not been nominated
Private Viewer	ALL documents including documents where the participant has been nominated as a private viewer

5.4.2 Actions

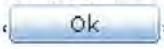
1 Find the Document:
   a Perform 'Standard Search' or 'Advanced Search' **or**
   b From the 'Documents homepage', 'My Documents' **or**
   c From 'QIS2 homepage' under 'My QIS Events'

2 Find and click on the appropriate document

3 Click on the ' 

' action button and Click on the ' 

' action button.

4 From 'Information' – 'The document was successfully added to Favourite Documents' – Click on ' 

'

5.5 Delete Favourite Documents

5.5.1 Access

Users	ALL documents that user has added to their own Favourite document list.

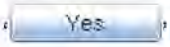
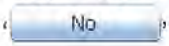
5.5.2 Actions

1 Find the Document:

a From the 'Documents homepage, 'My Favourite Documents'

2 Tick the box next to the appropriate Document

3 Click on the '  ' action button

4 From 'Confirm Delete' – 'Are you sure?' – Click on '  ' to delete or '  ' if changes are not to be saved.

5.6 Create a Download Pack

5.6.1 Access

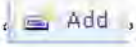
ALL users — ALL users are able to create a 'name' for a download pack

5.6.2 Actions

Option 1

1 Click the '+' symbol next to the 'Documents' menu

2 Click on the 'Favourites' module menu item

3 Click on the ' 

' action button

4 Enter the 'Download Pack' * name

5 Click on the ' 

' action button or Click on the ' 

' action button if changes are not to be saved.

Option 2 – create a download pack including adding a document

1 Find the Document:

a Perform 'Standard Search' or 'Advanced Search' **or**

b From the 'Documents homepage', 'My Documents' **or**

c From 'QIS2 homepage' under 'My QIS Events'

2 Find and click on the appropriate document

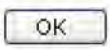
3 Click on the ' 

' action button and Click on the ' 

' action button.

4 From 'Add to Favourite Downloads Pack' – Tick the box next to 'Add to a new Favourite Download Pack'.

5 Enter the 'Download Pack' name

6 Click on the ' 

' button or Click on the ' 

' button if 'Download Pack' is not to be saved.

7 From the 'Add to Favourite Downloads Pack – The document was successfully added! - Click on the ' 

' button

5.7 Edit a Download Pack

5.7.1 Access

ALL Users	ALL download packs that user has added to their own Download Packs list.

5.7.2 Actions

Option 1

1 Click the '+' symbol next to the 'Documents' menu

2 Click on the 'Favourites' module menu item

3 Click on the ' Edit ' action button

4 Update the 'Download Pack' * name

5 Click on the ' Save ' action button or Click on the ' Cancel ' action button if changes are not to be saved.

Option 2

1 Click on the 'Documents' module menu item to display the module Home Page.

2 From 'Download Packs' tick the box next to the appropriate Download Pack

3 Click on the ' Edit ' action button

4 Select the appropriate 'Download Pack' from the ' Download Pack ' drop down list

5 Click on the ' Edit ' action button to update the 'Download Pack' name

6 Click on the ' Save ' action button or Click on the ' Cancel ' action button if changes are not to be saved.

5.8 Add Document to Download Pack

Please note you can only add an 'active' document to a download pack.

Note: when a document is archived it is automatically removed from download pack.

5.8.1 Access

ALL Users	ALL download packs that a user has added to their own Download Packs list.

5.8.2 Actions

1 Find the Document:

a Perform 'Standard Search' or 'Advanced Search' **or**

b From the 'Documents homepage, 'My Documents' **or**

c From 'QIS2 homepage' under 'My QIS Events'

2 Find and click on the appropriate document

3 Click on the '  ' action button and Click on the '  ' action button.

4 Select 'Download Pack' from the drop down list

5 Click on the '  ' button

6 From the 'Add to Favourite Downloads Pack – The document was successfully added! - Click on the '  ' button

5.9 Delete a Download Pack

5.9.1 Access

ALL Users	ALL download packs that user has added to their own Download Packs list.

5.9.2 Actions

Option 1

1 Click the '+' symbol next to the 'Documents' menu

2 Click on the 'Favourites' module menu item

3 Select the appropriate 'Download Pack' from the ' Download Pack ' drop down list

4 Click on the ' Delete ' action button

5 From 'Confirm Delete' – 'Are you sure?' – Click on ' Yes ' to delete or ' No ' if changes are not to be saved.

Option 2

1 Click on the 'Documents' module menu item to display the module Home Page

2 From 'Download Packs' tick the box next to the appropriate Download Pack

3 Click on the ' Delete ' action button

4 From 'Confirm Delete' – 'Are you sure?' – Click on ' Yes ' to delete or ' No ' if changes are not to be saved.

5.10 Delete a Document from a Download Pack

Please note you can only add an 'active' document to a download pack. Archived documents are automatically removed from your download pack without notice.

5.10.1 Access

ALL Users	ALL download packs that user has added to their own Download Packs list.

5.10.2 Actions

Option 1

1 Click the '+' symbol next to the 'Documents' menu

2 Click on the 'Favourites' module menu item

3 Select the appropriate 'Download Pack' from the 'Download Pack' drop down list

4 Tick the box next to the appropriate document

5 Click on the 'Delete Document' action button.

Option2

1 Click on the 'Documents' module menu item to display the module Home Page.

2 From 'Download Packs' tick the box next to the appropriate Download Pack

3 Click on the 'Edit' action button

4 Select the appropriate 'Download Pack' from the 'Download Pack' drop down list

5 Tick the box next to the appropriate document

6 Click on the 'Delete Document' action button

5.11 Download your Download Pack

5.11.1 Access

ALL Users	ALL download packs that user has added to their own Download Packs list.

5.11.2 Actions

1 Find the Download Pack:

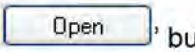
a From the 'Documents homepage, 'Download Packs'

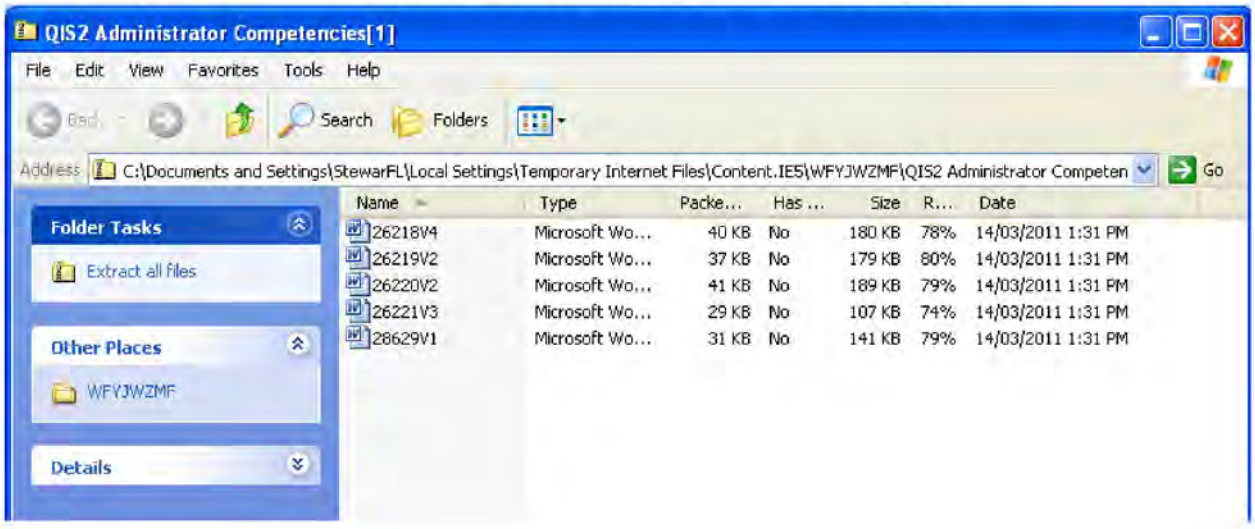
2 Tick the box next to the appropriate Download Pack

3 Click on the '  ' action button

4 From the 'File download – Do you want to open or save this file?



5 Click on the '  ' button and the following folder will be displayed:



OR:

6 Click on the 'Save' button to save the documents and Click on the File Location to save the 'Compressed (zipped) Folder'. E.g: Desktop.

OR:

7 Click on the 'Cancel' button if changes are not to be saved.

5.12 Create New Document

5.12.1 Definitions

Document Type	Description
Checklist	5 - Hierarchy Number: A checklist lays out tasks to be done according to time of day or other factors. Tasks are presented as a list with checkboxes down the side. A tick or check is placed in the box after action item has been completed. Examples of checklists are 'to-do' lists or schedules. Audit checklists are also included in this document type
Duty Statement	4 - Hierarchy Number: Details tasks required to be performed by individuals. May be defined by role or position
Form	5 - Hierarchy Number: Developed where there is a need to record particular information such as: data, information or results captured from performing a procedure or method. These are the documents on which records are made. They provide evidence that a course of action, procedure or policy has been progressed. Forms are commonly a document with blank spaces to be filled in with particulars. See below for other document types that fall into this category.
Framework/ Requirement	1 - Documents the rules governing an organization. The highest document in the hierarchy since other documents eg branch and department/discipline procedures must comply.
Guideline	2 - Hierarchy Number: Guidelines provide extra information regarding the implementation of a policy or procedure They are used to clarify how policies should be implemented. Compliance is not mandatory; they do however reflect best practice principles and therefore should be taken into consideration. Documented at corporate, branch and local levels.
Information Document	5 - Hierarchy Number: Includes information required to perform tasks etc. includes patient collection instructions. Usually separate from a method or procedure but should be referenced as applicable.
Manual	1- Hierarchy Number: Quality Manual and 2 - Hierarchy Number: Laboratory Manual are entered in QIS2 as Document Type Manual. A type of document that describes singularly or by relationship with other documents, the collective requirements of governing or delivering a business service. May be soft or hard manuals; eg CSR manual. May include different document types eg policy, procedures, methods, forms as required.
Organisation Chart	1 - Hierarchy Number: Describe the responsibilities, authorities and relationships of staff.
Policy	1 - Hierarchy Number: Statement of intent. Derived from established requirements or organisational mandate. Describes "what is done". Examples include • CaSS Policy • Branch or Service Policy • Discipline/Team Policy
Register	5 - Hierarchy Number: A Controlled List (data) Examples include: • Table of contents for a Manual • Telephone List

Standard Operating Procedure	3 - Hierarchy Number: Details the purpose and scope of nominated processes and identifies: • who does it • how it is done • when it is done • what resources are used to do it • what records are kept • what reports are required
Template	A Division or Branch-wide QIS document having a preset format, used as a starting point for a particular document or record so that the format does not have to be recreated each time it is used.
Terms of Reference	4 - Hierarchy Number: Description of meetings held, to include purpose, objectives attendees, frequency etc
Test Method	4 - Hierarchy Number: Test methods are the means through which test results are generated from the sample or test submitted to the laboratory. To include media and reagent recipes
Training Protocol	4 - Hierarchy Number: Documents used for training staff to assist in the development of staff skills, job knowledge and competence. Examples include • Training delivery presentation • Training module • Course manual Not to be used for Procedures, training plans or forms used for recording training outcomes
Work Instruction	4 - Hierarchy Number: Instructions for individual jobs: Defines how specific tasks that are referenced in a procedure are carried out.
Worksheet	5 - Hierarchy Number: Manipulates data or performs calculations. Used as an intermediary step between a work procedure and result generation. Not used for data capture: Example include • Excel macro

5.12.2 Access

Document Administrator Has the ability to add new documents based on their scope.

5.12.3 Actions

1 Click the '+' symbol next to the 'Documents' menu

2 Select 'New Document' module menu item

3 Enter 'Local Document Identifier' *if applicable*

4 Enter 'Title' *

5 View 'Version' number

6 View 'Document Status'

7 Enter 'Document' * -> use the 'Browse' function to find and Click on the document

8 Select 'Document Type' * from the drop down box

9 Enter 'Document Abstract' *

10 Enter 'Keywords'

11 Select 'Valid From' *if applicable. Refers to a date when this document, and the information contained within it, becomes applicable to the business.*

12 Enter 'Review Period (In Months) *

13 Select 'Notification Review Period (In Months) *

14 Select 'Organisational Unit Scope' * Start typing details in the selection box and choose appropriate option. *Refers to the scope that the document applies.*

15 Select 'Service Scope' * Start typing details in the selection box and choose appropriate option

16 Select 'Site/Location Scope' * Start typing details in the selection box and choose appropriate option

17 Select 'Author'

18 Select 'Update Responsibility' * Start typing details in the selection box and choose appropriate option

19 View 'Document Administrator'. *This will be auto populated bases on the UR, but can be changed if required.*

20 Select 'Approver' * Start typing details in the selection box and choose appropriate option

21 Select 'Reviewer'(s) (if applicable) Start typing details in the selection box and choose appropriate option. *Reviewers offer comments and feedback on the document before it is approved and published.*

22 Select 'Private Viewer'(s) (if applicable) Start typing details in the selection box and choose appropriate option. *Private Viewers restrict the view of the document to participants only.*

23 Is 'Resource Document', *tick box if a document that can be used for support or help. Must be division-wide or branch wide. Includes documents such as templates and QIS2 user manuals. Does not include procedures, methods or work instructions.*

24 Is 'Workplace Process', *tick box if the document assessors a competency in a process and is required to be recorded as a competency in the PD Module.*

25 Is 'Calibration Procedure', *tick box if the document is required to be associated with calibration tests.*

26 View 'Force Footer'. *This will default to selected, but can be changed if required*

27 Enter 'Revision Notes' *(if applicable)*

28 Click on the '  ' action button or Click on the '  ' action button if changes are not to be saved.

5.13 Submit Document for Review

5.13.1 Access

Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.13.2 Event

- Update Responsibility – Home Page



- Update Responsibility – Documents Module Home Page



5.13.3 Actions

1 Find the Document:

   a Perform 'Standard Search' or 'Advanced Search' **or**

   b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**

   c From 'QIS2 homepage' under 'My QIS Events'

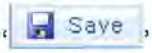
2 Find and click on the appropriate Document

3 Click on the ' 

' action button

4 Select 'Review Due By Date' *. *Defaults to two weeks from the 'submit' date but can be changed if required.*

   Note: If there are reviewers they have until the 'Review Due by Date' has past, at which point the Approver will receive an event to action. The reviewers still has until the Approver actions the event.

5 Click on the ' 

' action button or Click on the ' 

' action button if changes are not to be saved.

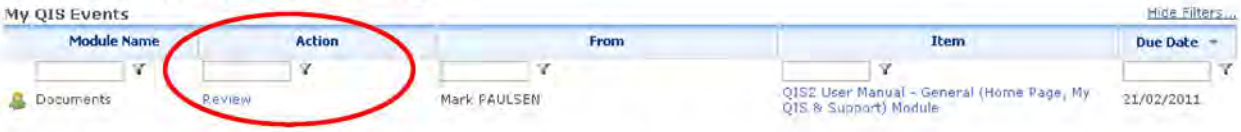
5.14 Review – Accept, No Change Required (Reviewer)

5.14.1 Access

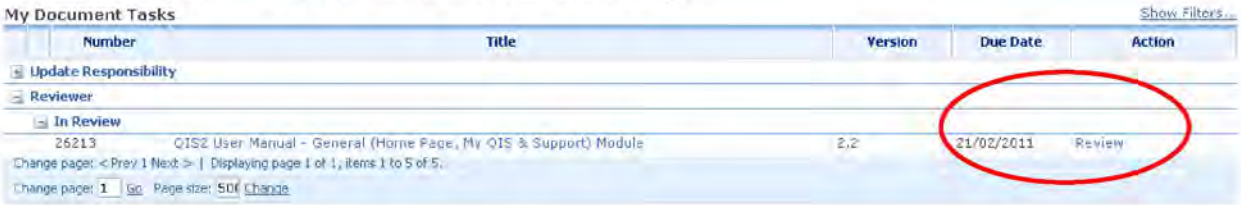
Reviewer	ALL documents where the user has the participant role of Reviewer

5.14.2 Event

- Reviewer – Home Page



- Reviewer – Documents Module Home Page



5.14.3 Actions

1 Find the Document:
   a Perform 'Standard Search' or 'Advanced Search' **or**
   b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c From 'QIS2 homepage' under 'My QIS Events'
2 Find and click on the appropriate Document
3 Click on the ' Accept ' action button
4 Enter 'Comments' *
5 Click on the ' Save ' action button or Click on the ' Cancel ' action button if changes are not to be saved.

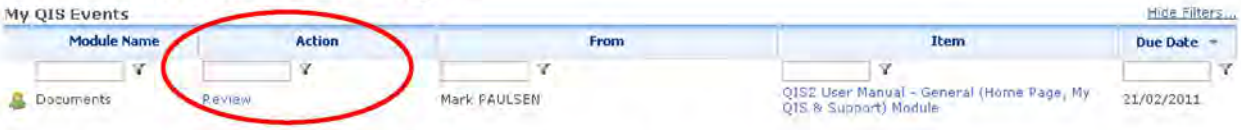
5.15 Review – Requires Changes (Reviewer)

5.15.1 Access

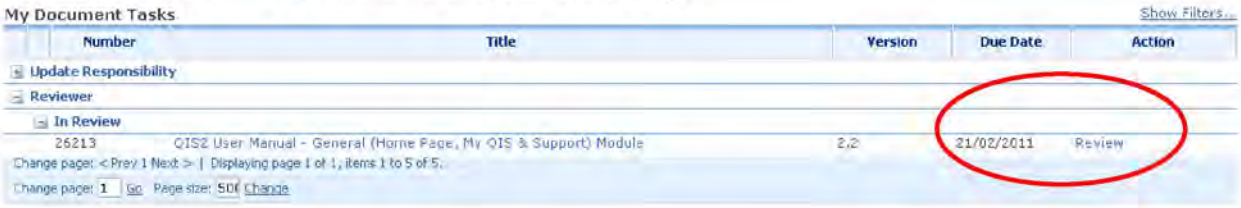
Reviewer	ALL documents where the user has the participant role of Reviewer

5.15.2 Event

- Reviewer – Home Page



- Reviewer – Documents Module Home Page



5.15.3 Actions

1 Find the Document:

   a Perform 'Standard Search' or 'Advanced Search' **or**

   b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**

   c From 'QIS2 homepage' under 'My QIS Events'

2 Find and click on the appropriate Document

3 Click on the ' 

' action button

4 Enter 'Comments' *

5 Click on the ' 

' action button or Click on the ' 

' action button if changes are not to be saved.

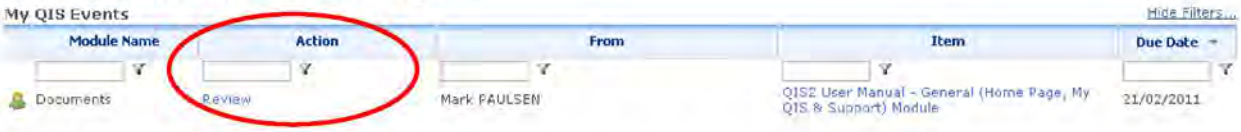
5.16 Review – Not Reviewed (Reviewer)

5.16.1 Access

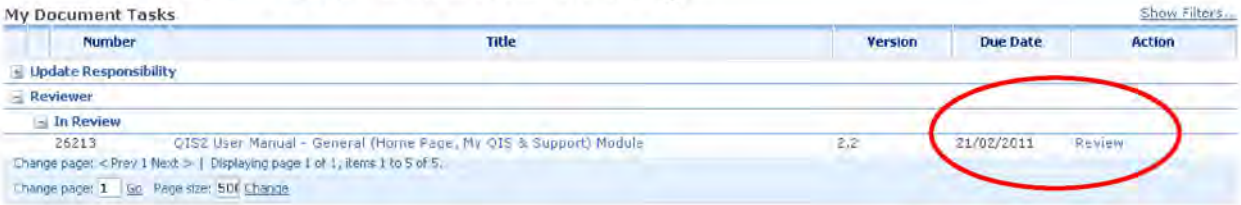
Reviewer	ALL documents where the user has the participant role of Reviewer

5.16.2 Event

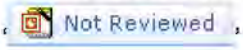
- Reviewer – Home Page



- Reviewer – Documents Module Home Page



5.16.3 Actions

1 Find the Document:
   a Perform 'Standard Search' or 'Advanced Search' **or**
   b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c From 'QIS2 homepage' under 'My QIS Events'
2 Find and click on the appropriate Document
3 Click on the ' 

' action button
4 Enter 'Comments' *
5 Click on the ' 

' action button or Click on the ' 

' action button if changes are not to be saved.

5.17 Approve a Document

When a document is submitted for review and reviewers have been added the 'Approver' does not receive the 'Approve' action until after the review due by date has past. They will however receive an 'FYI' event on the Documents module home page.

5.17.1 Access

Approver	ALL documents where the user has the participant role of Approver
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.17.2 Event

- Approver – Home Page



- Approver – Documents Module Home Page



5.17.3 Actions

1 Find the Document:
   a Perform 'Standard Search' or 'Advanced Search' **or**
   b From the 'Documents' homepage, 'My Document Tasks' **or**
   c From 'QIS2 homepage' under 'My QIS Events'
2 Find and click on the appropriate Document
3 Click on the ' Approve ' action button
4 Enter 'Comments' *
5 Click on the ' Save ' action button or Click on the ' Cancel ' action button if changes are not to be saved.

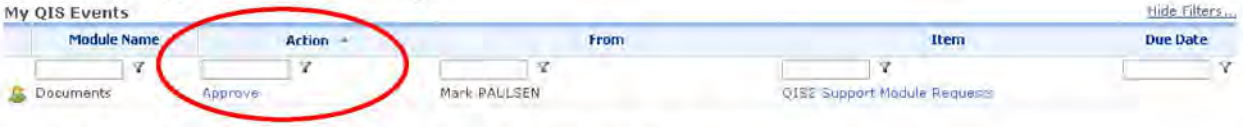
5.18 Reject Approval of a Document

5.18.1 Access

Approver	ALL documents where the user has the participant role of Approver
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.18.2 Event

- Approver – Home Page



- Approver – Documents Module Home Page



5.18.3 Actions

1 Find the Document:
   a Perform 'Standard Search' or 'Advanced Search' **or**
   b From the 'Documents' homepage, 'My Document Tasks' **or**
   c From 'QIS2 homepage' under 'My QIS Events'
2 Find and click on the appropriate Document
3 Click on the ' 

' action button
4 Enter 'Comments' *
5 Click on the ' 

' action button or Click on the ' 

' action button if changes are not to be saved.

5.19 Reviews and Approvals – Print Comments

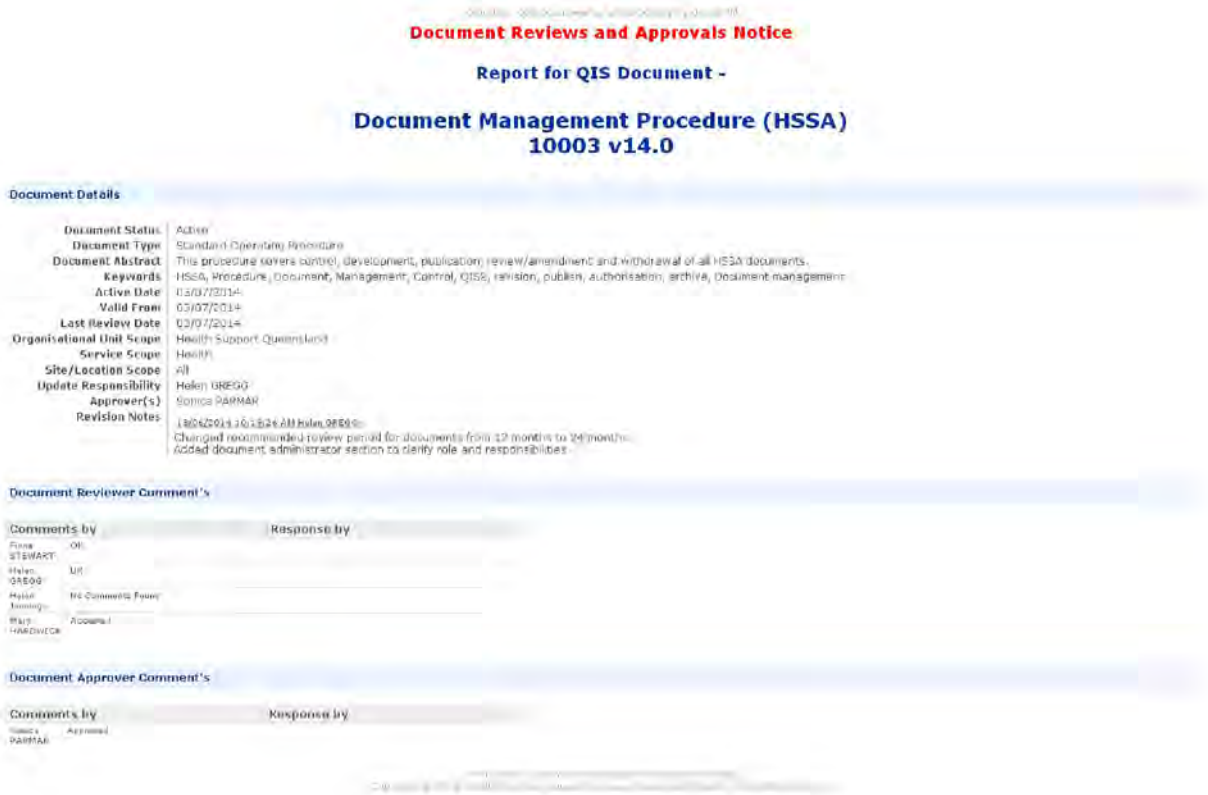
Available from the Reviews and Approvals tab are 'Print Comments' which provides an overview of any comments made by all Reviewers including the Approver comments.

5.19.1 Access

ALL users	ALL documents where a private viewer has not been nominated

5.19.2 Actions

1 Find the Document:
   a Perform 'Standard Search' or 'Advanced Search' **or**
   b From the 'Documents' homepage, 'My Document Tasks' **or**
   c From 'QIS2 homepage' under 'My QIS Events'
2 Find and click on the appropriate Document
3 Click on the 'Reviews and Approvals' tab
4 Click on the 'Print Comments' action button



Document Reviews and Approvals Notice

Report for QIS Document -

Document Management Procedure (HSSA)
10003 v14.0

Document Details

Document Status	Active
Document Type	Standard Operating Procedure
Document Abstract	This procedure covers control, development, publication, review/amendment and withdrawal of all HSSA documents.
Keywords	HSSA, Procedure, Document, Management, Control, QISS, revision, publish, authorisation, archive, Document management
Active Date	03/07/2014
Valid From	03/07/2014
Last Review Date	03/07/2014
Organisational Unit Scope	Health Support Queensland
Service Scope	Health
Site/Location Scope	All
Update Responsibility	Helen GREGG
Approver(s)	Sonica PARMAR
Revision Notes	18/04/2014 10:15:24 AM Helen GREGG: Changed recommended review period for documents from 12 months to 24 months. Added document administrator section to clarify role and responsibilities.

Document Reviewer Comment's

Comments by	Response by
Fiona STEWART: Ok	
Helen GREGG: Ok	
Helen Gregg: No Comments Found	
Mark HARDWICK: Accepted	

Document Approver Comment's

Comments by	Response by
Sonica PARMAR: Approved	

5.20 Revise DRAFT Document

The 'Revise' action will appear for the Update Responsibility when the 'Approver' has rejected the Draft Document.

This function will update the Version number:

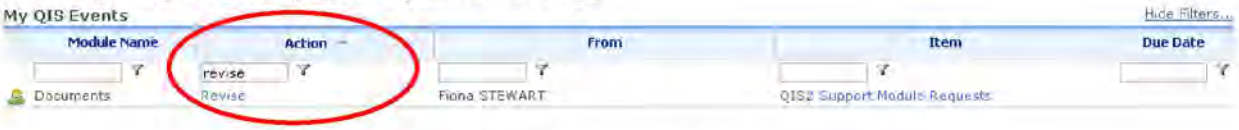
- Draft. Document currently under review or In Review. Document currently under review (2.1) to the next minor version number (2.2).

5.20.1 Access

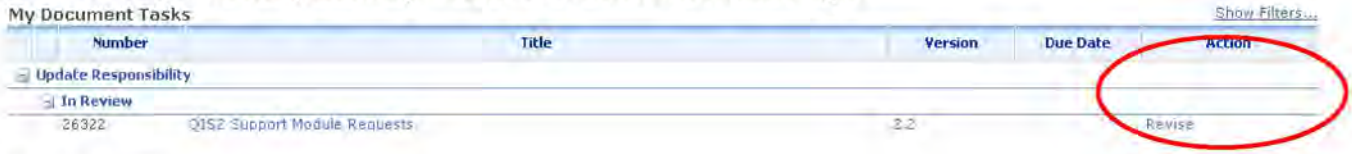
Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.20.2 Event

- Update Responsibility – Home Page



- Update Responsibility – Documents Module Home Page



5.20.3 Actions

Option 1

1 Find the Document:

a From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**

b From 'QIS2 homepage' under 'My QIS Events'

2 Find the appropriate Document

3 Click on the ' Revise ' action from the events page

4 View the 'Approvers' comments

a) Click on the ' Respond ' action button *if applicable*

b) Enter 'Response' *

c) Click on the ' Save ' action button or Click on the ' Cancel ' action button if changes are not to be saved.

5 Click on the ' Revise ' action button

6 From the 'Confirm Revise Document' – Are you sure you wish to revise the Document? – Click on ' Yes ' to revise or ' No ' if changes are not to be saved.

Option 2

1 Find the Document:

a Perform 'Standard Search' or 'Advanced Search'

2 Find and click on the appropriate Document

3 Click on the 'Reviews and Approvals' tab

4 View the 'Approvers' comments

a) Click on the 'Respond' action button *if applicable*

b) Enter 'Response' *

c) Click on the 'Save' action button or Click on the 'Cancel' action button if changes are not to be saved.

5 Click on the 'Revise' action button

6 From the 'Confirm Revise Document' – Are you sure you wish to revise the Document? – Click on 'Yes' to revise or 'No' if changes are not to be saved.

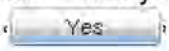
5.21 Delete DRAFT Document

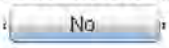
5.21.1 Access

Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.21.2 Actions

1 Find the Document:
   a Perform 'Advanced Search' **or**
   b From the 'Documents' homepage, 'My Document Tasks' **or**
   c From 'QIS2 homepage' under 'My QIS Events'
2 Find and click on the appropriate Document
3 Click on the ' 

' action button
4 From the 'Confirm Delete Document Revision' – Are you sure you want to delete the selected Document Version? – Click on ' 

' to delete or ' 

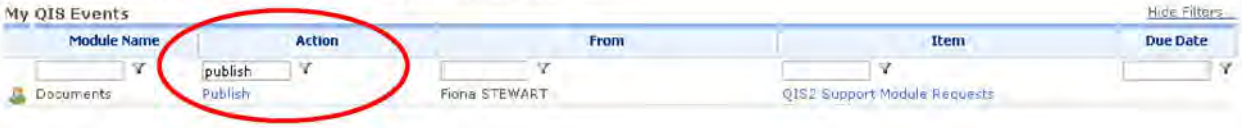
' if changes are not to be saved.

5.22 Publish a Document

Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.22.1 Event

- Update Responsibility – Home Page



- Update Responsibility – Documents Module Home Page



5.22.2 Actions

1 Find the Document:

a Perform 'Standard Search' or 'Advanced Search' **or**

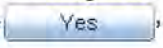
b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**

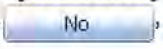
c From 'QIS2 homepage' under 'My QIS Events'

2 Find and click on the appropriate Document

3 Click on the ' 

' action button

4 From the 'Confirm Publishing Document' – Are you sure you wish to publish the Document? – Click on ' 

' to publish or ' 

' if changes are not to be saved.

5.23 Edit Document Details

The 'Edit' action button is available when a document has the status:

- 'Draft. Document currently under review' – all details on the document can be edited
- 'Active' – Approver(s) and Reviewer(s) fields cannot be changed as they are applicable to the current published version.

OU and Service details can be changed by the document administrator, but only to within their 'Scope'. E.g. an FSS document administrator will be unable to update the OU and Service details to a Pathology Queensland as this is out of their scope.

5.23.1 Access

Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.23.2 Actions

1 Find the Document:
   a Perform 'Standard Search' or 'Advanced Search' **or**
   b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c From 'QIS2 homepage' under 'My QIS Events'
2 Find and click on the appropriate Document
3 Click on the ' 

' action button
4 Update details as required
5 Click on the ' 

' action button or Click on the ' 

' action button if changes are not to be saved.

5.24 Active Document – Review, No Changes Required

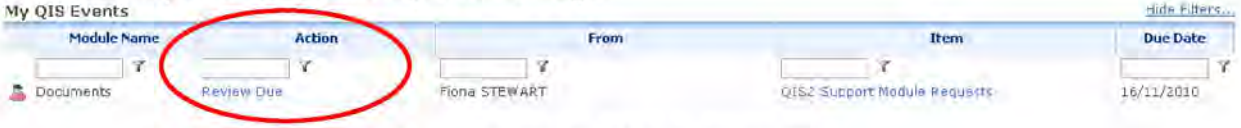
This function will update the 'Last Review Date' to today's date and update the 'Next Review Date'. The formula for the Next Review Date is the Last Review Date + the Review Period (in Months).

5.24.1 Access

Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.24.2 Event

- Update Responsibility – Home Page

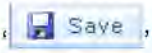


- Update Responsibility – Documents Module Home Page



5.24.3 Actions

1 Find the Document:
   a Perform 'Standard Search' or 'Advanced Search' **or**
   b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c From 'QIS2 homepage' under 'My QIS Events'
2 Find and click on the appropriate Document
3 Click on the '  ' action button

4 Tick 'Reviewed. No Changes Required'
5 View the 'Review Date'
6 Click on the '  ' action button or Click on the '  ' action button if changes are not to be saved.

The following details will be automatically added:

Revision Notes	19/04/2010 10:58:16 AM Fiona STEWART: Reviewed. No Change Required

5.25 Active Document – Review

This function will update the Version number:

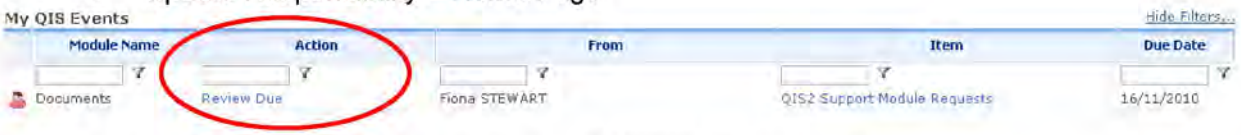
- Active (4.0) document to the next minor version number (4.1)

5.25.1 Access

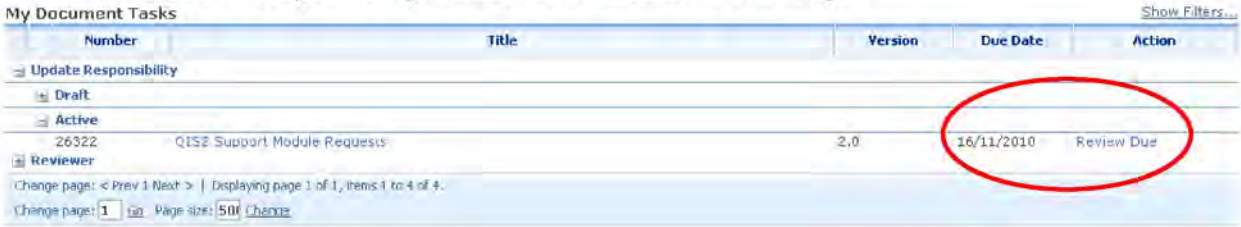
Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.25.2 Event

- Update Responsibility – Home Page



- Update Responsibility – Documents Module Home Page



5.25.3 Actions

Option 1

1 Find the Document:

a Perform 'Standard Search' or 'Advanced Search' **or**

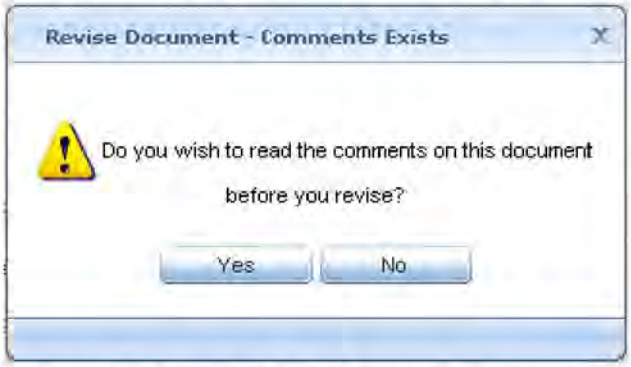
b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**

c From 'QIS2 homepage' under 'My QIS Events'

2 Find and click on the appropriate Document

3 Click on the ' Revise ' action button

a From the 'Revise Document – Comments Exists' – Do you wish to read the comments on this document before you revise? – Click on ' Yes ' to be redirected to the ' Comments ' tab **or**



Note: This action will only occur when comments have been added to a document.

b From the 'Revise Document – Comments Exists' – Do you wish to read the comments on this document before your revise? – Click on ' No '.

4 From the 'Confirm Revise Document' – Are you sure you wish to revise the Document? – Click on ' Yes ' to revise or ' No ' if changes are not to be saved.

Option 2

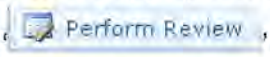
1 Find the Document:

a Perform 'Standard Search' or 'Advanced Search' **or**

b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**

c From 'QIS2 homepage' under 'My QIS Events'

2 Find and click on the appropriate Document

3 Click on the ' 

', action button

Note: 'Perform Review' action button is only available when the 'Notification Review Period (in months)' prior to the 'Next Review Date' is reached.

4 Click on the ' 

', action button or Click on the ' 

', action button if changes are not to be saved.

5.26 Add Notification List

Notification lists can be added on all document status expect Archived and Superseded, but event will only be sent when document is Active.

5.26.1 Access

ALL Users	ALL documents where a private viewer has not been nominated
Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.26.2 Actions

1 Find the Document:

a Perform 'Standard Search' or 'Advanced Search' **or**

b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**

c From 'QIS2 homepage' under 'My QIS Events'

2 Find and click on the appropriate Document

3 Click on the ' Notifications ' tab

4 Click on the ' Add Notifiee ' action button

5 Select 'Document Participant' * Start typing details in the selection box and choose appropriate option. E.g. Notifiee User, Organisational Unit or User Group

Note: wait for document participant to be added to the list before selecting another document participant, screen will refresh.

6 Click on the ' Save ' action button or Click on the ' Cancel ' action button if changes are not to be saved.

5.27 Add Self to Notification List

5.27.1 Access

ALL users	ALL documents where a private viewer has not been nominated

5.27.2 Actions

1. Find the Document:
   a. Perform 'Standard Search' or 'Advanced Search' **or**
   b. From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c. From 'QIS2 homepage' under 'My QIS Events'
2. Find and click on the appropriate Document
3. Click on the 'Notifications' tab
4. Click on the 'Add Myself as Notifiee' action button

5.28 Acknowledge a Notification

The notification list is separated into 3 '**User Membership Type**' and the sections will be displayed in the following order:

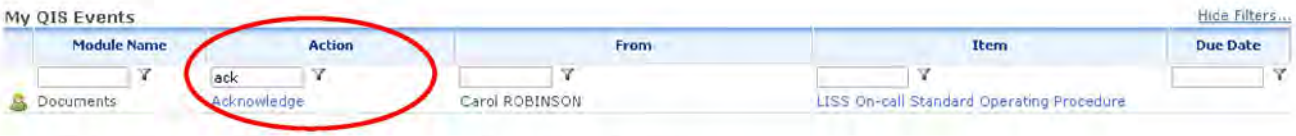
1 Users
2 User Group
3 Organisational Unit

5.28.1 Access

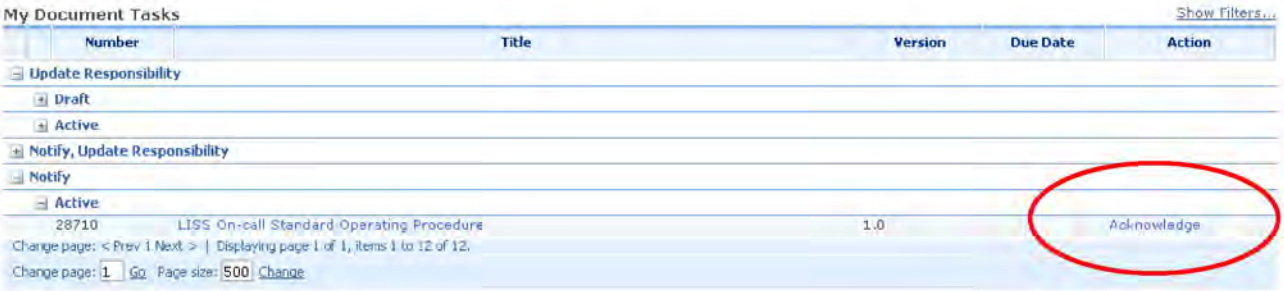
Notifiee	ALL documents where a private viewer has not been nominated and user has been added to a document 'Notification' list.

5.28.2 Events

- Notifiee – Home Page



- Notifiee – Documents Module Home Page



5.28.3 Actions

Option 1

1 Find the Document:

a From the 'Documents' homepage, 'My Document Tasks' **or**

b From 'QIS2 homepage' under 'My QIS Events'

2 Find the appropriate Document

3 Click on the ' Acknowledge ' action

Note: The 'Notifiee's' name will be displayed at the top of the ' User Membership Type ' section. E.g. 'User Group'

4 Find 'your name' and Tick the box next to your name (if not already done). *Note: it is only when 'your name' is selected that the required action button will be available.*

5 Click on the ' Acknowledge Notification ' action button

Option 2

1 Find the Document:

a Perform 'Standard Search' or 'Advanced Search' **or**

2 Find and click on the appropriate Document

3 Click on the ' Notifications ' tab

Note: The 'Notifiee's' name will be displayed at the top of the ' User Membership Type ' section. E.g. 'User Group'

6 Find 'your name' and Tick the box next to your name (if not already done). *Note: it is only when 'your name' is selected that the required action button will be available.*

7 Click on the ' Acknowledge Notification ' action button

5.29 Delete 'User' from Notification List

'User Membership Type' of 'User' can only be deleted from a notification list when participant has a 'Notification Status' of 'Pending'.

5.29.1 Access

Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.29.2 Actions

1. Find the Document:
   a. Perform 'Standard Search' or 'Advanced Search' **or**
   b. From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c. From 'QIS2 homepage' under 'My QIS Events'
2. Find and click on the appropriate Document
3. Click on the 'Notifications' tab
4. Tick the box next to a Notifiee in the user list
5. Click on the 'Delete User' action button
6. From 'Confirm Delete' – 'Are you sure?' – Click on 'Yes' to delete or 'No' if changes are not to be saved.

5.30 Delete 'User Group' from Notification List

' User Membership Type ' of 'User Groups' can only be deleted from a notification list when all participants have a ' Notification Status ' of 'Pending'.

5.30.1 Access

Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.30.2 Actions

7 Find the Document:

- d Perform 'Standard Search' or 'Advanced Search' **or**
- e From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
- f From 'QIS2 homepage' under 'My QIS Events'

8 Find and click on the appropriate Document

9 Click on the ' Notifications ' tab

10 Tick the box next to a Notifiee in the user group

11 Click on the ' ✕ Delete Group ' action button

12 From 'Confirm Delete' – 'Are you sure you want to delete the entire User Group from this Notification List?' – Click on ' Yes ' to delete or ' No ' if changes are not to be saved.

5.31 Delete 'OU' from Notification List

' User Membership Type ' of 'Organisational Units' can only be deleted from a notification list when all participants have a ' Notification Status ' of 'Pending'.

5.31.1 Access

Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.31.2 Actions

1. Find the Document:
   a. Perform 'Standard Search' or 'Advanced Search' **or**
   b. From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c. From 'QIS2 homepage' under 'My QIS Events'
2. Find and click on the appropriate Document
3. Click on the ' Notifications ' tab
4. Tick the box next to a Notifiee in the OU
5. Click on the ' ✕ Delete OU ' action button
6. From 'Confirm Delete' – 'Are you sure you want to delete the entire Organisation Unit from this Notification List?' – Click on ' Yes ' to delete or ' No ' if changes are not to be saved.

5.32 Delete Self from Notification List

The 'Notifiee' is only able to delete their own notification when the ' User Membership Type ' is 'User' and the status is 'Pending'.

5.32.1 Access

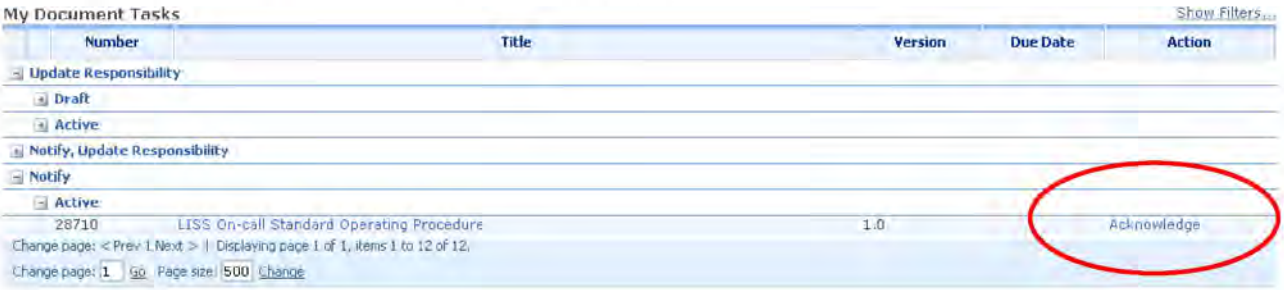
Notifiee	ALL documents where a private viewer has not been nominated and user has been added as a **'User'** to a document 'Notification' list.

5.32.2 Events

- Notifiee – Home Page



- Notifiee – Documents Module Home Page



5.32.3 Actions

Option 1

1 Find the Document:

a From the 'Documents' homepage, 'My Document Tasks' **or**

b From 'QIS2 homepage' under 'My QIS Events'

2 Find the appropriate Document

3 Click on the ' Acknowledge ' action

Note: The 'Notifiee's' name will be displayed at the top of the ' User Membership Type ' section. E.g. 'User'

4 Find 'your name' and Tick the box next to your name (if not already done). *Note: it is only when 'your name' is selected that the required action button will be available.*

5 Click on the ' ✕ Remove Myself as Notifiee ' action button

Option 2

1 Find the Document:

a Perform 'Standard Search' or 'Advanced Search' **or**

2 Find and click on the appropriate Document

3 Click on the 'Notifications' tab

Note: The 'Notifiee's' name will be displayed at the top of the 'User Membership Type' section. E.g. 'User'

4 Find 'your name' and Tick the box next to your name (if not already done). *Note: it is only when 'your name' is selected that the required action button will be available.*

5 Click on the 'Remove Myself as Notifiee' action button

5.33 Add a Comment

5.33.1 Access

ALL users	ALL documents where a private viewer has not been nominated

5.33.2 Actions

1 Find the Document:

a Perform 'Standard Search' or 'Advanced Search' **or**

b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**

c From 'QIS2 homepage' under 'My QIS Events'

2 Find and click on the appropriate Document

3 Click on the ' Comments ' tab

4 Click on the ' Add ' action button

5 Enter 'Comments' *

6 Tick the box next to 'Notify Update Responsibility' *if applicable*

Note: if you are the document update responsibility the above box will not be available and the update responsibility will not receive a notification for the comment.

7 Click on the ' Save ' action button or Click on the ' Cancel ' action button if changes are not to be saved.

5.34 Respond to a Comment

5.34.1 Access

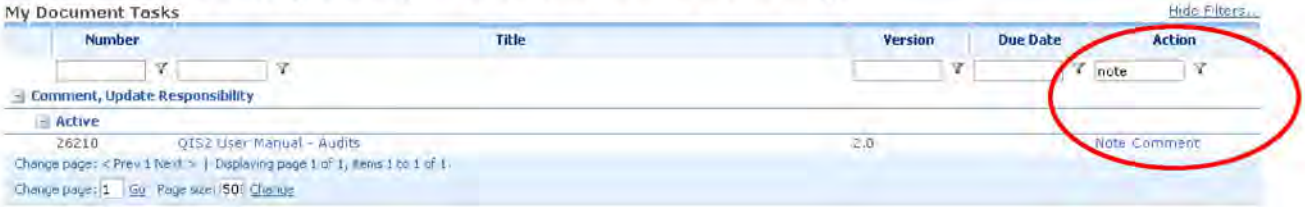
Update Responsibility	ALL documents where the user has the participant role of Update Responsibility

5.34.2 Events

- Update Responsibility – Home Page



- Update Responsibility – Documents Module Home Page



5.34.3 Actions

Option 1

1 Find the Document:

a From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**

b From 'QIS2 homepage' under 'My QIS Events'

2 Find the appropriate Document

3 Click on the ' Note Comment ' action

4 Tick the box next to the 'Pending' comment *if applicable*

5 Click on the ' Respond ' action button

6 Enter 'Response'. The ability to enter a response is only available if the user is the 'Update Responsibility' of the document and the 'Comments By' participant.

7 View 'Comment Noted'. *This will be automatically default ticked.*

8 Click on the ' Save ' action button or Click on the ' Cancel ' action button if changes are not to be saved.

Option 2

1 Find the Document:
   a Perform 'Standard Search' or 'Advanced Search'
2 Find and click on the appropriate Document
3 Click on the 'Comments' tab
4 Tick the box next to the 'Pending' comment *if applicable*
5 Click on the 'Respond' action button
6 Enter 'Response'. The ability to enter a response is only available if the user is the 'Update Responsibility' of the document and the 'Comments By' participant.
7 View 'Comment Noted'. *This will be automatically default ticked.*
8 Click on the 'Save' action button or Click on the 'Cancel' action button if changes are not to be saved.

5.35 Edit Comments

This function is only available if a user has made a comment on a document.

5.35.1 Access

Comments By	ALL documents where the user has added a comment against a document

5.35.2 Actions

Option 1 – Not yet responded to

1 Find the Document:
   a Perform 'Standard Search' or 'Advanced Search' **or**
   b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c From 'QIS2 homepage' under 'My QIS Events'
2 Find and click on the appropriate Document
3 Click on the 'Comments' tab
4 Tick the box next to the appropriate comment *if applicable*
5 Click on the 'Edit' action button
6 Enter 'Comments'.
   Note this new comment will be appended to the previous comment.
7 Click on the 'Save' action button or Click on the 'Cancel' action button if changes are not to be saved.

Option 2 – Response added

1 Find the Document:
   a Perform 'Standard Search' or 'Advanced Search' **or**
   b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c From 'QIS2 homepage' under 'My QIS Events'
2 Find and click on the appropriate Document
3 Click on the 'Comments' tab
4 Tick the box next to the appropriate comment *if applicable*
5 Click on the 'Edit' action button
6 Enter 'Comments'.
   Note this new comment will be appended to the previous comment.
7 Click on the 'Save' action button or Click on the 'Cancel' action button if changes are not to be saved.

5.36 Delete Comment

This function is only available if a user has made a comment on a document and the comment has not received a response.

5.36.1 Access

Comments By	ALL documents where the user has added a comment against a document

5.36.2 Actions

1. Find the Document:
   a. Perform 'Standard Search' or 'Advanced Search' **or**
   b. From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c. From 'QIS2 homepage' under 'My QIS Events'
2. Find and click on the appropriate Document
3. Click on the 'Comments' tab
4. Tick the box next to the appropriate comment *if applicable*
5. Click on the 'Delete' action button
6. From 'Confirm Delete' – 'Are you sure?' – Click on 'Yes' to delete or 'No' if changes are not to be saved.

5.37 Comments – Print Comments

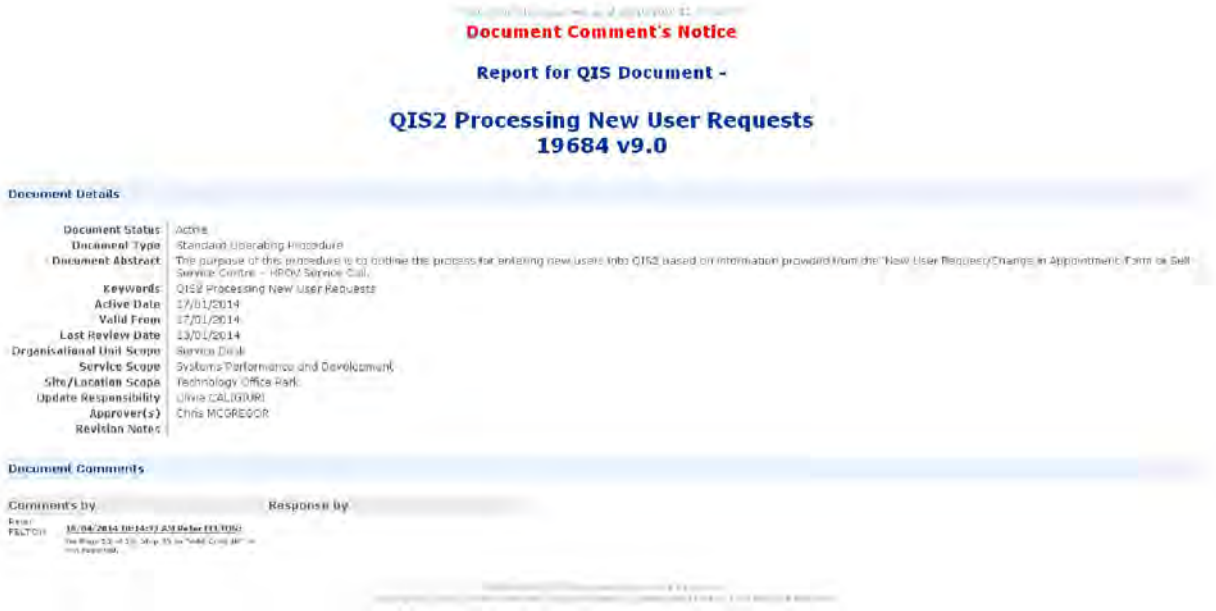
Available from the 'Comments' tab are 'Print Comments' which provides an overview of ALL comments created.

5.37.1 Access

ALL users	ALL documents where a private viewer has not been nominated

5.37.2 Actions

1 Find the Document:
   a Perform 'Standard Search' or 'Advanced Search' **or**
   b From the 'Documents' homepage, 'My Document Tasks' **or**
   c From 'QIS2 homepage' under 'My QIS Events'
2 Find and click on the appropriate Document
3 Click on the 'Comments' tab
4 Click on the 'Print Comments' action button



Document Comment's Notice

Report for QIS Document -

QIS2 Processing New User Requests
19684 v9.0

Document Details

Document Status	Active
Document Type	Standard Operating Procedure
Document Abstract	The purpose of this procedure is to outline the process for entering new users into QIS2 based on information provided from the 'New User Request/Change in Appointment Form or Self Service Centre – HPRM Service Call.
Keywords	QIS2 Processing New User Requests
Active Date	17/01/2014
Valid From	17/01/2014
Last Review Date	13/01/2014
Organisational Unit Scope	Service Desk
Service Scope	Systems Performance and Development
Site/Location Scope	Technology Office Park
Update Responsibility	Olivia CALLIGURI
Approver(s)	Chris MCGREGOR
Revision Notes	

Document Comments

Comment's by	Response by
From: FELTON	18/04/2014 09:14:33 AM Helen FELTON

5.38 Print Controlled Copy Notice

5.38.1 Access

ALL users	ALL documents where a private viewer has not been nominated

5.38.2 Actions

1 Find the Document:
   a Perform 'Standard Search' or 'Advanced Search' **or**
   b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c From 'QIS2 homepage' under 'My QIS Events'
2 Find and click on the appropriate Document
3 Click on the 'Controlled Copies' tab
4 Click on the 'Print Notice' action button
5 From the 'Controlled Document Copy Notice'
   a) Enter 'Physical Location' *
   b) Select 'Organisational Unit' Start typing details in the selection box and choose appropriate option
   c) Select 'Site Location' Start typing details in the selection box and choose appropriate option
   d) Enter 'Number of Printed Copies' *
6 Click on the 'Print' button or Click on the 'Cancel' button if changes are not to be saved.
7 From the 'Print' popup window Click on the 'Print' button or Click on the 'Cancel' button is changes are not to be saved.

Note: The 'Controlled Document Copy Notice' popup window will not automatically close after a print run. Details should be update from the current window if another print run is required. To close the window select the .

Details of the Print notice will be added to the 'Controlled Copies' tab and the 'Who Printed Copies' user will be automatically added to the Document Notification list with the 'Controlled Copy' icon shown against the users name.

This icon can be selected and the user will be taken to the 'Controlled Copies' tab.

5.39 Recall Active Controlled Copies

5.39.1 Access

Controlled Copy Owner	ALL documents where the user has added a controlled copy against a document
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Controlled Copy Owner.

5.39.2 Actions

1 Find the Document:
   a Perform 'Standard Search' or 'Advanced Search' **or**
   b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c From 'QIS2 homepage' under 'My QIS Events'
2 Find and click on the appropriate Document
3 Click on the 'Controlled Copies' tab
4 Tick the box next to the appropriate controlled copy if applicable
5 Click on the 'Recall' action button
6 Enter 'Reason For Recall' *
7 Click on the 'Save' action button or Click on the 'Cancel' action button if changes are not to be saved.

5.40 Recall Superseded/Archived Controlled Copies

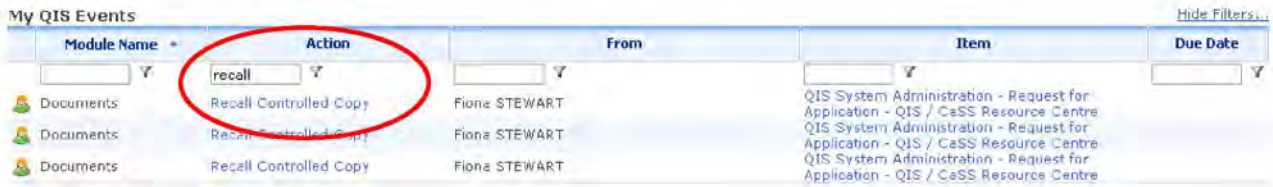
A Controlled Copy Owner will receive an event to 'Recall' for every individual controlled copy record that they have in QIS2.

5.40.1 Access

Controlled Copy Owner	ALL documents where the user has added a controlled copy against a document
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Controlled Copy Owner.

5.40.2 Events

- Controlled Copy Owner – Home Page



- Controlled Copy Owner – Documents Module Home Page



5.40.3 Actions

1 Find the Document:

   a From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**

   b From 'QIS2 homepage' under 'My QIS Events'

2 Find and click on the appropriate Document

3 Click on the ' Recall Controlled Copy ' action

4 Tick the box next to the appropriate controlled copy *if applicable*

5 Click on the ' Recall ' action button

6 Enter 'Reason For Recall' *

7 Click on the ' Save ' action button or Click on the ' Cancel ' action button if changes are not to be saved.

5.41 Delete Controlled Copies

5.41.1 Access

Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Controlled Copy Owner.

5.41.2 Actions

1 Find the Document:

a Perform 'Standard Search' or 'Advanced Search' **or**

2 Find and click on the appropriate Document

3 Click on the 'Controlled Copies' tab

4 Tick the box next to the appropriate controlled copy *if applicable*

5 Click on the 'Delete' action button

6 From 'Confirm Delete' – 'Are you sure?' – Click on 'Yes' to delete or 'No' if changes are not to be saved.

5.42 Archive a Document

Only 'Active' documents when a minor version has not been incremented are able to be archived.

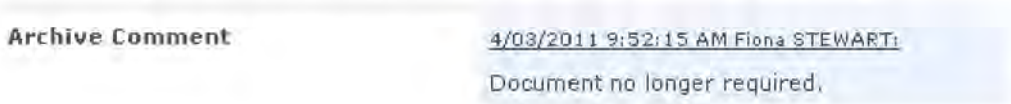
5.42.1 Access

Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.42.2 Actions

1. Find the Document:
   a. Perform 'Standard Search' or 'Advanced Search' **or**
   b. From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c. From 'QIS2 homepage' under 'My QIS Events'
2. Find and click on the appropriate Document
3. Click on the ' Archive ' action button.
4. Enter 'Archive Comments'*
5. Click on the ' Save ' action button or Click on the ' Cancel ' action button if changes are not to be saved.

The following details will be automatically added to the Meta-Data page:



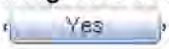
5.43 Un-archive a Document

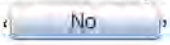
5.43.1 Access

Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.43.2 Actions

1 Find the Document:
   a Perform 'Standard Search' or 'Advanced Search' **or**
   b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c From 'QIS2 homepage' under 'My QIS Events'
2 Find and click on the appropriate Document
3 Click on the ' 

' action button.
4 From 'Confirm Unarchiving of Document' – 'Are you sure you wish to unarchive the document?' – Click on ' 

' or ' 

' if changes are not to be saved.

5.44 Add an Association

5.44.1 Access

Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.44.2 Actions

1 Find the Document:
   a Perform 'Standard Search' or 'Advanced Search' **or**
   b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c From 'QIS2 homepage' under 'My QIS Events'
2 Find and click on the appropriate Document
3 Click on the 'Associations' tab
4 Click on the 'Add' action button
5 Select 'Module' * from the drop down box
6 Select 'QIS Record' * (Validate or Search)
7 Enter 'Association Description' *
8 Click on the 'Save' action button or Click on the 'Cancel' action button if changes are not to be saved.

5.45 Edit an Association

5.45.1 Access

Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.45.2 Actions

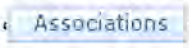
1. Find the Document:
   a. Perform 'Standard Search' or 'Advanced Search' **or**
   b. From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c. From 'QIS2 homepage' under 'My QIS Events'
2. Find and click on the appropriate Document
3. Click on the 'Associations' tab
4. Tick the box next to the appropriate Association
5. Click on the 'Edit' action button
6. Update details as required
7. Click on the 'Save' action button or Click on the 'Cancel' action button if changes are not to be saved.

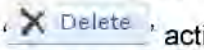
5.46 Delete an Association

5.46.1 Access

Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.46.2 Actions

1. Find the Document:
   - a Perform 'Standard Search' or 'Advanced Search' **or**
   - b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   - c From 'QIS2 homepage' under 'My QIS Events'
2. Find and click on the appropriate Document
3. Click on the '  ' tab

4. Tick the box next to the appropriate Association
5. Click on the '  ' action button

6. 'Are you sure?' – Click on 'Yes'

5.47 Add a Record

5.47.1 Definitions

Record Storage Type	Description
CD/DVD	Compact Disk or Digital Video Disk (DVD)
Compactor	File storage type
Digital Data Store (DDS)	File storage type
Filing Cabinet	File storage type
Folder	File storage type
Internet	a global network of interconnected computers, enabling users to share information along multiple channels
Library	a collection of information, sources, resources, books, and services
Local PC-Hard Drive	Personal computer
Logbooks	File storage type
Network Directory	Within your network folders
Not Applicable	Does not apply
Off-site	File storage type
QH Recfind	Queensland Health Recfind system
Removable Disk (USB etc.)	Removal disk or Universal Serial Bus (USB)
Storeroom	File storage type

5.47.2 Access

Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.47.3 Actions

1 Find the Document:
   a Perform 'Standard Search' or 'Advanced Search' **or**
   b From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c From 'QIS2 homepage' under 'My QIS Events'
2 Find and click on the appropriate Document
3 Click on the '  ' tab
4 Click on the '  ' action button
5 Enter 'Record Name' *
6 Enter 'Record Description' *
7 Select 'Storage Type' * from the drop down box
8 Enter 'Location' *
9 Click on the '  ' action button or Click on the '  ' action button if changes are not to be saved.

5.48 Edit a Record

5.48.1 Access

Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.48.2 Actions

1. Find the Document:
   a. Perform 'Standard Search' or 'Advanced Search' **or**
   b. From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c. From 'QIS2 homepage' under 'My QIS Events'
2. Find and click on the appropriate Document
3. Click on the 'Records' tab
4. Tick the box next to the appropriate Record
5. Click on the 'Edit' action button
6. Update details as required
7. Click on the 'Save' action button or Click on the 'Cancel' action button if changes are not to be saved.

5.49 Delete a Record

5.49.1 Access

Update Responsibility	ALL documents where the user has the participant role of Update Responsibility
Document Administrator	ALL documents where the Document Administrator is scoped to the same OU or above as the Update Responsibility

5.49.2 Actions

1. Find the Document:
   a. Perform 'Standard Search' or 'Advanced Search' **or**
   b. From the 'Documents' homepage, 'My Document Tasks' or 'My Documents' **or**
   c. From 'QIS2 homepage' under 'My QIS Events'
2. Find and click on the appropriate Document
3. Click on the 'Records' tab
4. Tick the box next to the appropriate Record
5. Click on the 'Delete' action button
6. 'Are you sure?' – Click on 'Yes'

5.50 Notification Search

The notification search is a person search, which will provide the documents that a person has been notified about.

5.50.1 Access

ALL users	ALL documents where a private viewer has not been nominated
Private Viewer	ALL documents including documents where the participant has been nominated as a private viewer

5.50.2 Notification Search (Standard)

1 Click on the '+' symbol next to the 'Documents' menu

2 Click on 'Notification Search'

3 Enter criteria in the standard search box. *E.g. persons name – Fiona*

4 Click on the '[Search]' button underneath or press Enter

For assistance with Standard Search refer to the 'Show search tips' link.



5.50.3 Notification Search (Advanced)

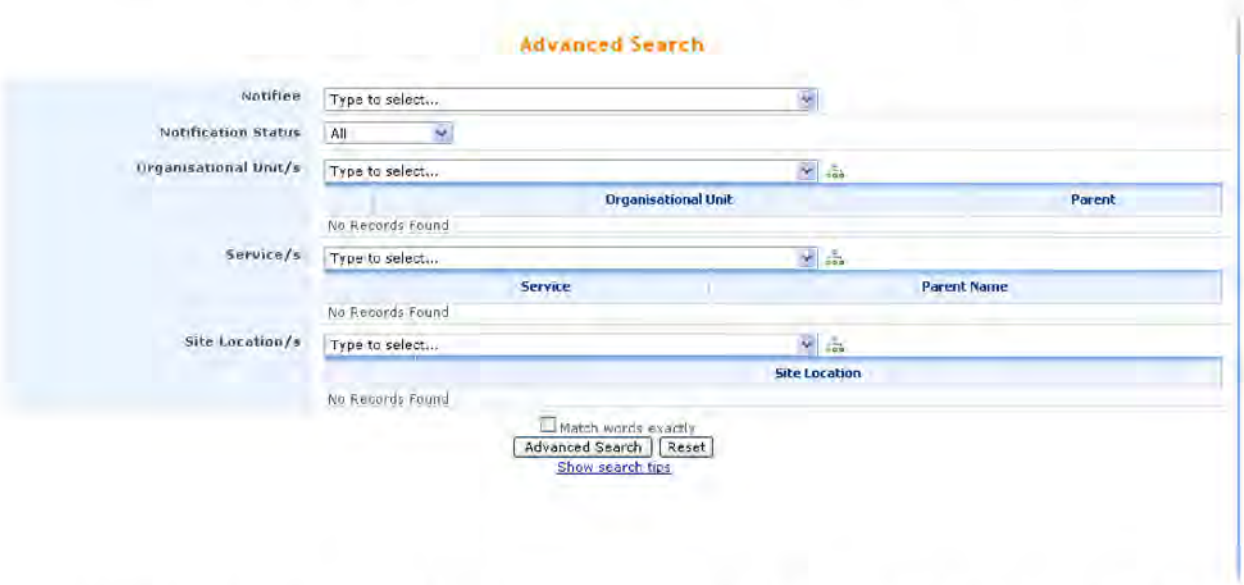
1 Click on the '+' symbol next to the 'Documents' menu

2 Click on 'Notification Search'

3 Enter criteria in the relevant fields under the advanced search

4 Click on the 'Advanced Search' button at the bottom of the page or press Enter

For assistance with Advanced Search refer to the 'Show search tips' link.



- 'Notified' = documents are returned only where the person is a notifiee (they may have acknowledged and therefore would appear in the acknowledged list)
- 'Acknowledged' documents are returned only where the person is a notifiee and has acknowledged the notification.
- 'All' = no status filter is applied

5.51 Resources

Resource: a document that can be used for support or help. Must be division-wide or branch wide. Includes documents such as templates and QIS2 user manuals. Does not include procedures, methods or work instructions.

5.51.1 Access

ALL users	ALL documents where a private viewer has not been nominated



5.52 Document Activity

1 Click on the '+' symbol next to the 'Documents' menu
2 Click on 'Reports'
3 Click on 'Document Activity'
4 Enter criteria in the search fields
5 Click on the 'Report' button underneath or press Enter

For details information on report criteria and results please see 26214 QIS2 User Manual – Report Module.

5.53 Notification Activity

1 Click on the '+' symbol next to the 'Documents' menu
2 Click on 'Reports'
3 Click on 'Notification Activity'
4 Enter criteria in the search fields
5 Click on the 'Report' button underneath or press Enter

The current overdue notifications will be displayed as of today.

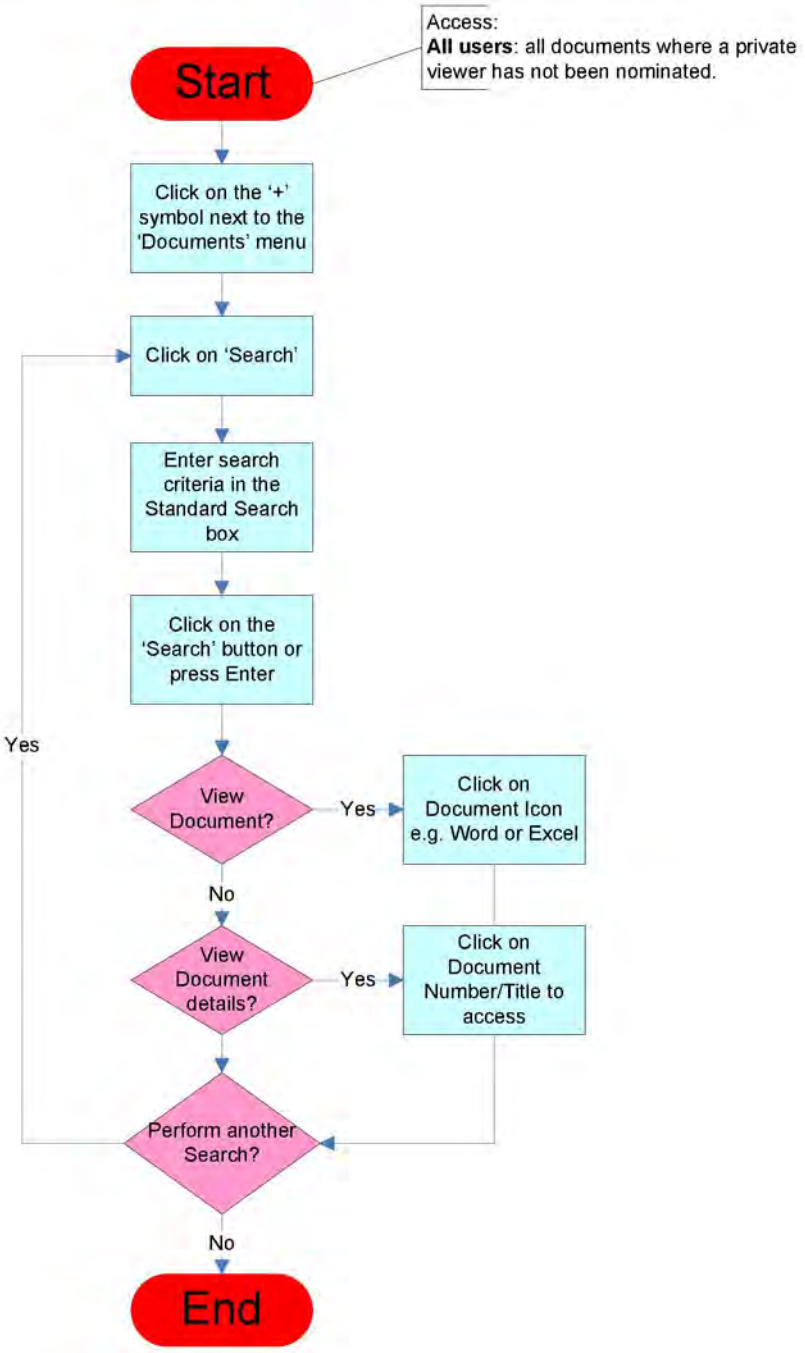
For details information on report criteria and results please see 26214 QIS2 User Manual – Report Module.

6 Workflows

6.1 Document Search Standard

Notes

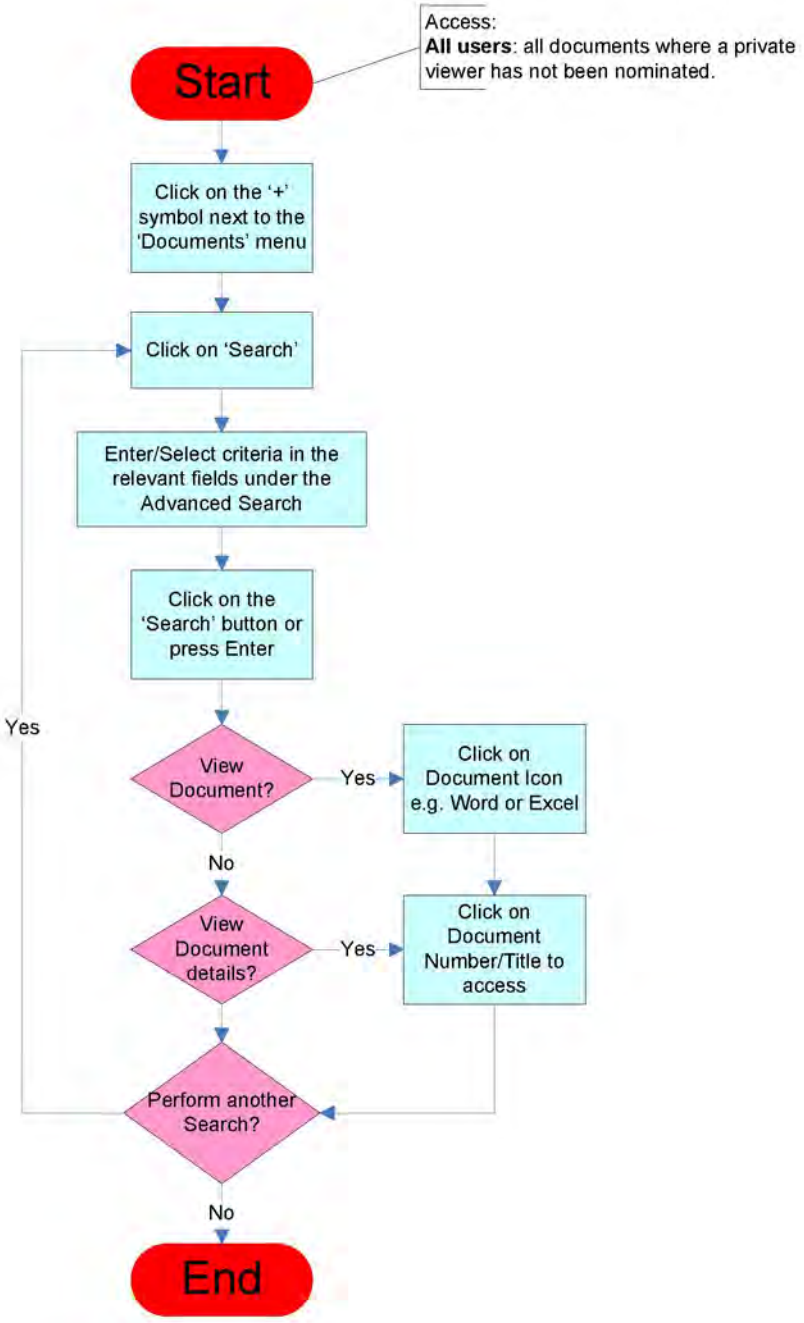
The Standard Search will search for the occurrence of the search criteria within Document meta-data and The document



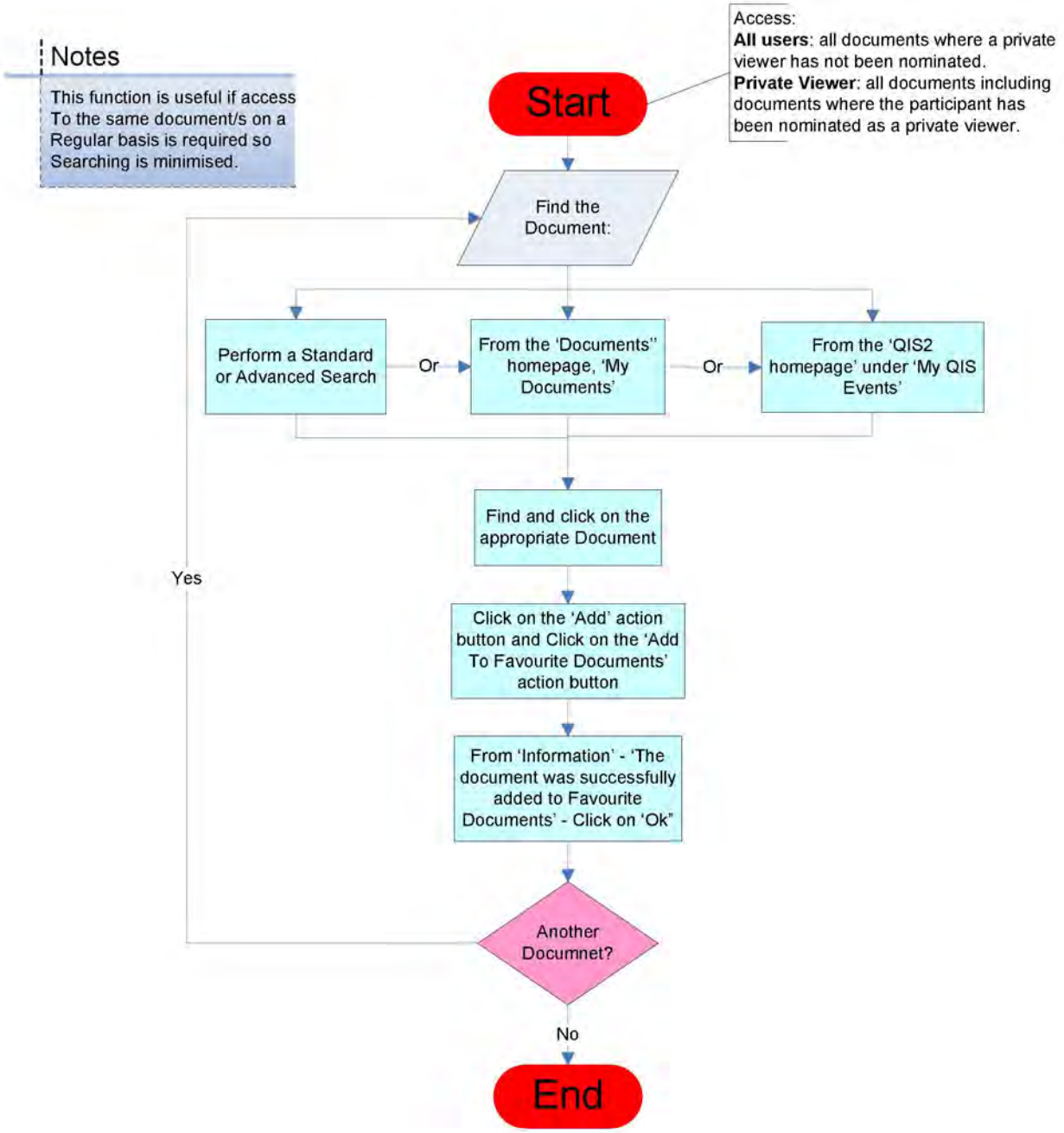
6.2 Document Search Advanced

Notes

The Advanced Search will search for the occurrence of the search criteria within Document meta-data based On the field that is being Searched upon.



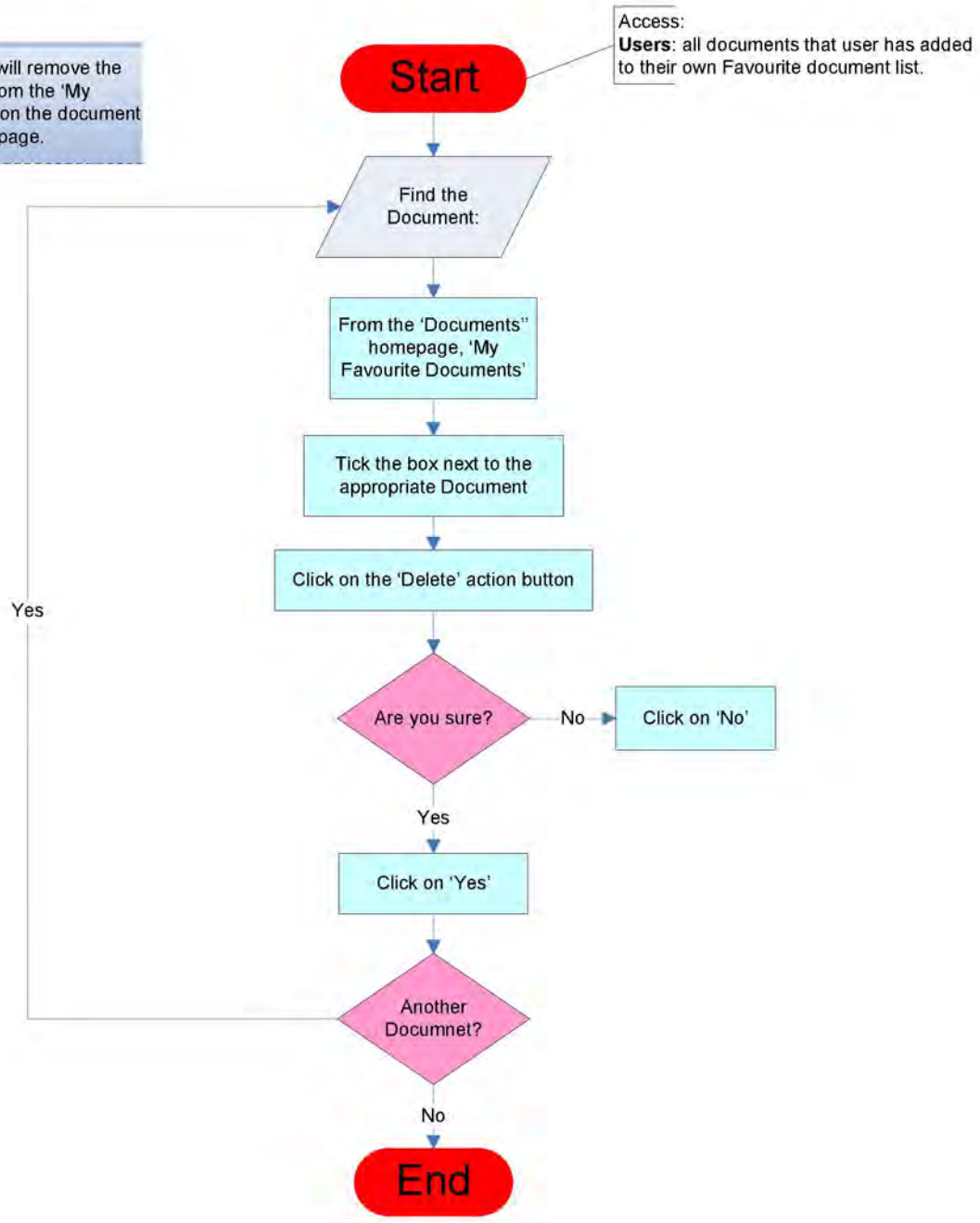
6.3 Add to Favourite Documents



6.4 Delete Favourite Documents

Notes

This function will remove the document/s from the 'My Favourite' list on the document Module homepage.

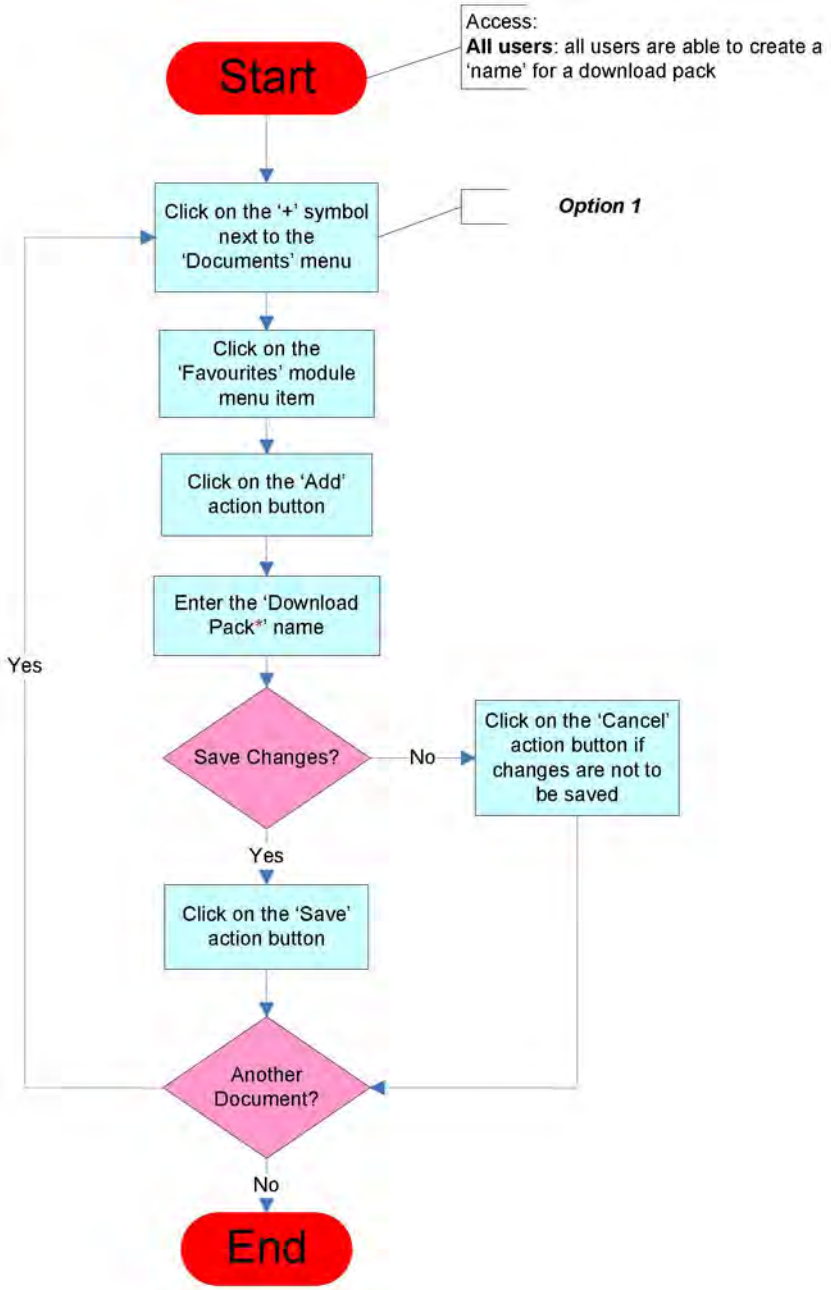


6.5 Create a Download Pack

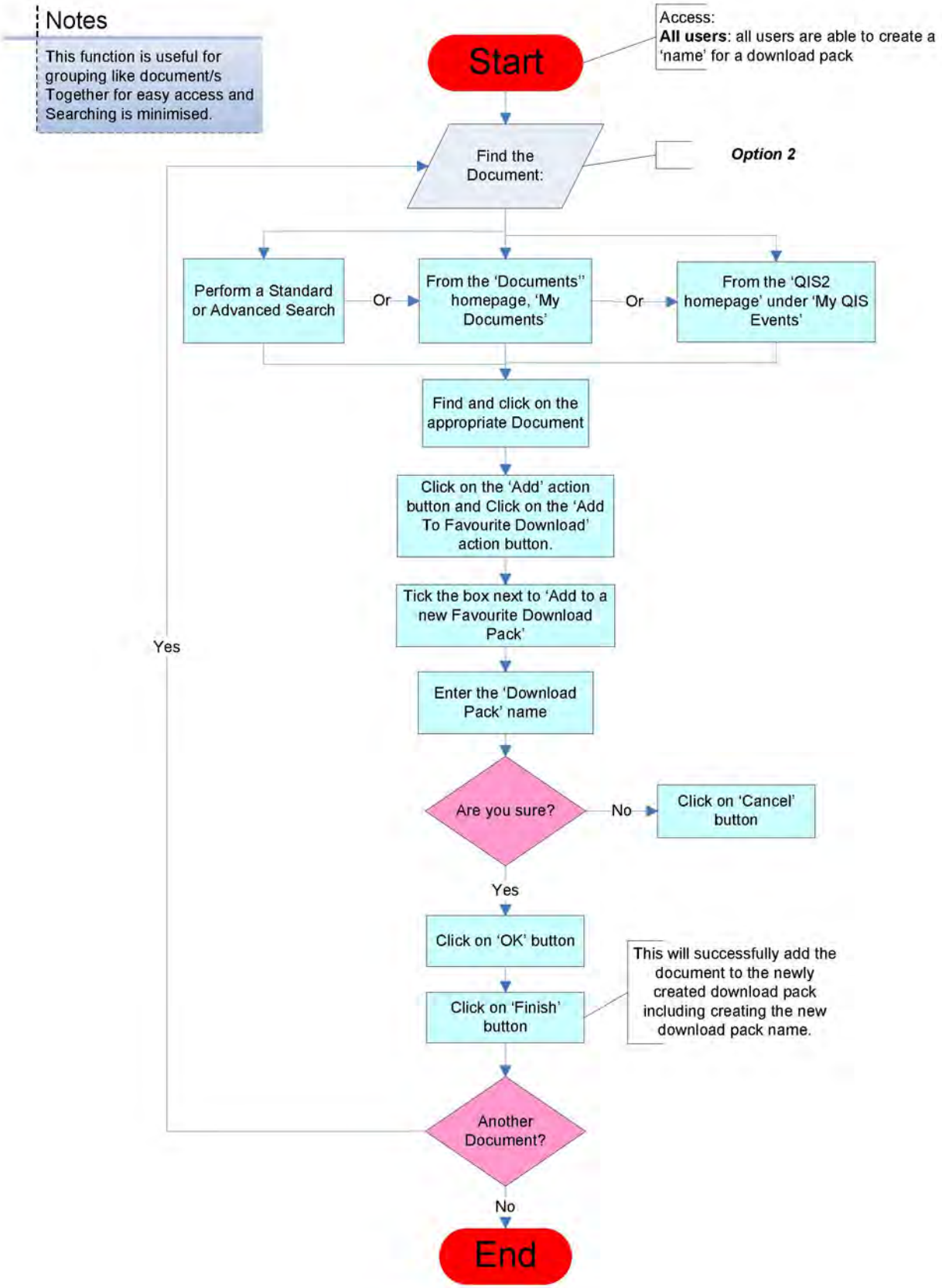
6.5.1 Option 1

Notes

This function is useful for grouping like document/s Together for easy access and Searching is minimised.



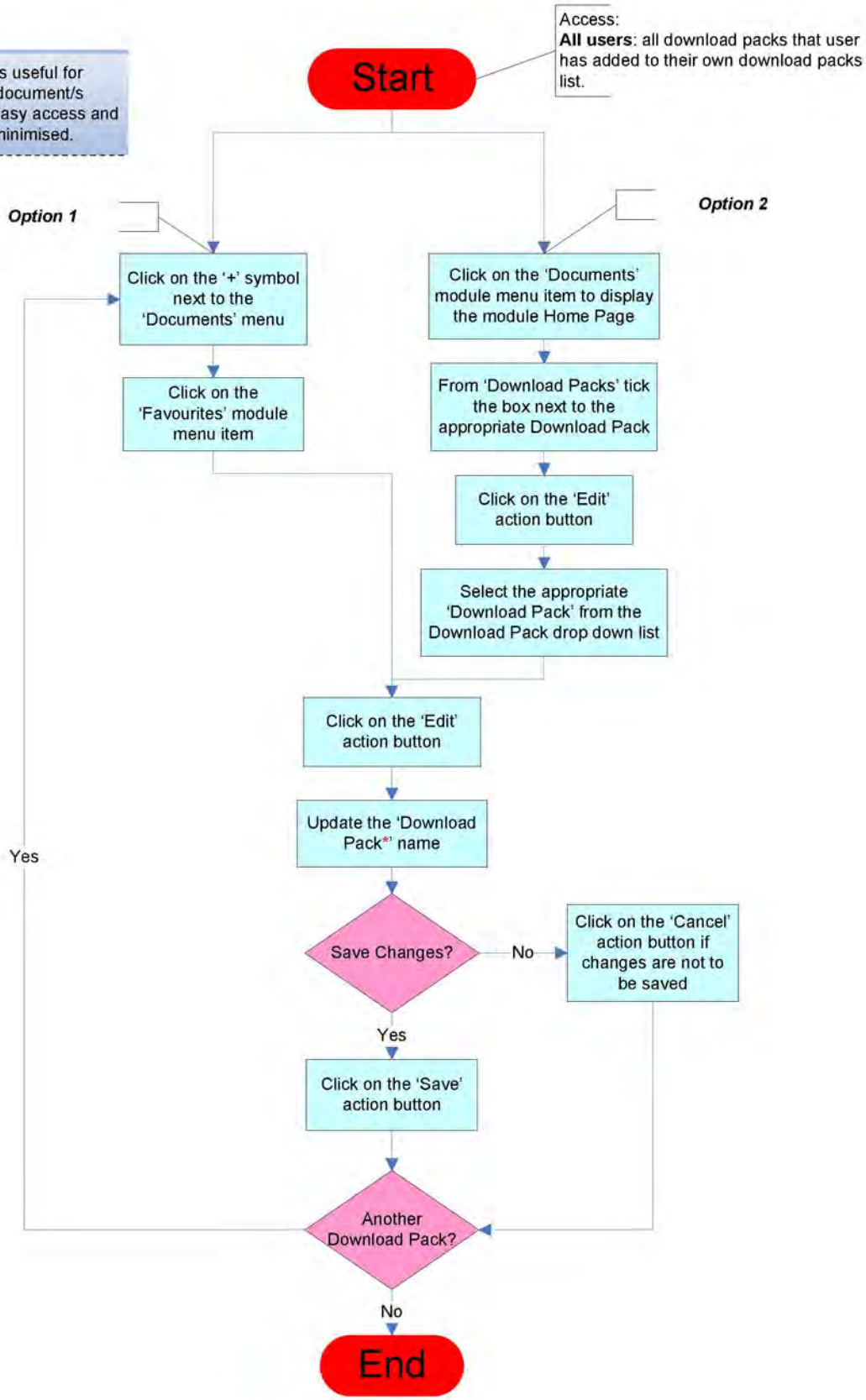
6.5.2 Option 2


Notes
This function is useful for grouping like document/s Together for easy access and Searching is minimised.
Start
Access:
All users: all users are able to create a 'name' for a download pack
Find the Document:
Option 2
Perform a Standard or Advanced Search
Or
From the 'Documents'' homepage, 'My Documents'
Or
From the 'QIS2 homepage' under 'My QIS Events'
Find and click on the appropriate Document
Click on the 'Add' action button and Click on the 'Add To Favourite Download' action button.
Tick the box next to 'Add to a new Favourite Download Pack'
Enter the 'Download Pack' name
Are you sure?
No
Click on 'Cancel' button
Yes
Click on 'OK' button
Click on 'Finish' button
This will successfully add the document to the newly created download pack including creating the new download pack name.
Another Document?
Yes
No
End

6.6 Edit a Download Pack

Notes

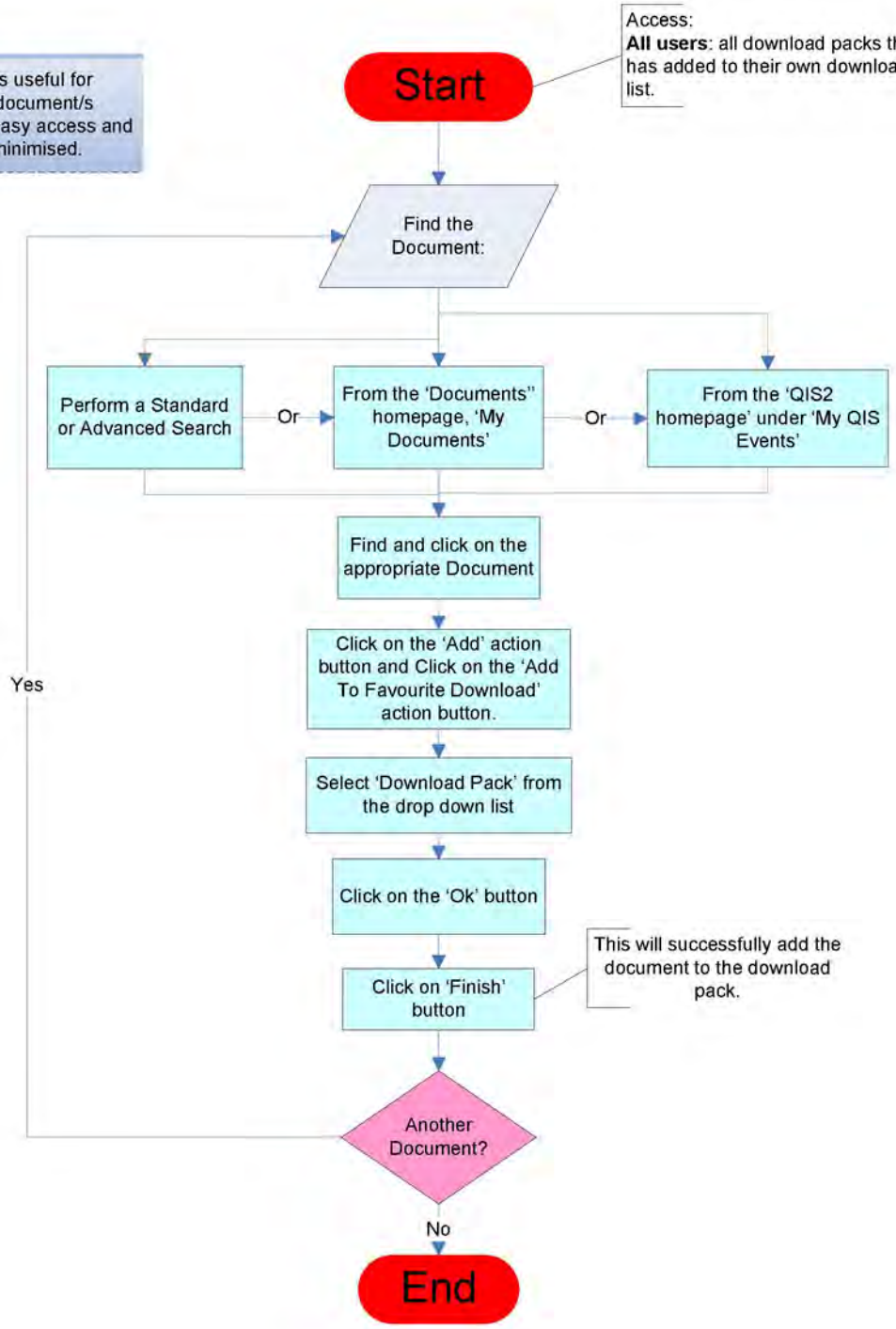
This function is useful for grouping like document/s Together for easy access and Searching is minimised.



6.7 Add Document to a Download Pack

Notes

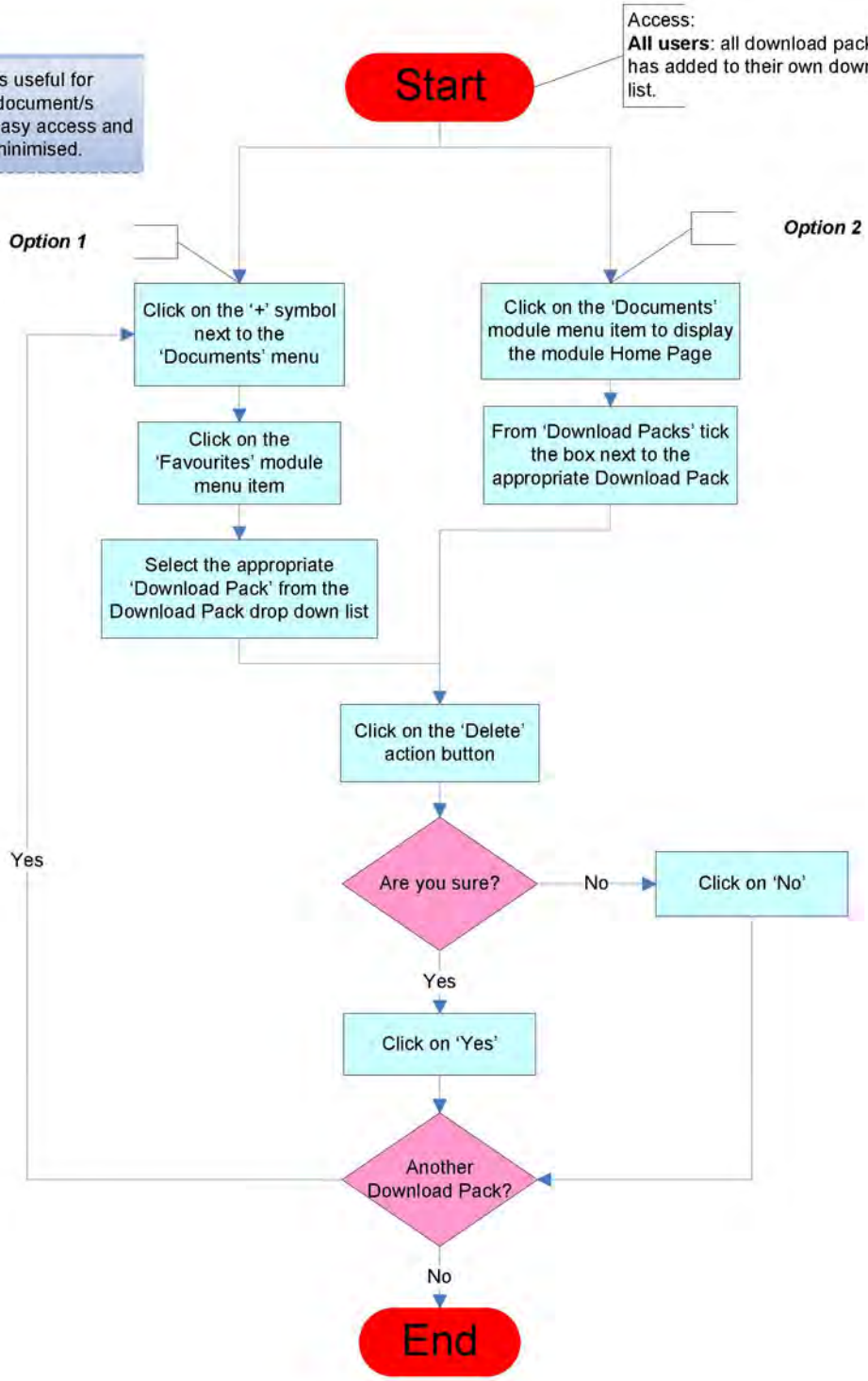
This function is useful for grouping like document/s Together for easy access and Searching is minimised.



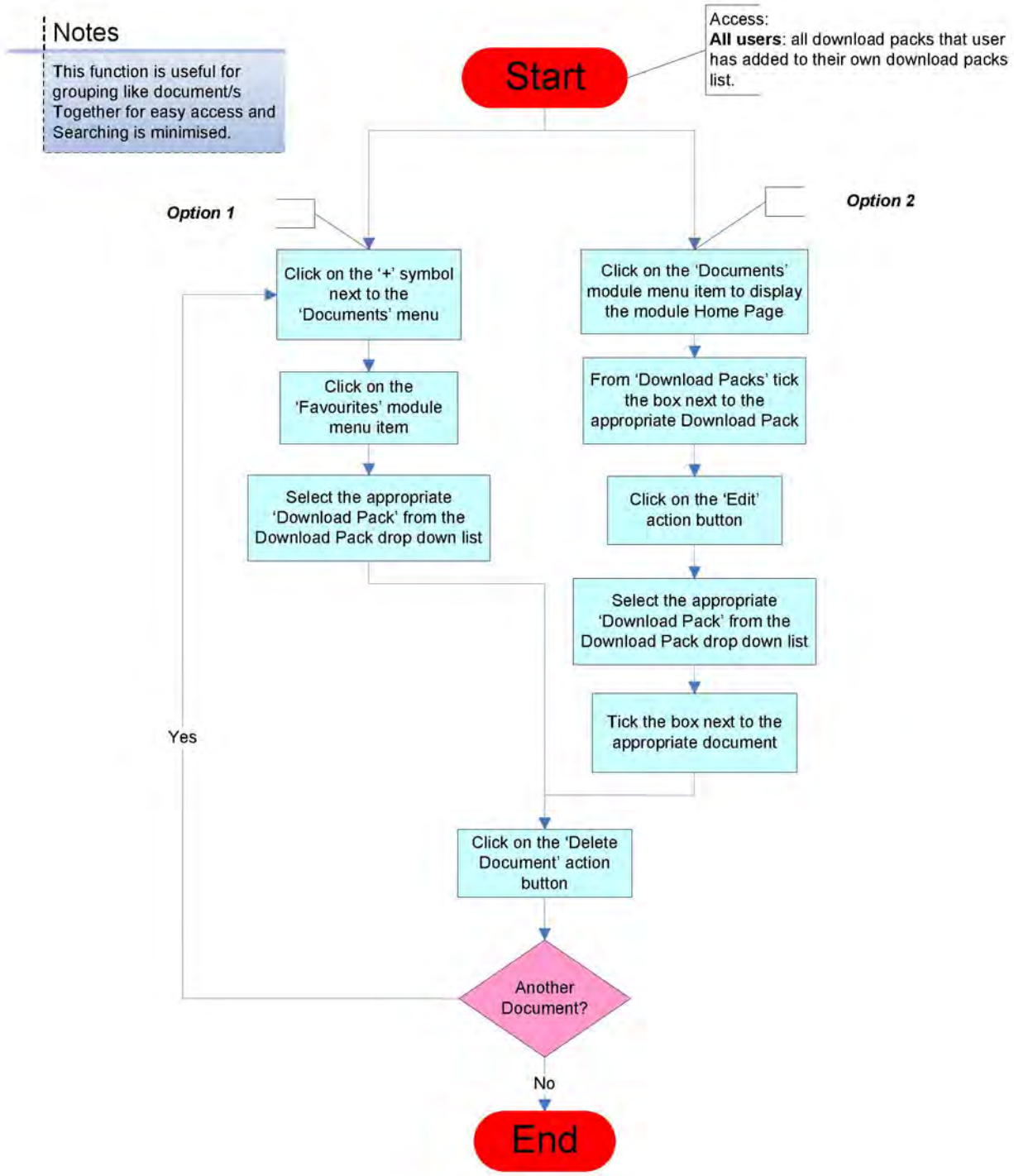
6.8 Delete a Download Pack

Notes

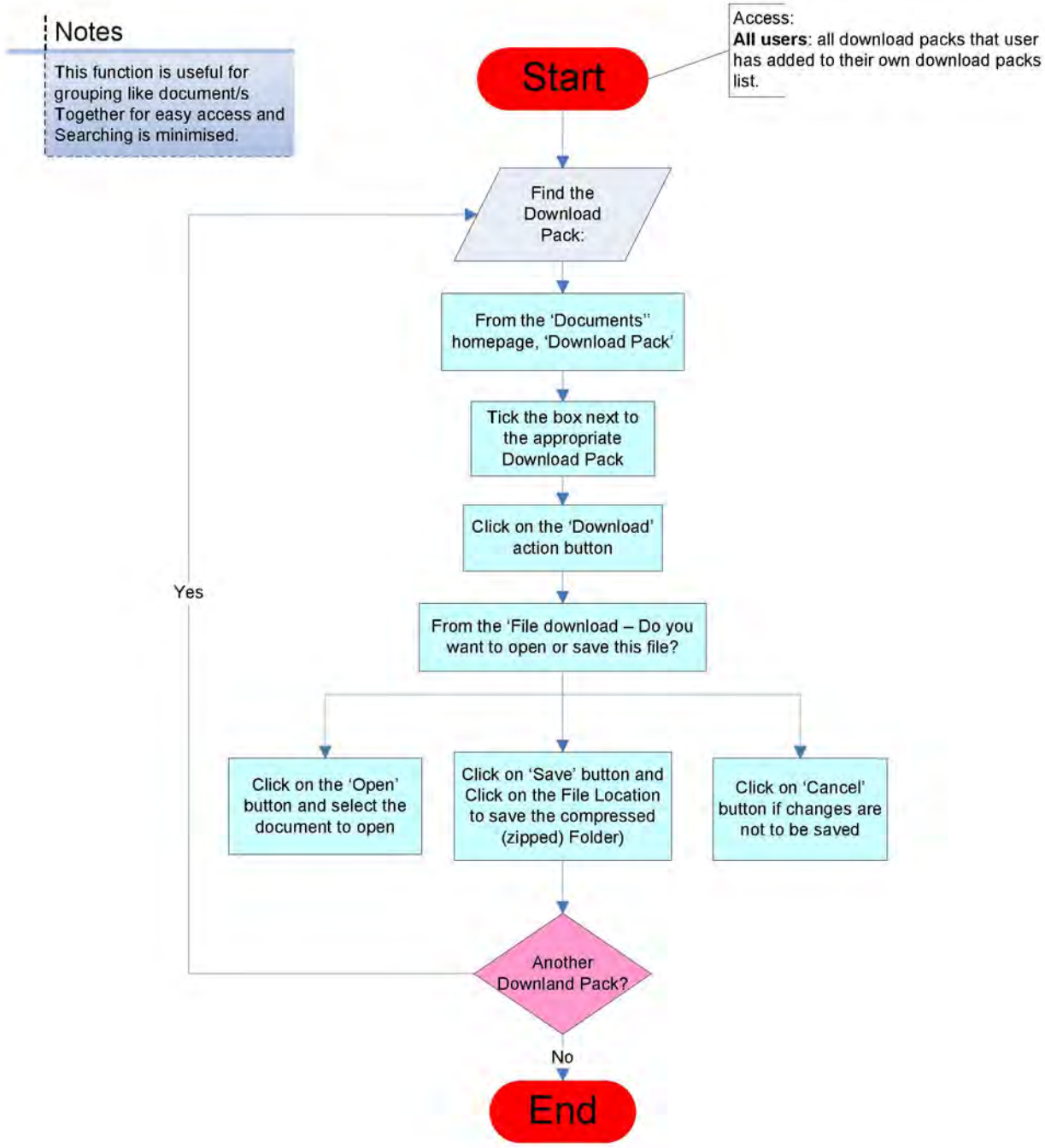
This function is useful for grouping like document/s Together for easy access and Searching is minimised.



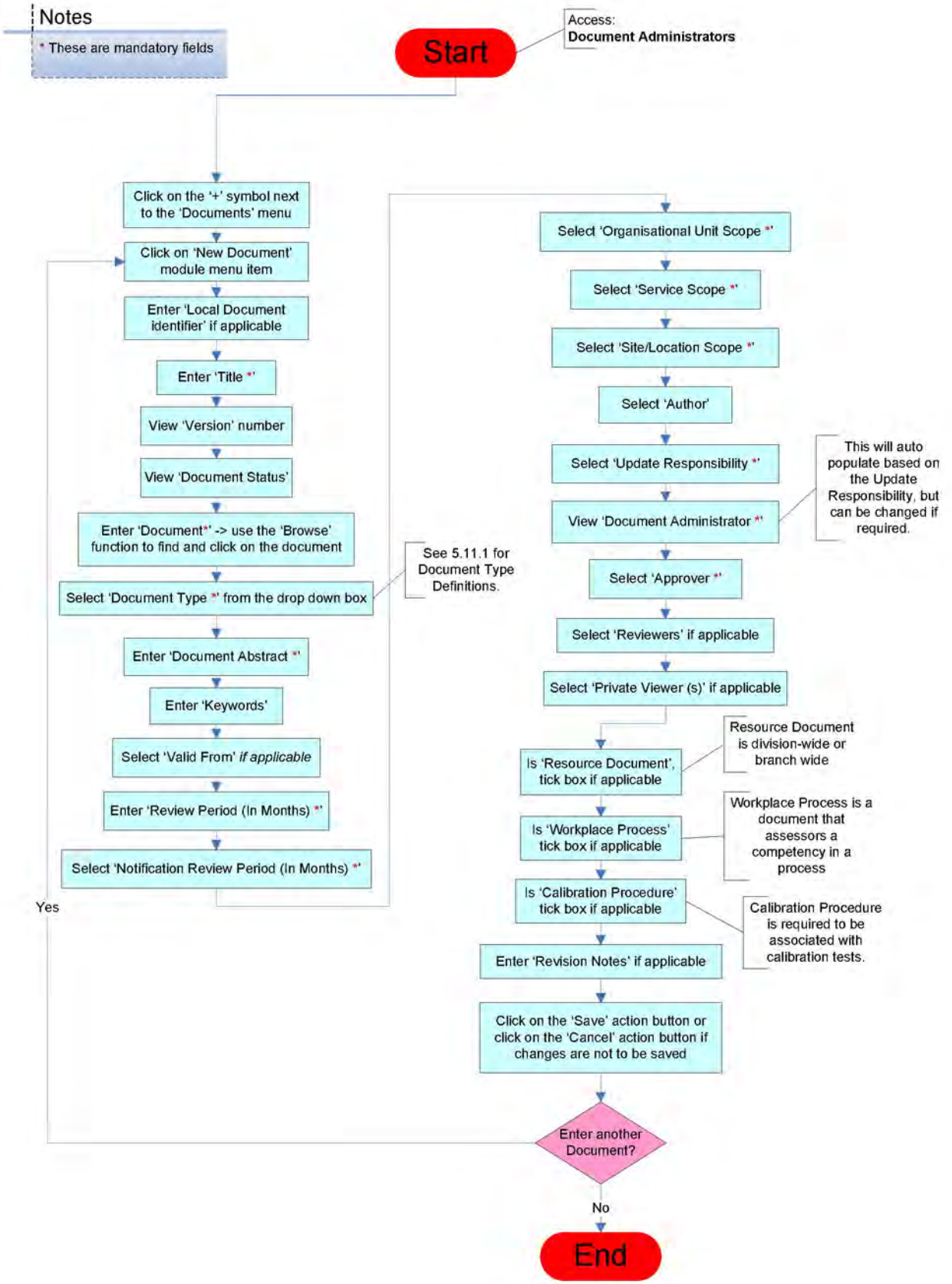
6.9 Delete a Document from a Download Pack



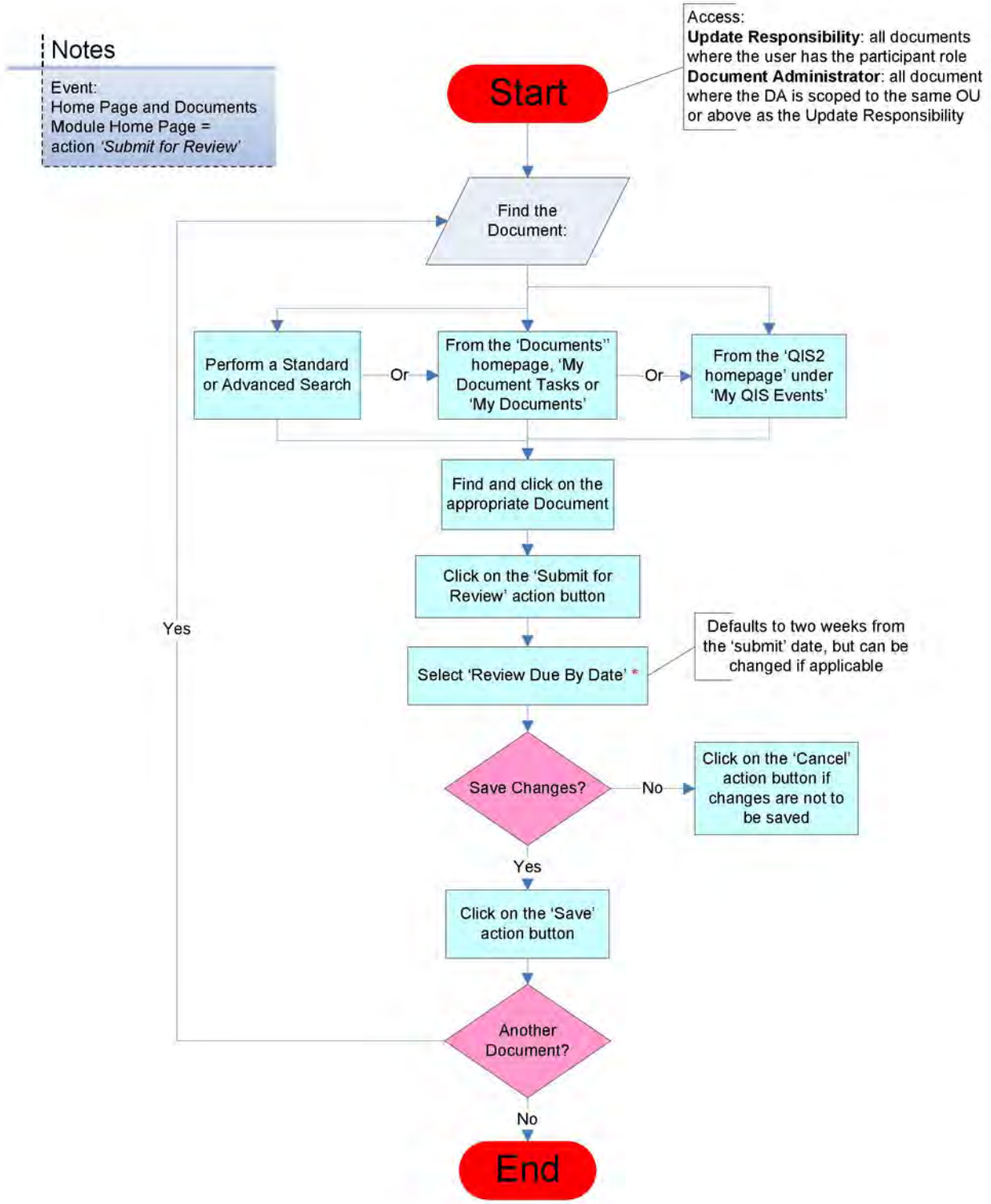
6.10 Download your Download Pack



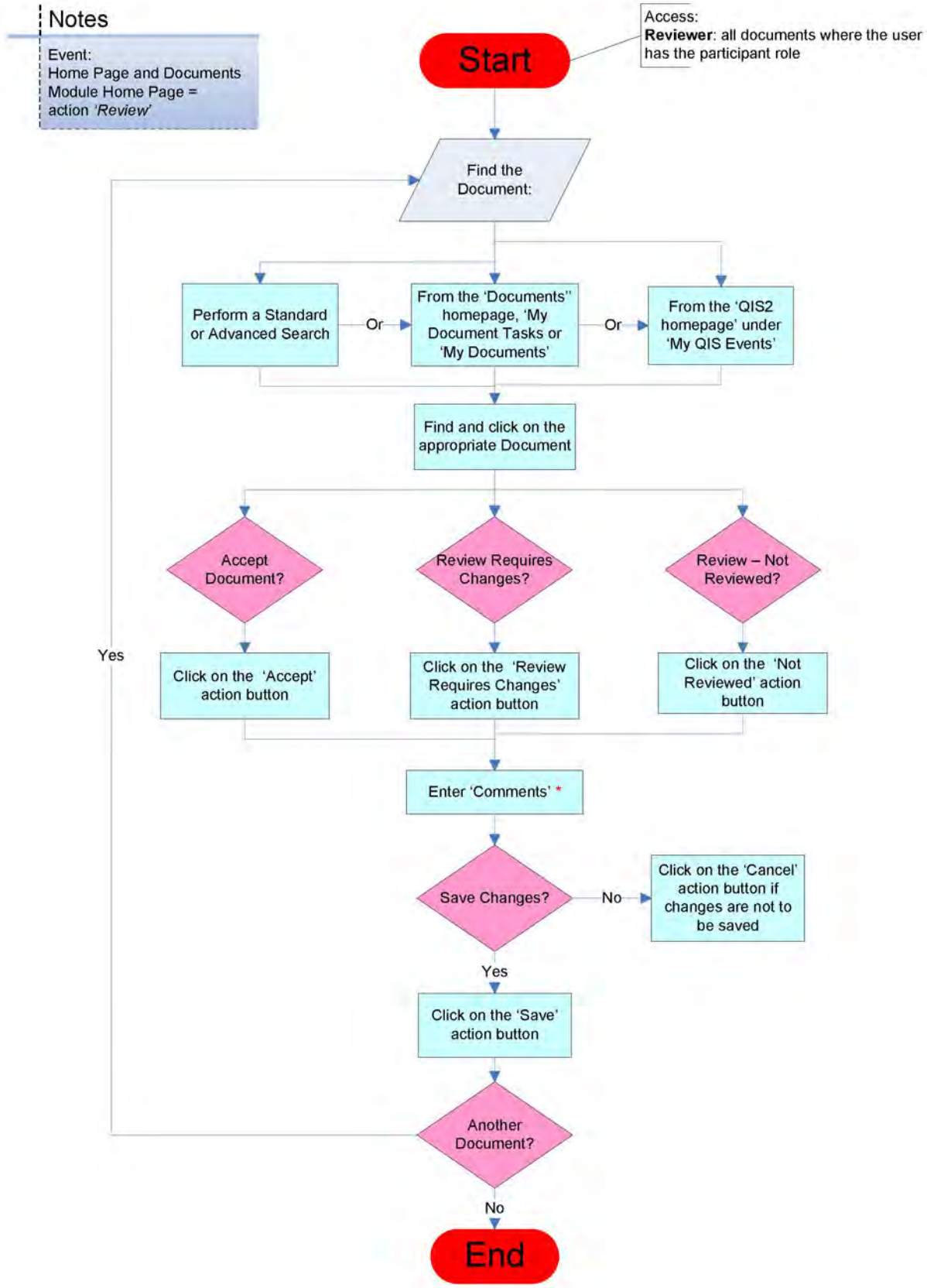
6.11 Create a New Document



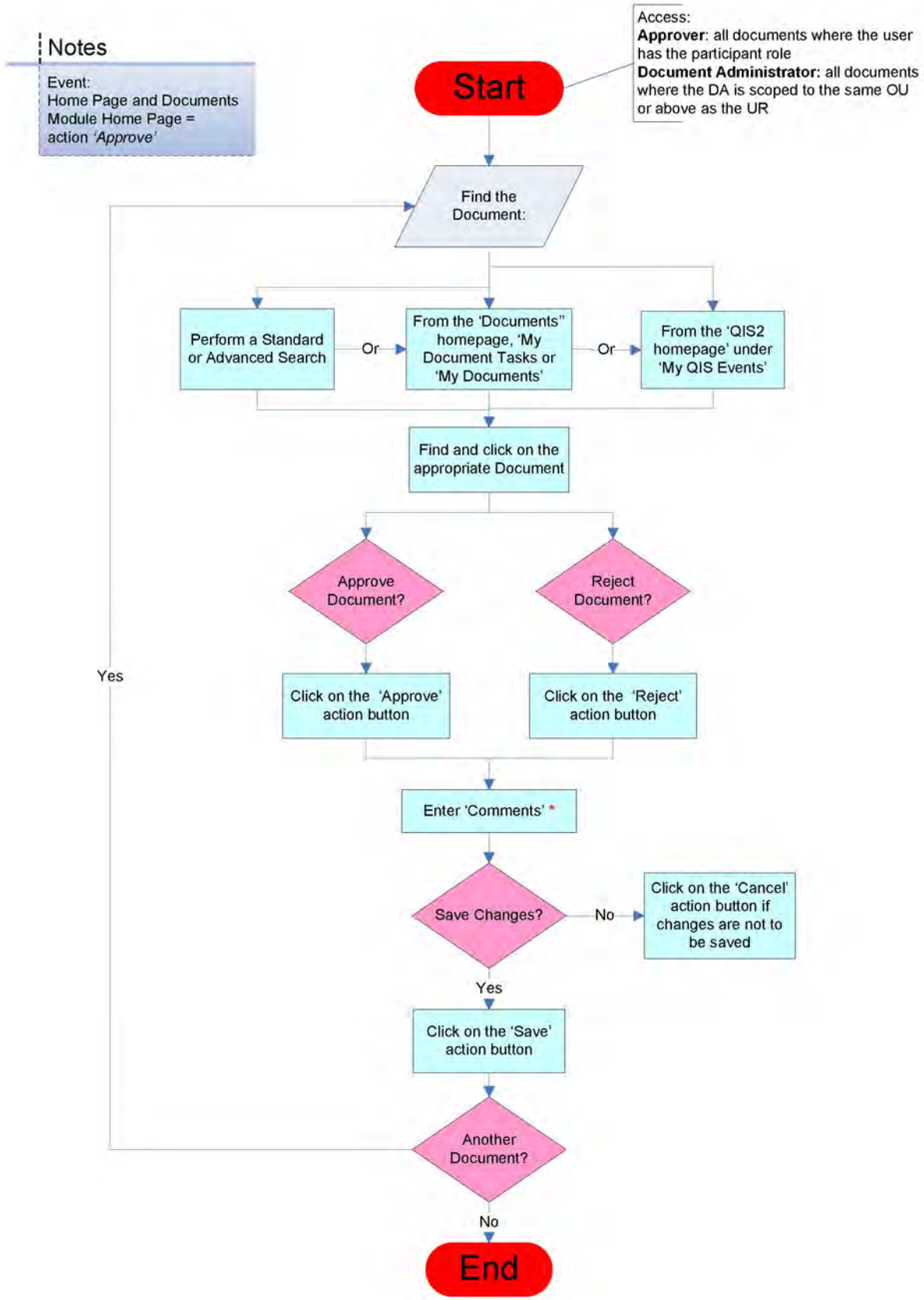
6.12 Submit Document for Review



6.13 Reviewer

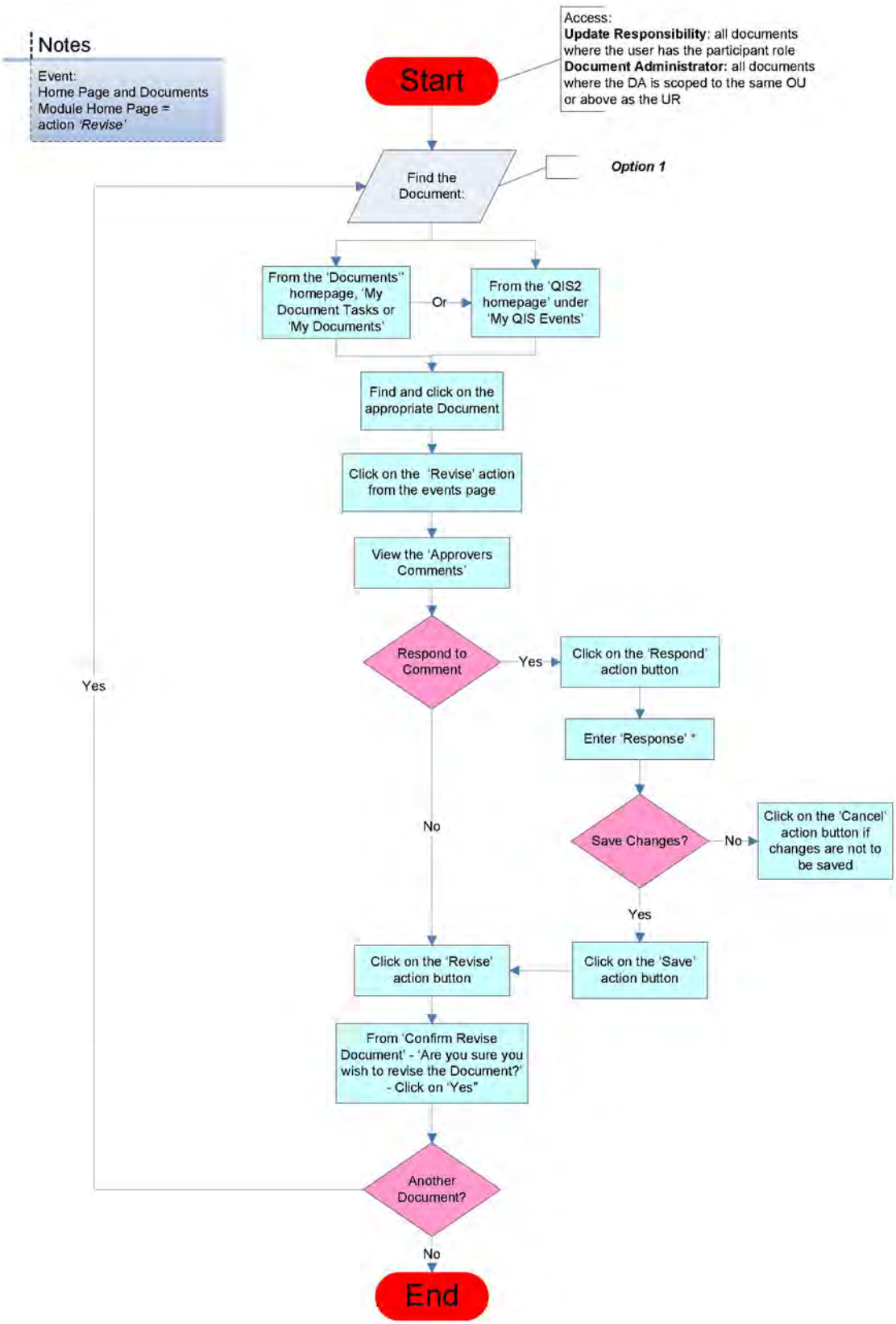


6.14 Approver

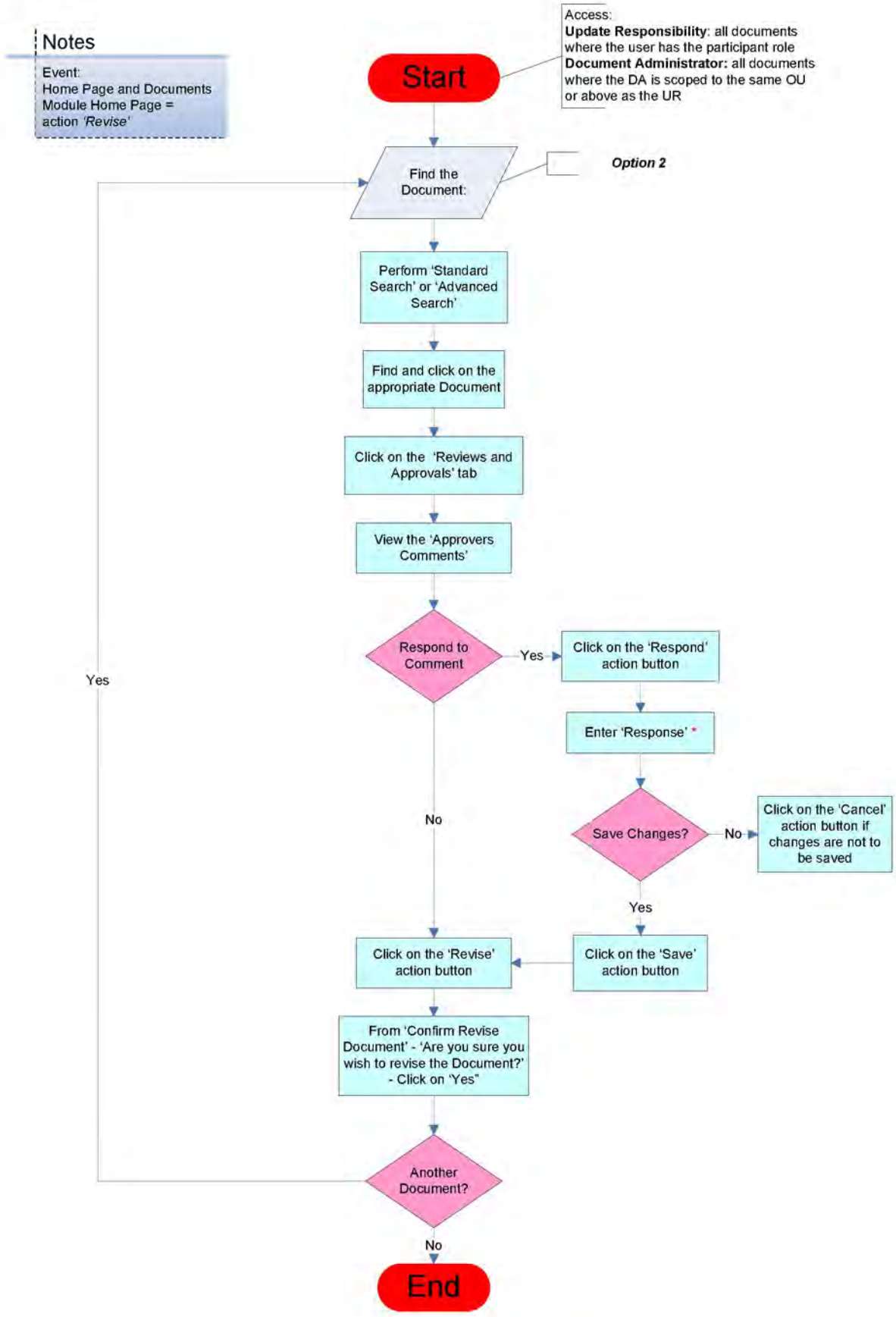


6.15 Revise a DRAFT Document

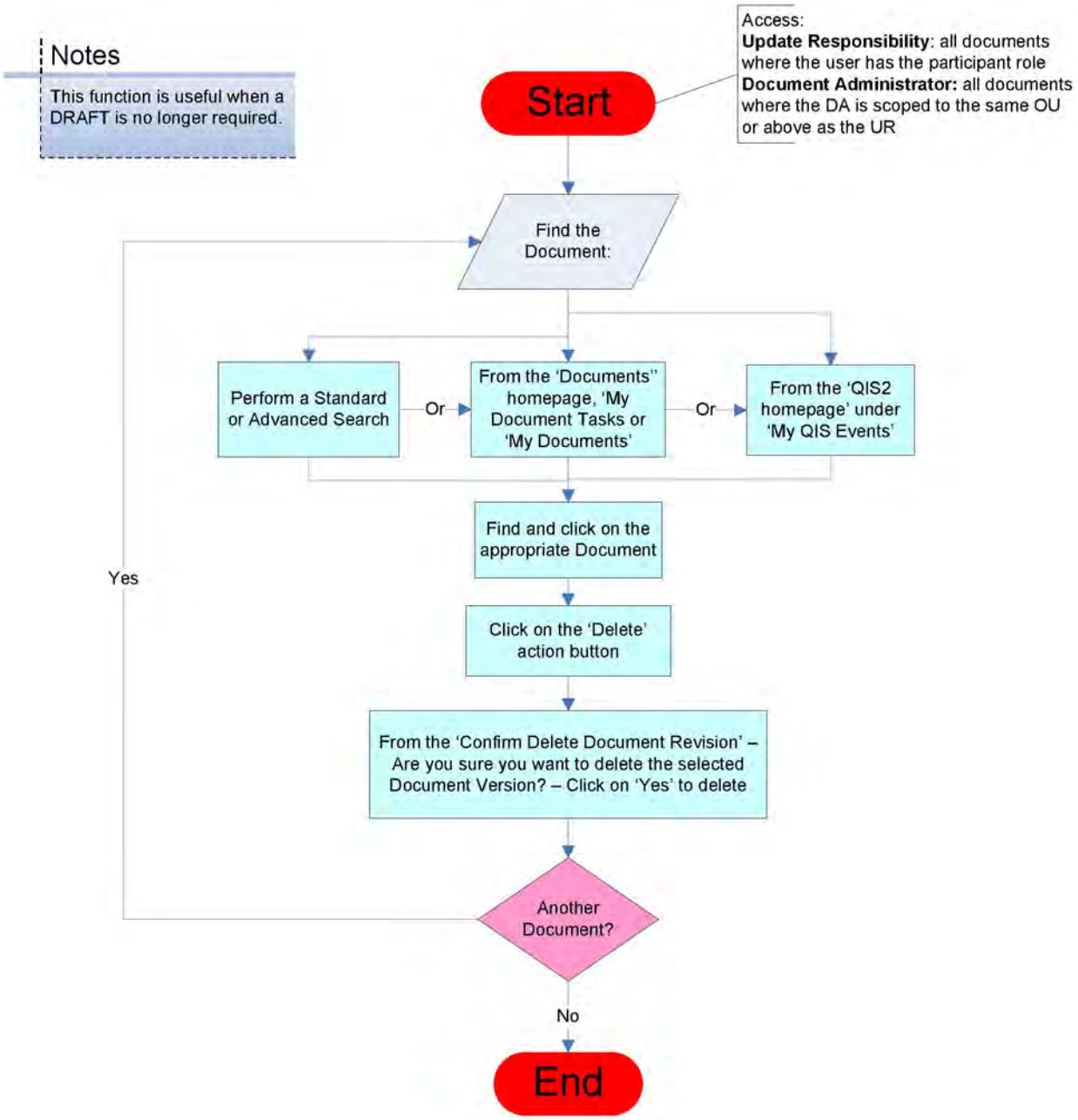
6.15.1 Option 1



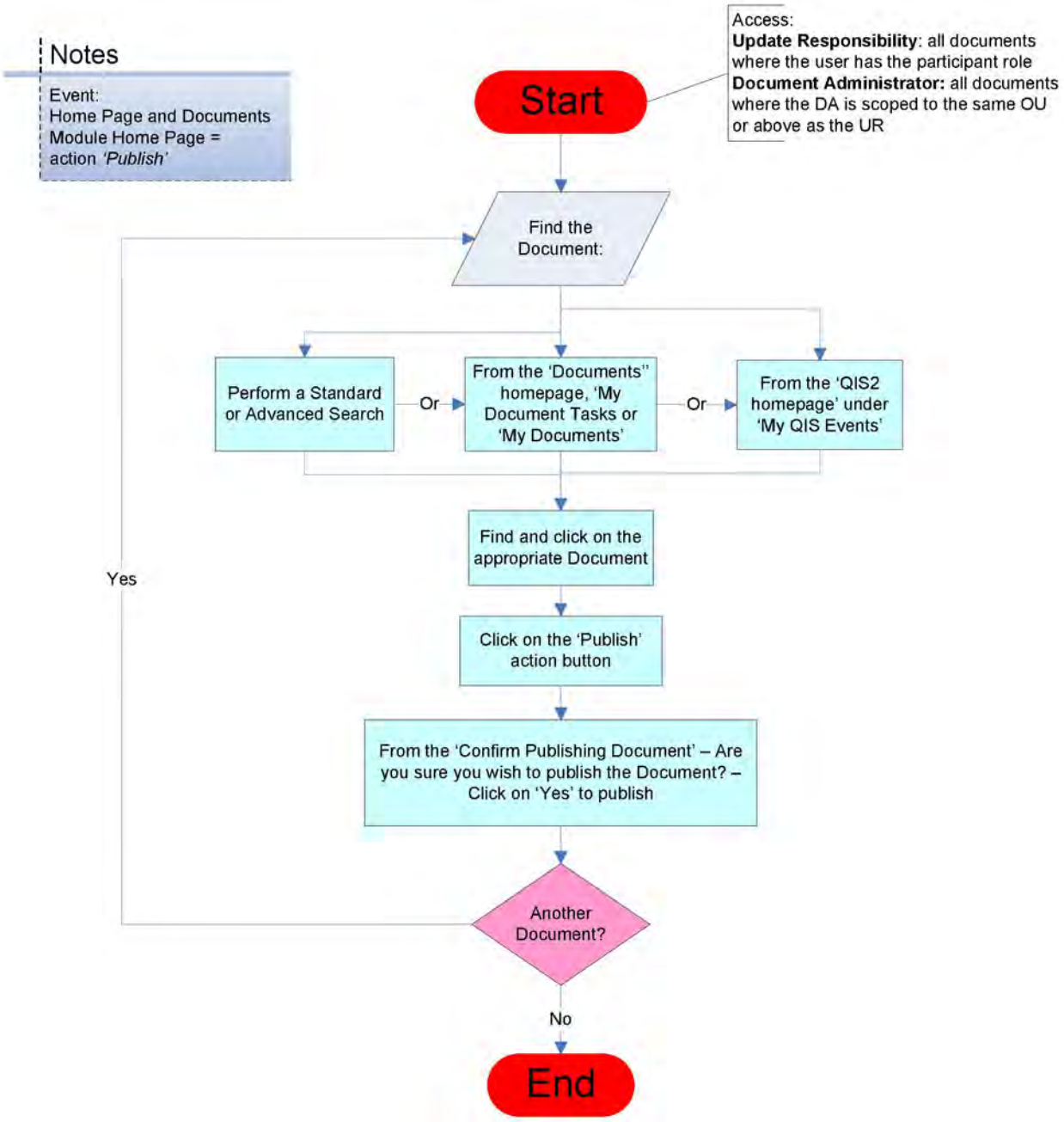
6.15.2 Option 2



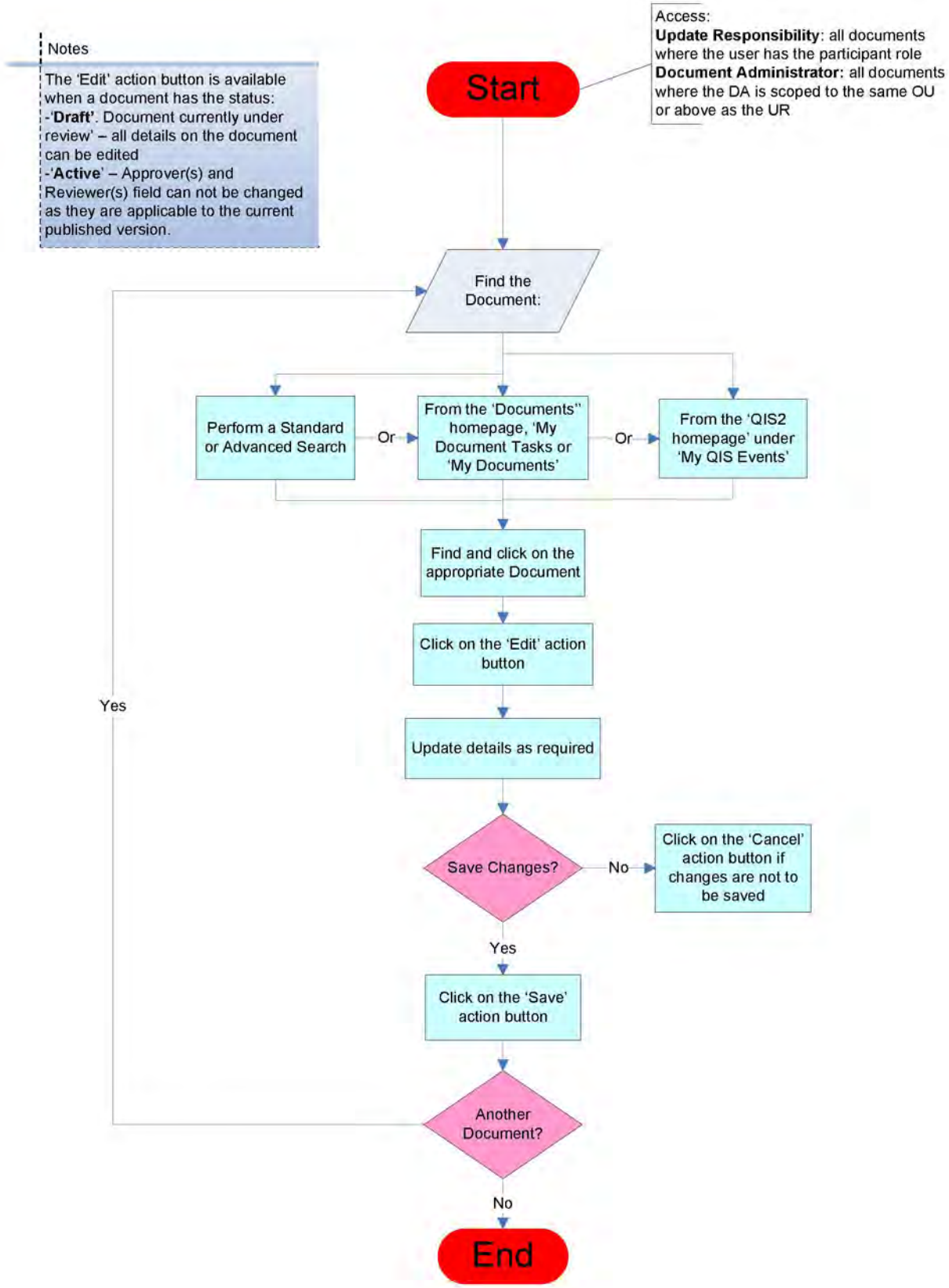
6.16 Delete DRAFT Document



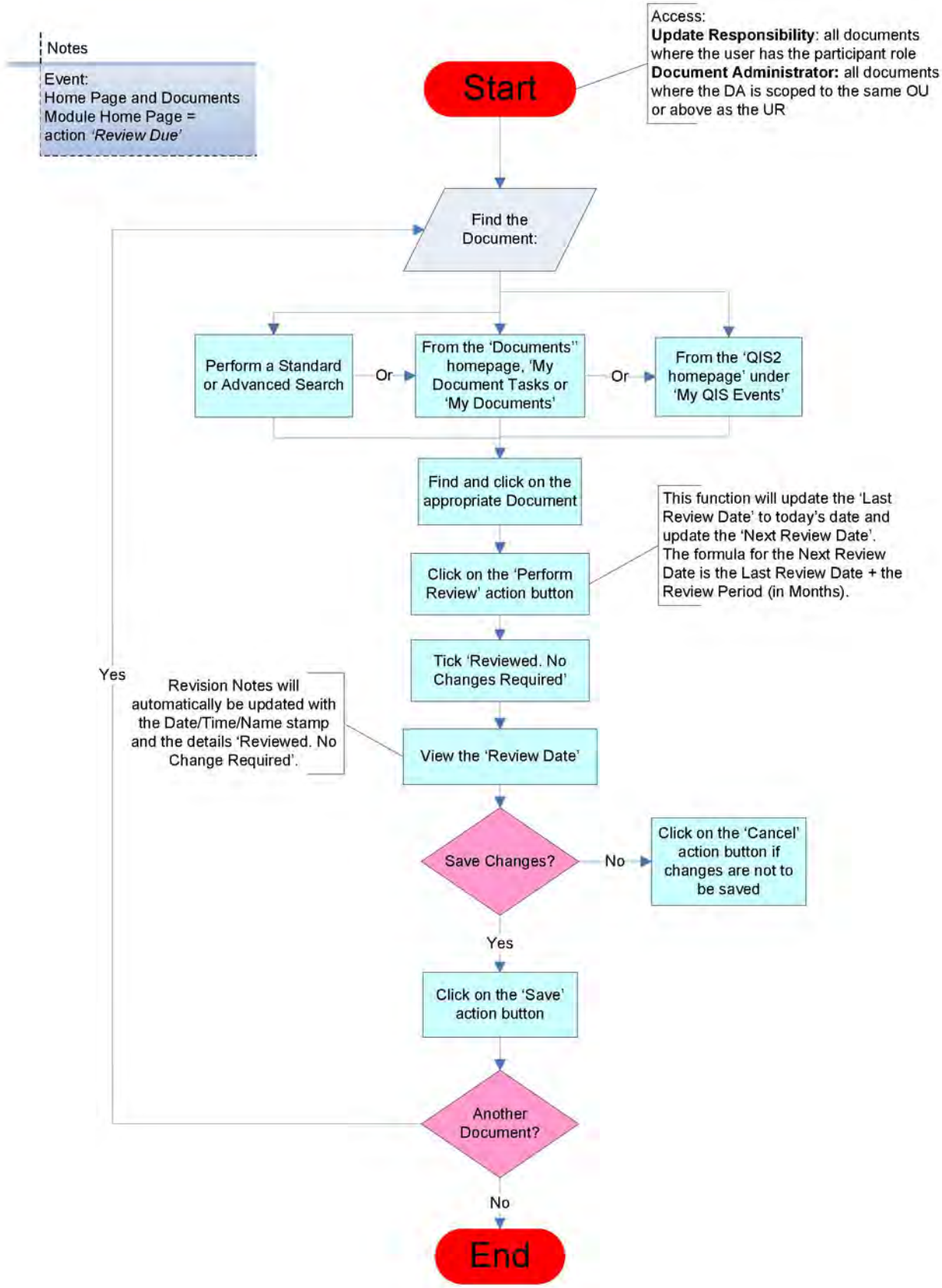
6.17 Publish a Document



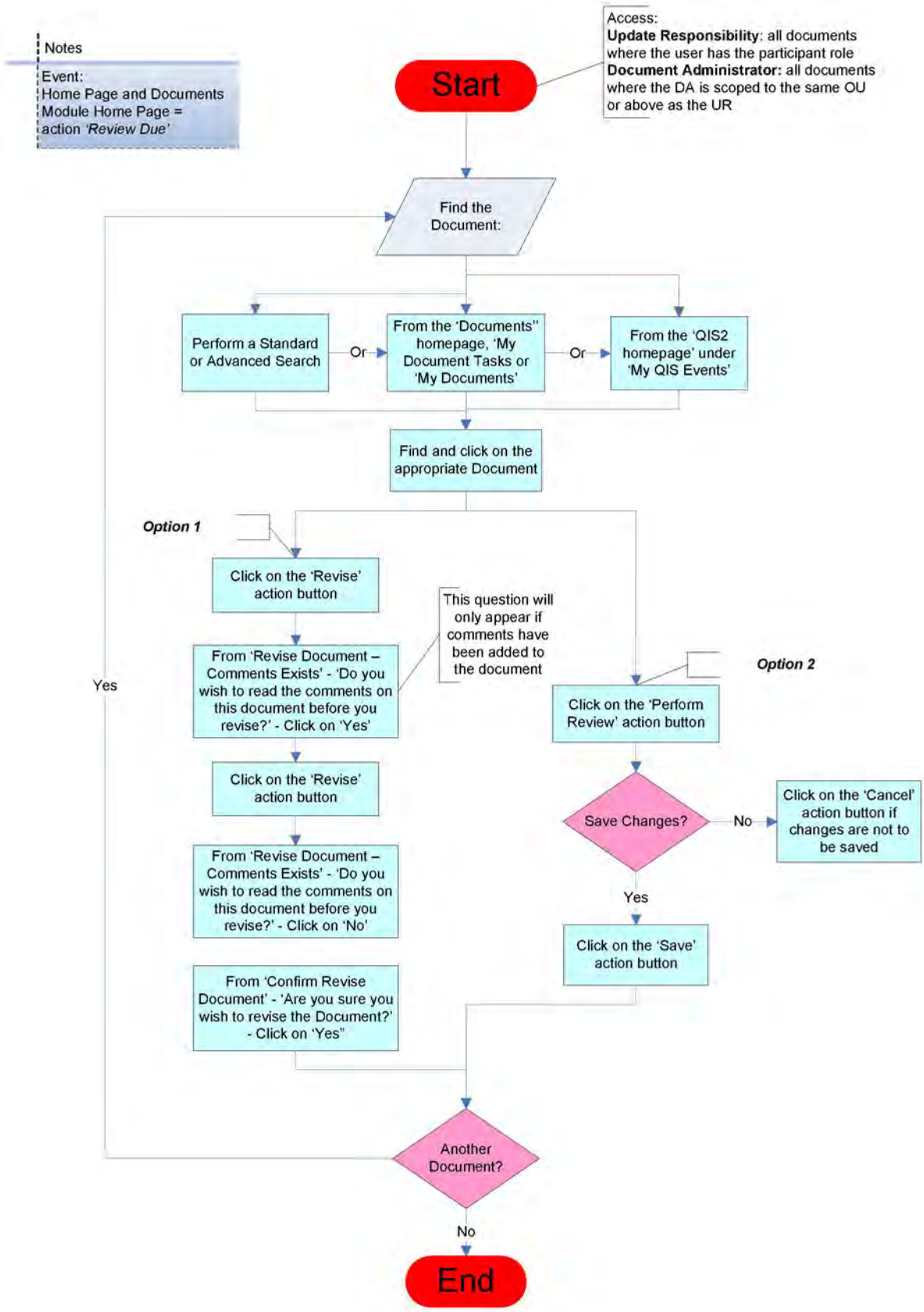
6.18 Edit Document Details



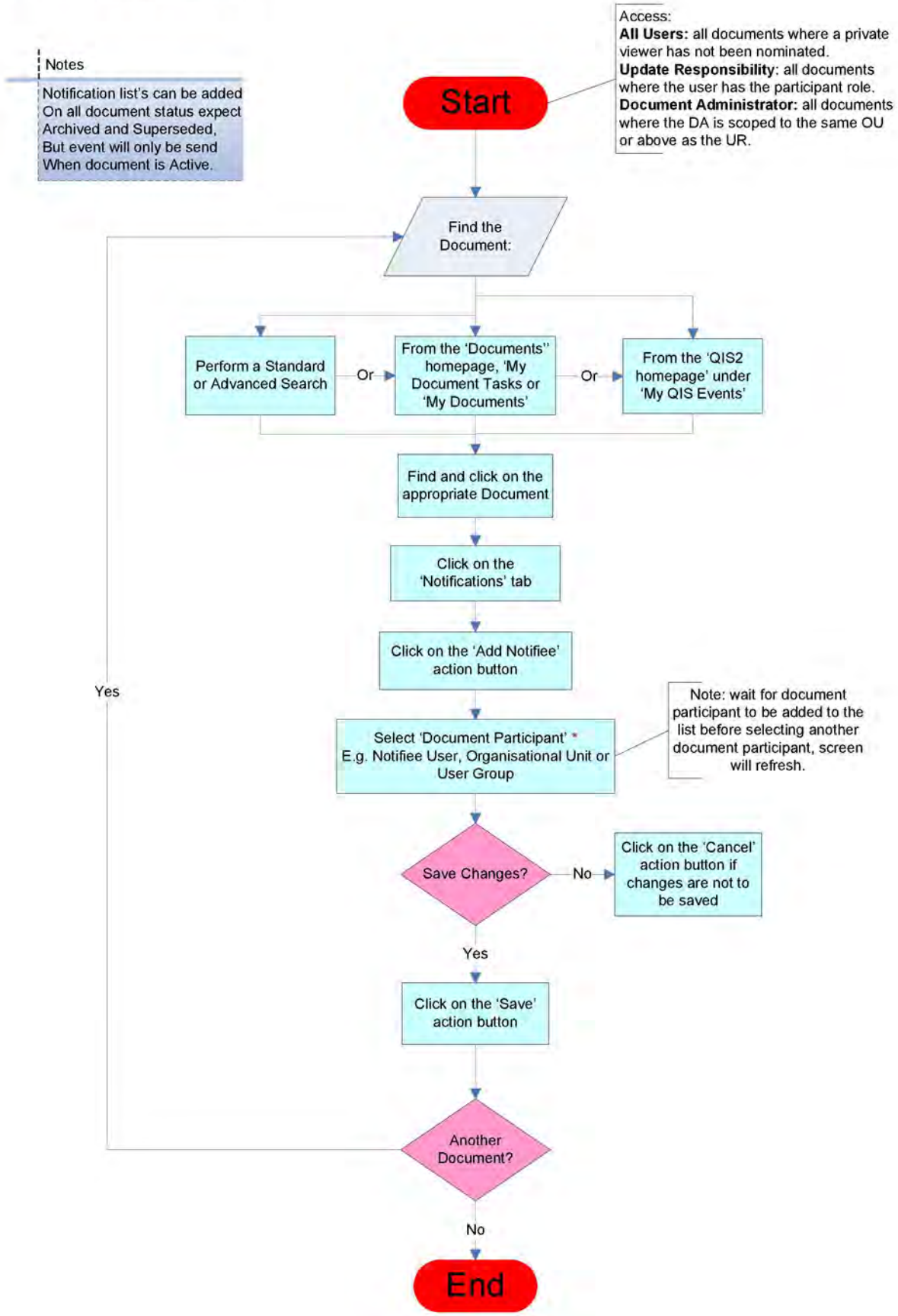
6.19 Active Document, Review, No changes required



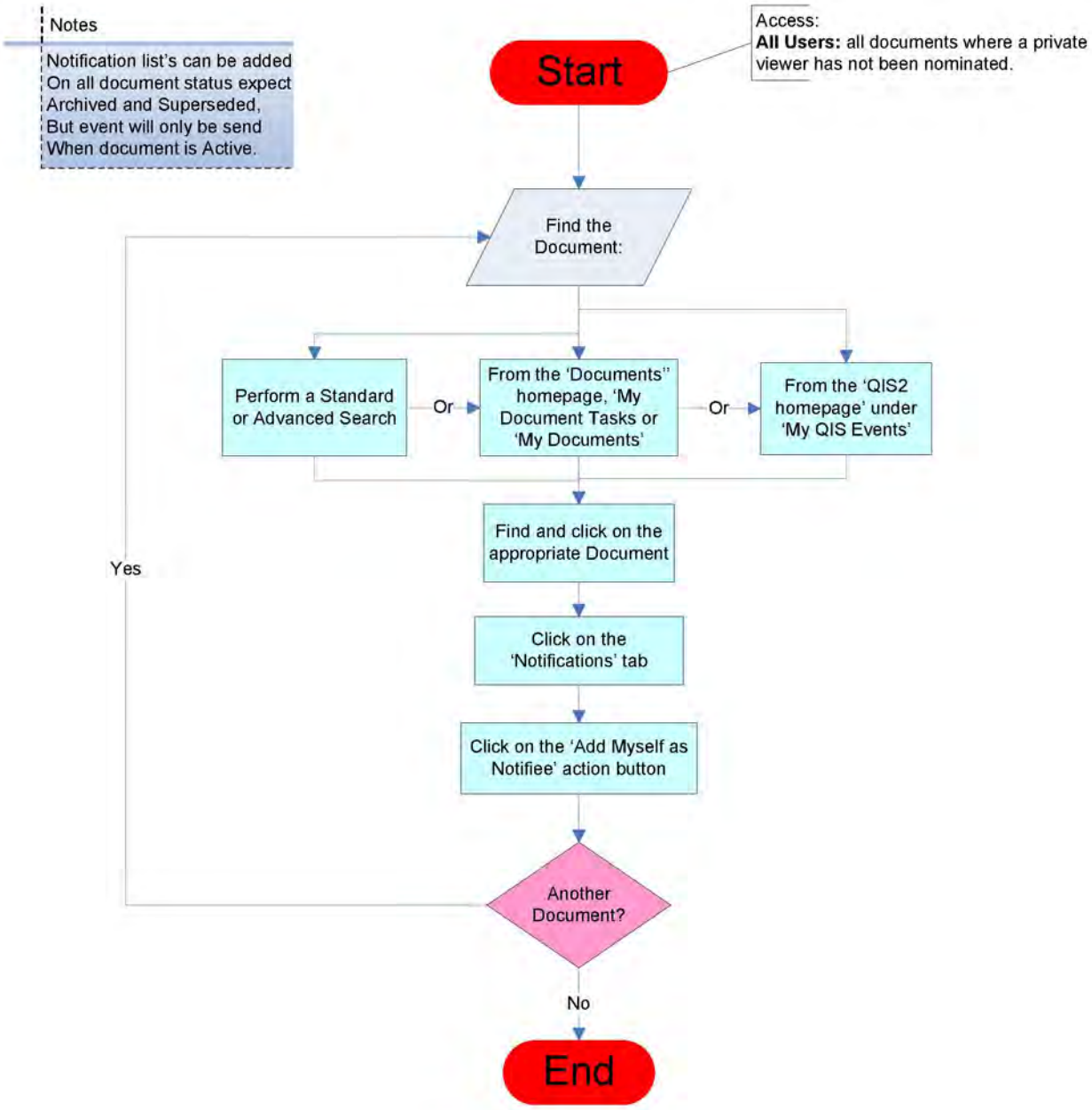
6.20 Active Document, Review



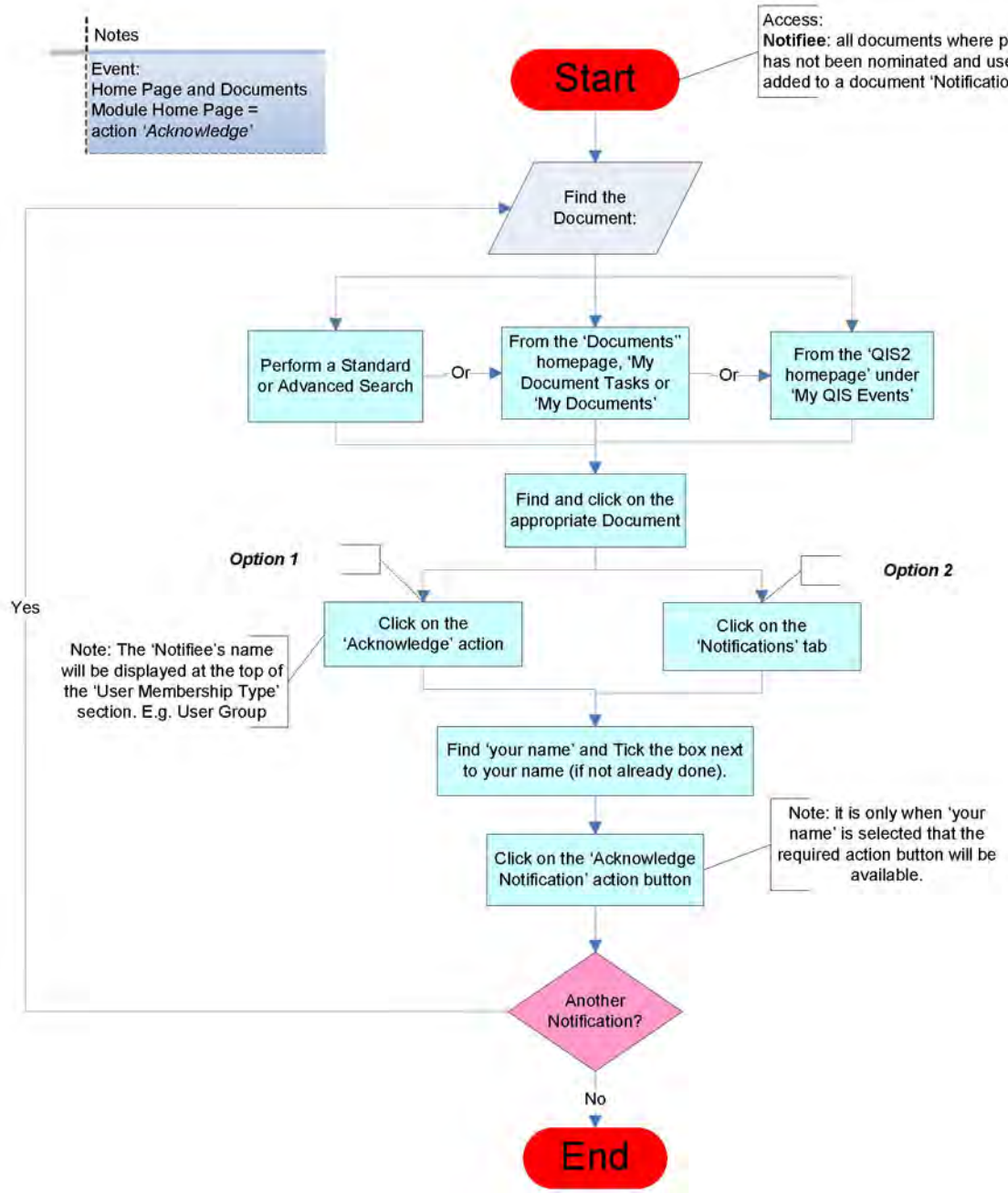
6.21 Add Notification List



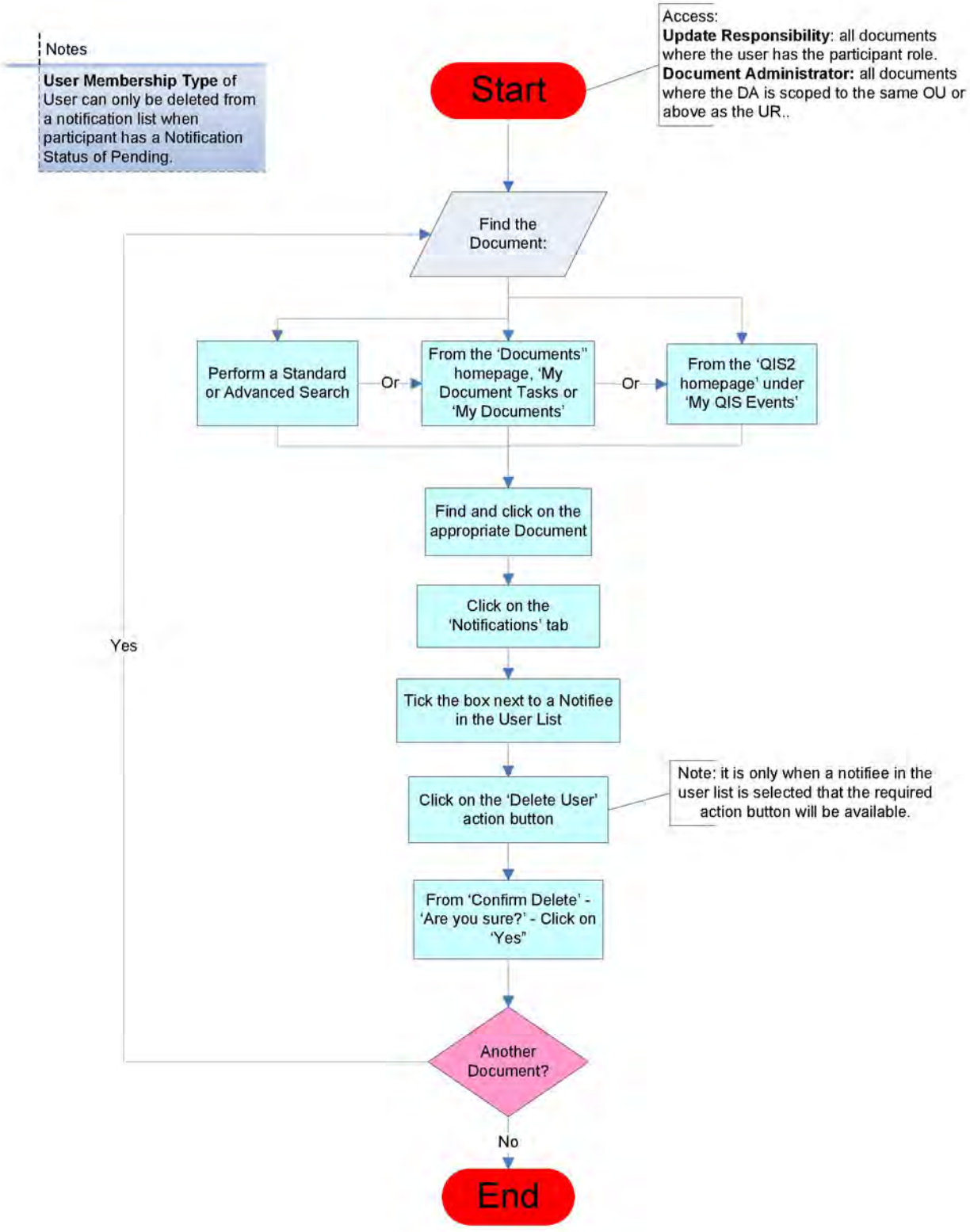
6.22 Add Self to Notification List



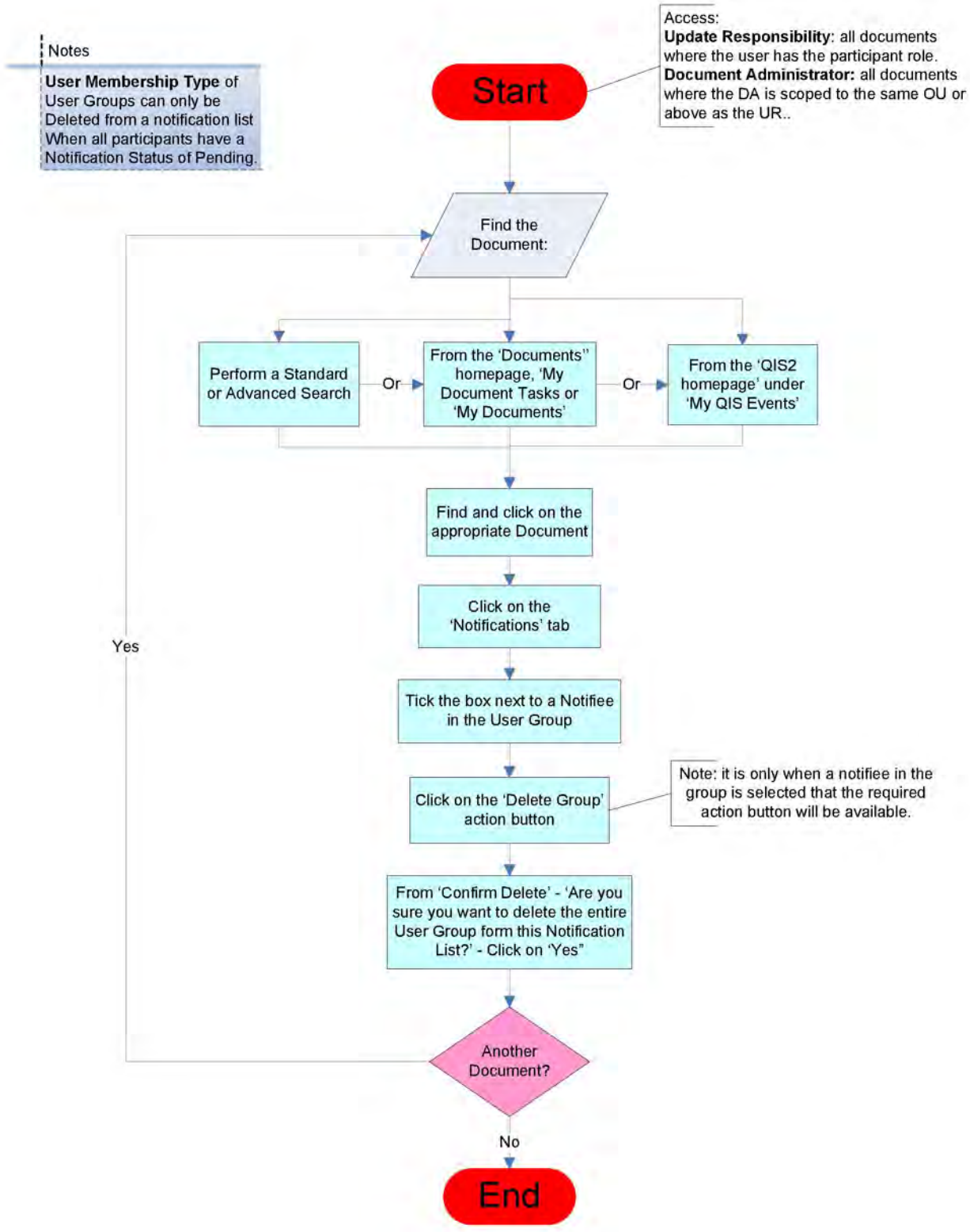
6.23 Acknowledge a Notification



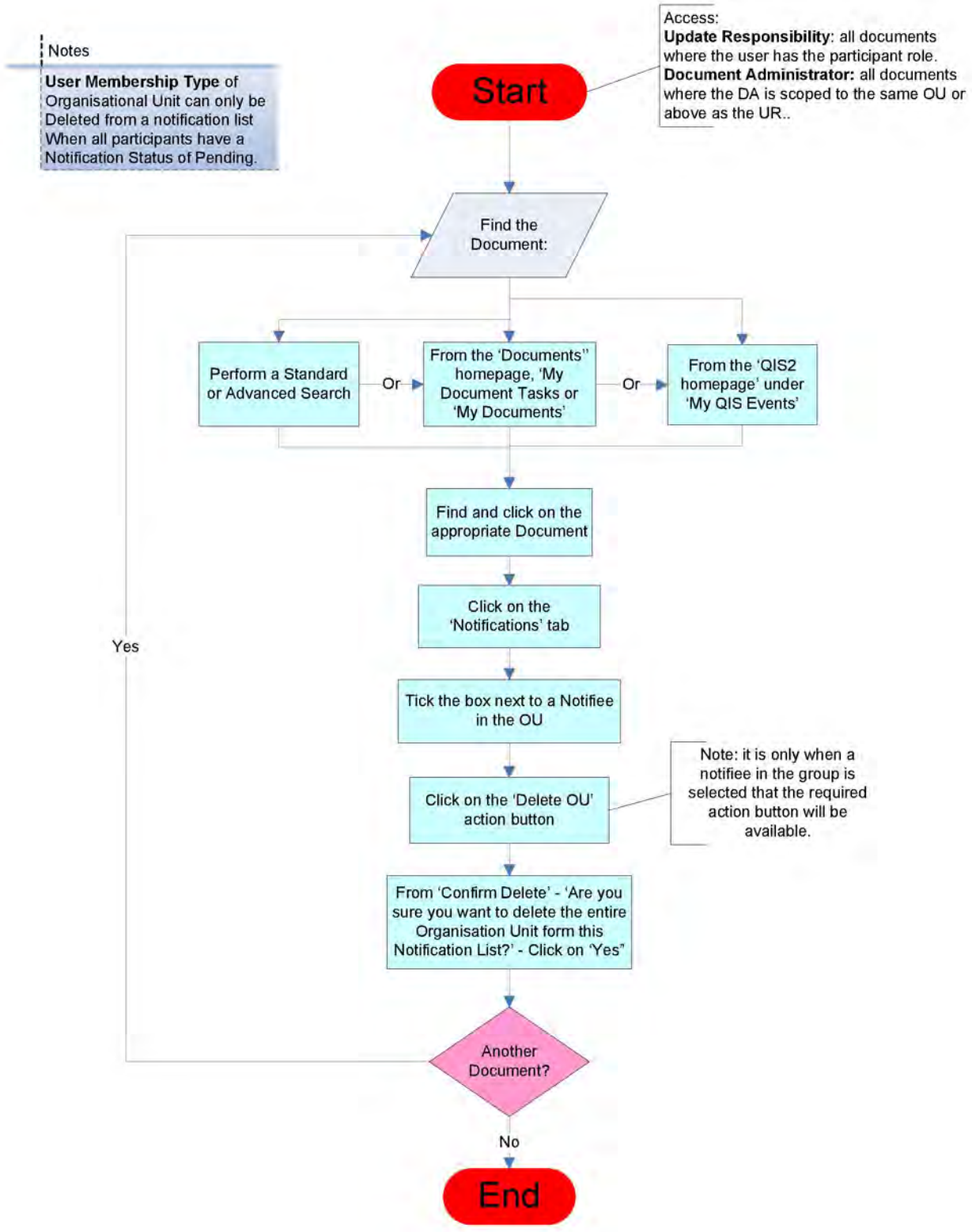
6.24 Delete 'User' from Notification List



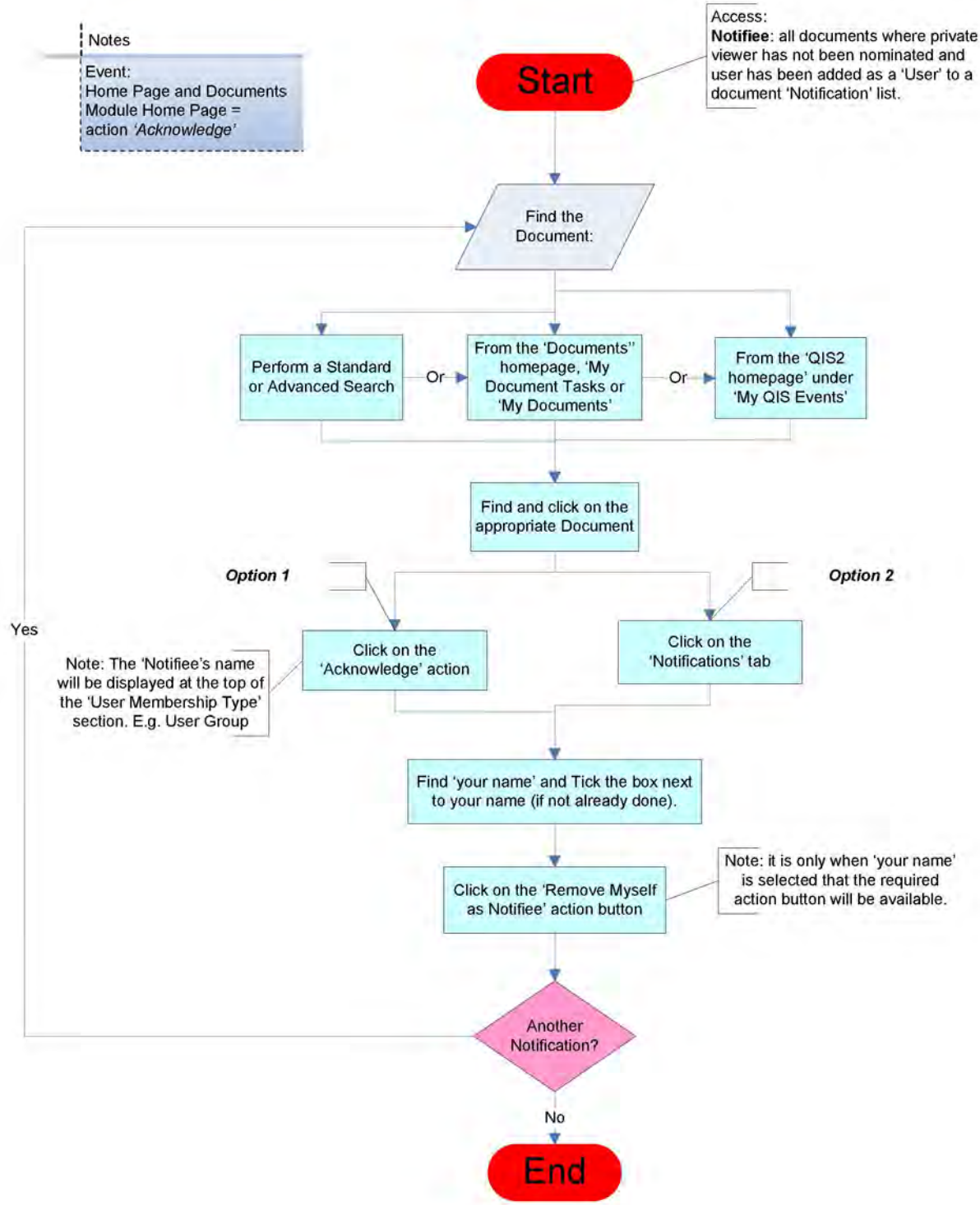
6.25 Delete 'User Group' from Notification List



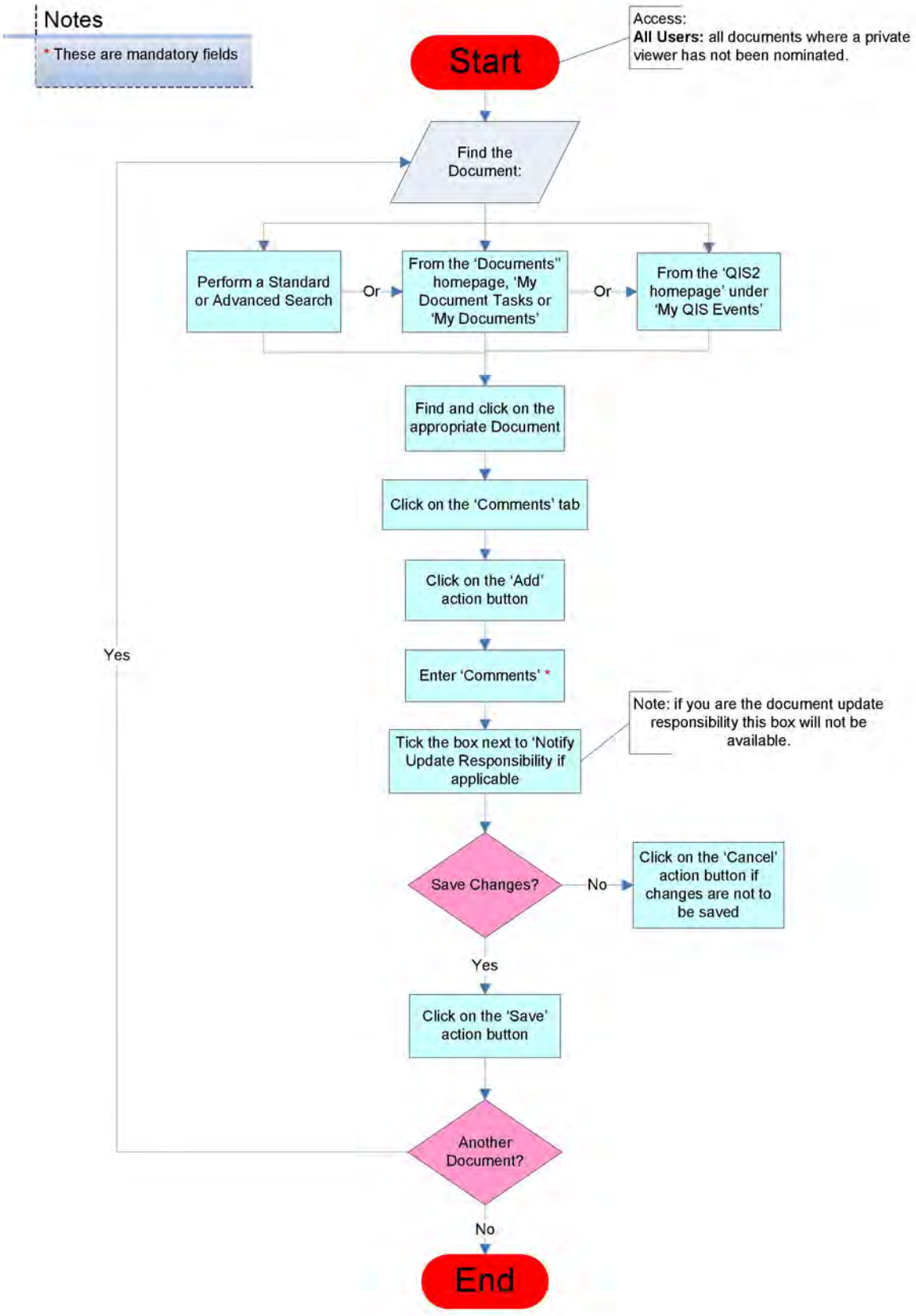
6.26 Delete 'OU' from Notification List



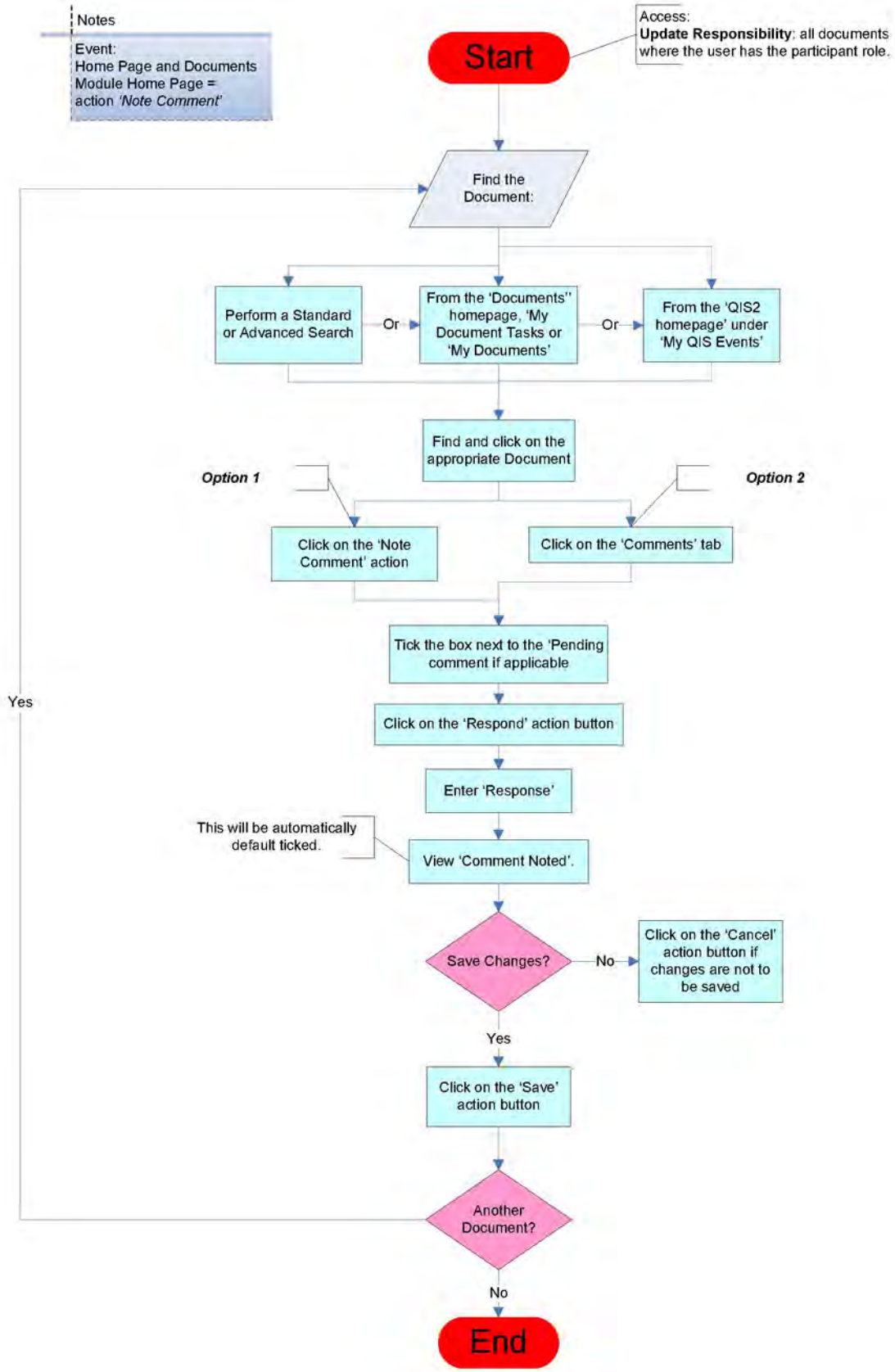
6.27 Delete Self from Notification List



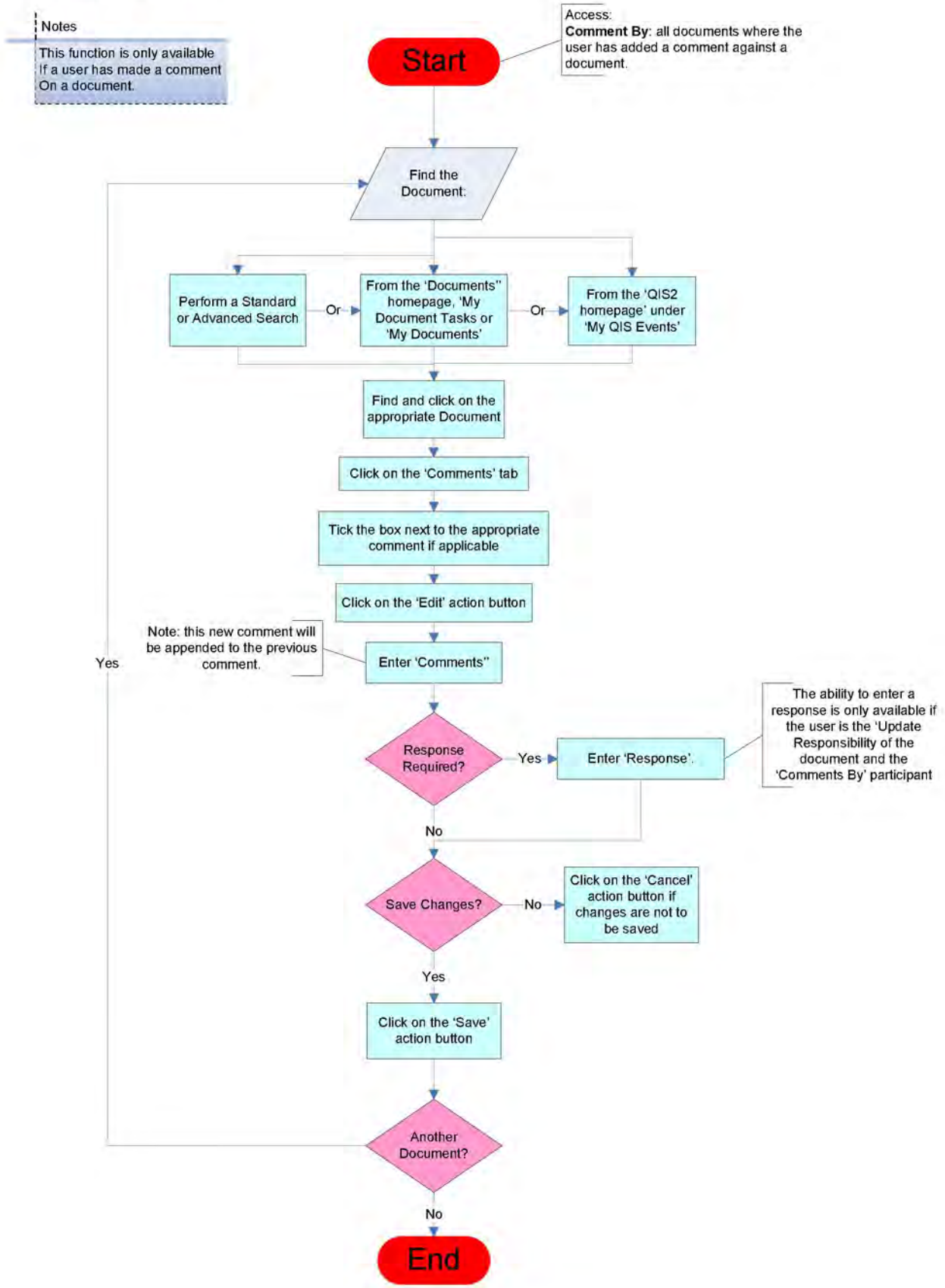
6.28 Add a Comment



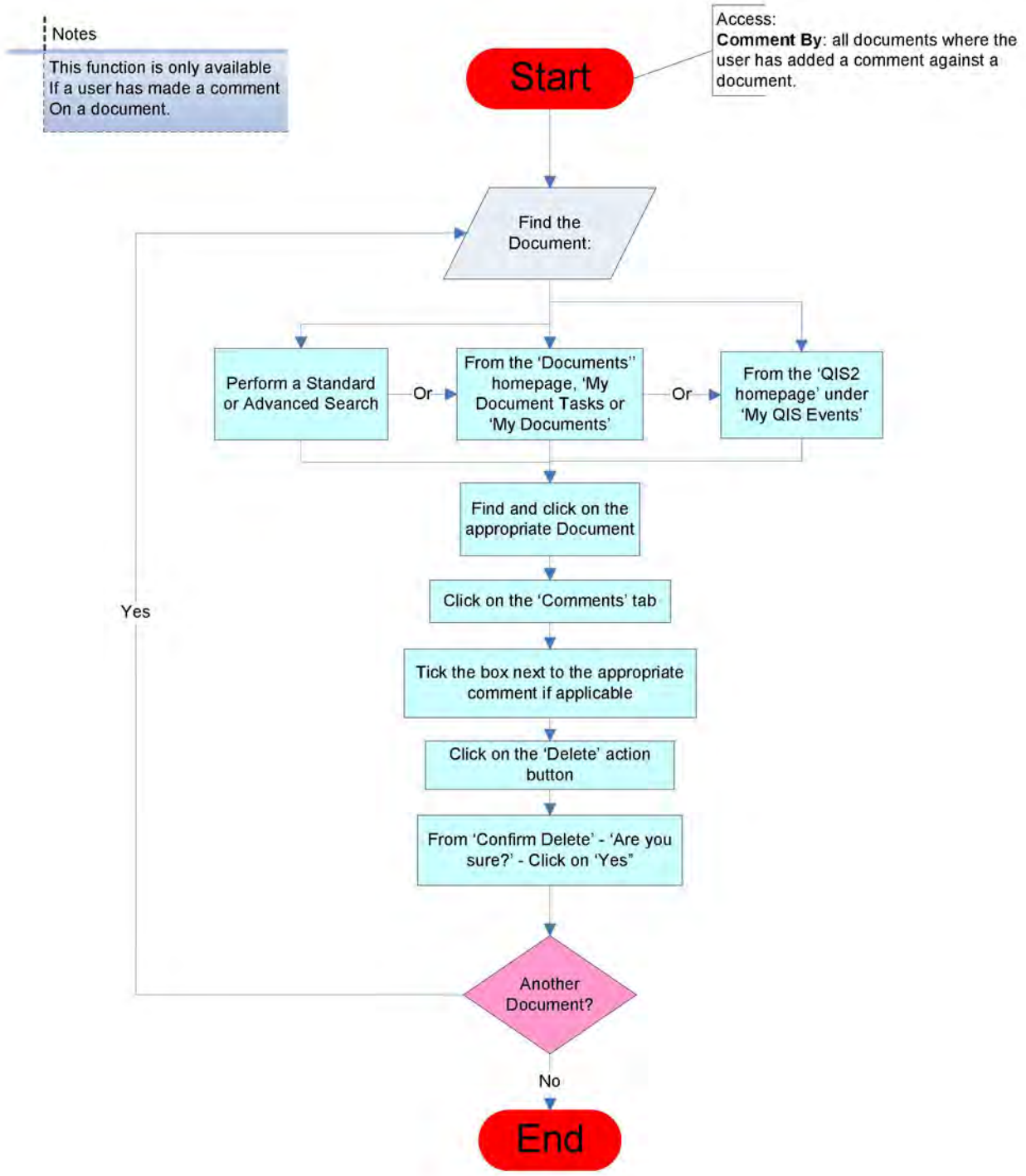
6.29 Respond to a Comment



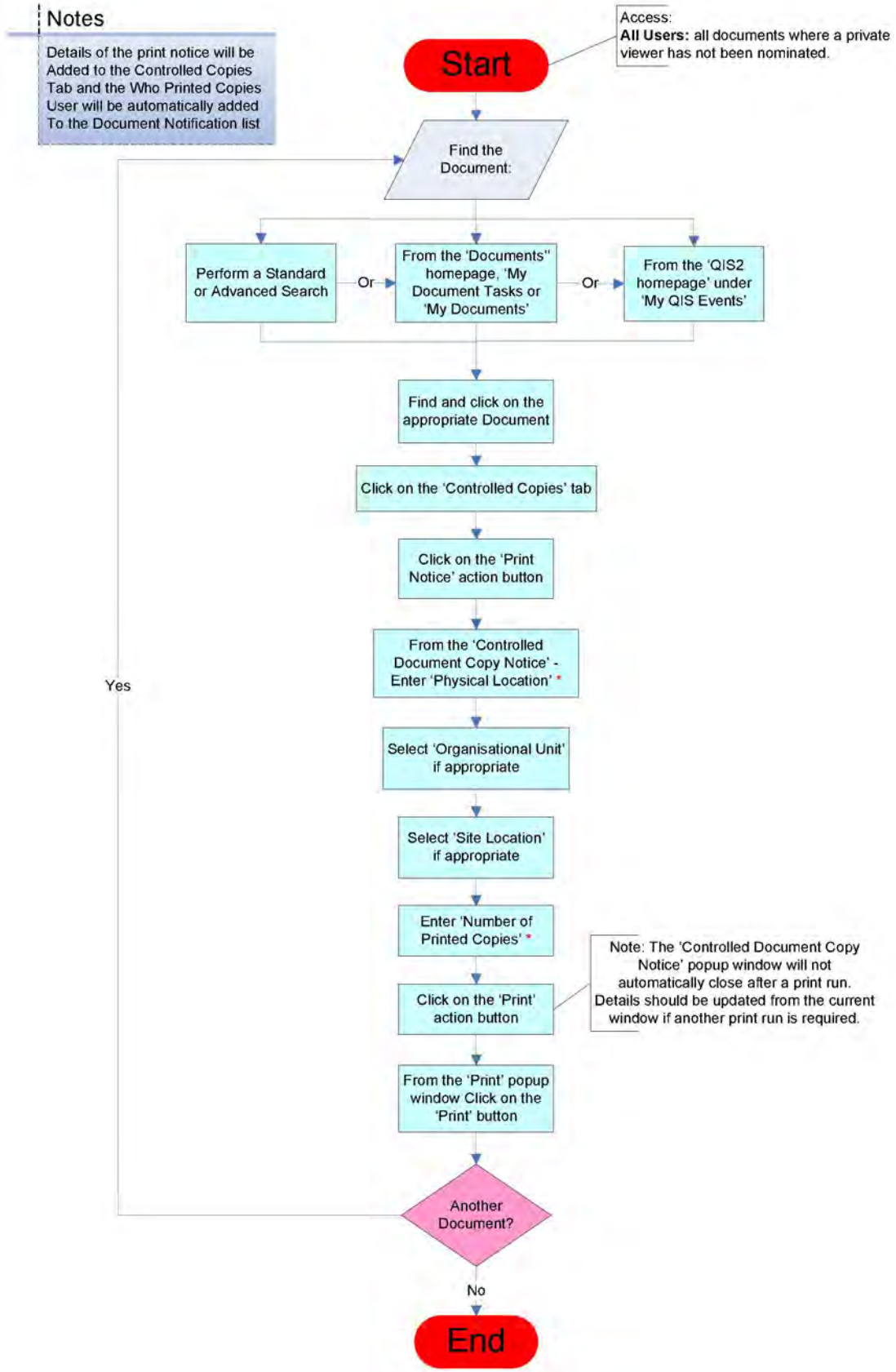
6.30 Edit Comments



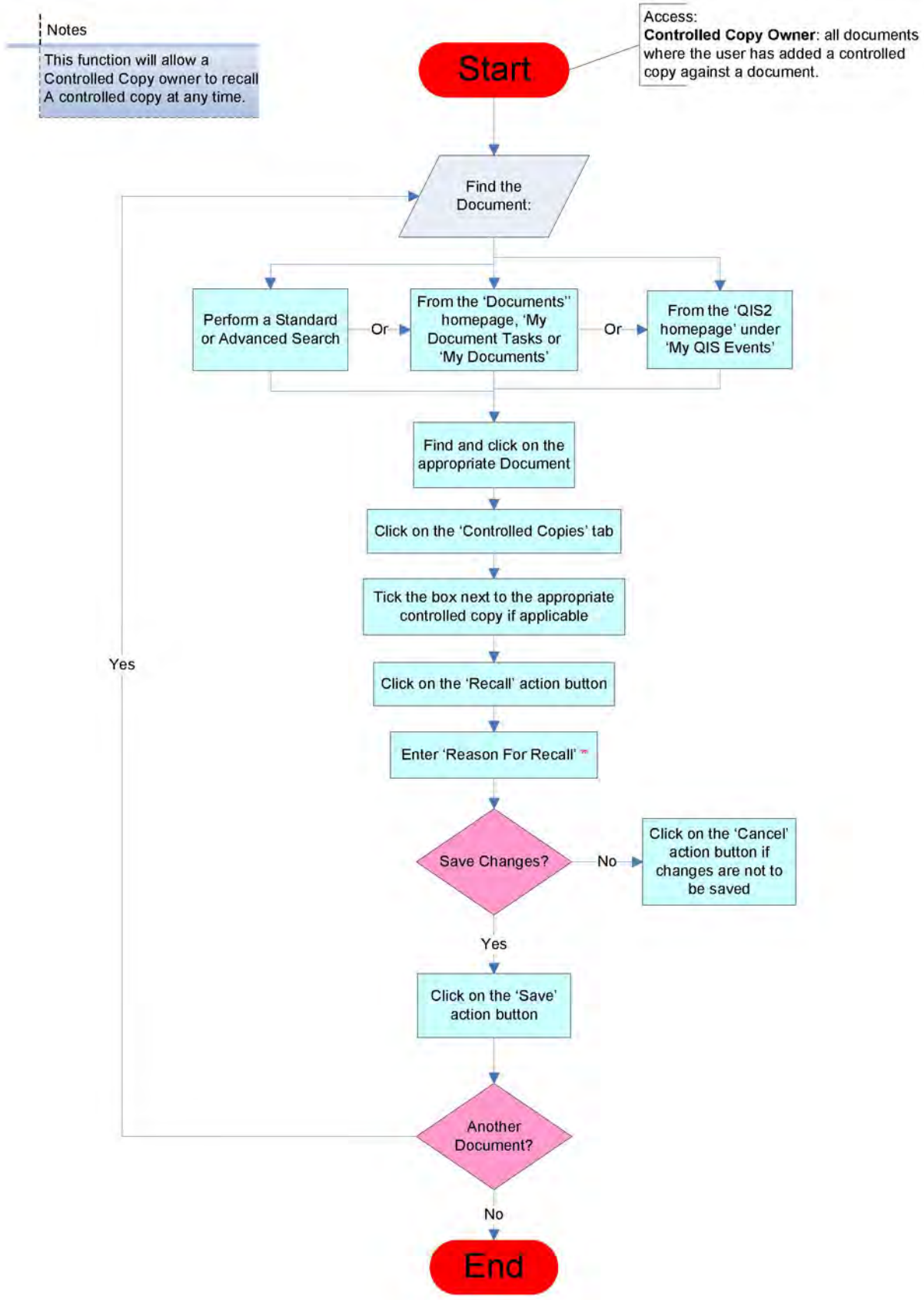
6.31 Delete Comment



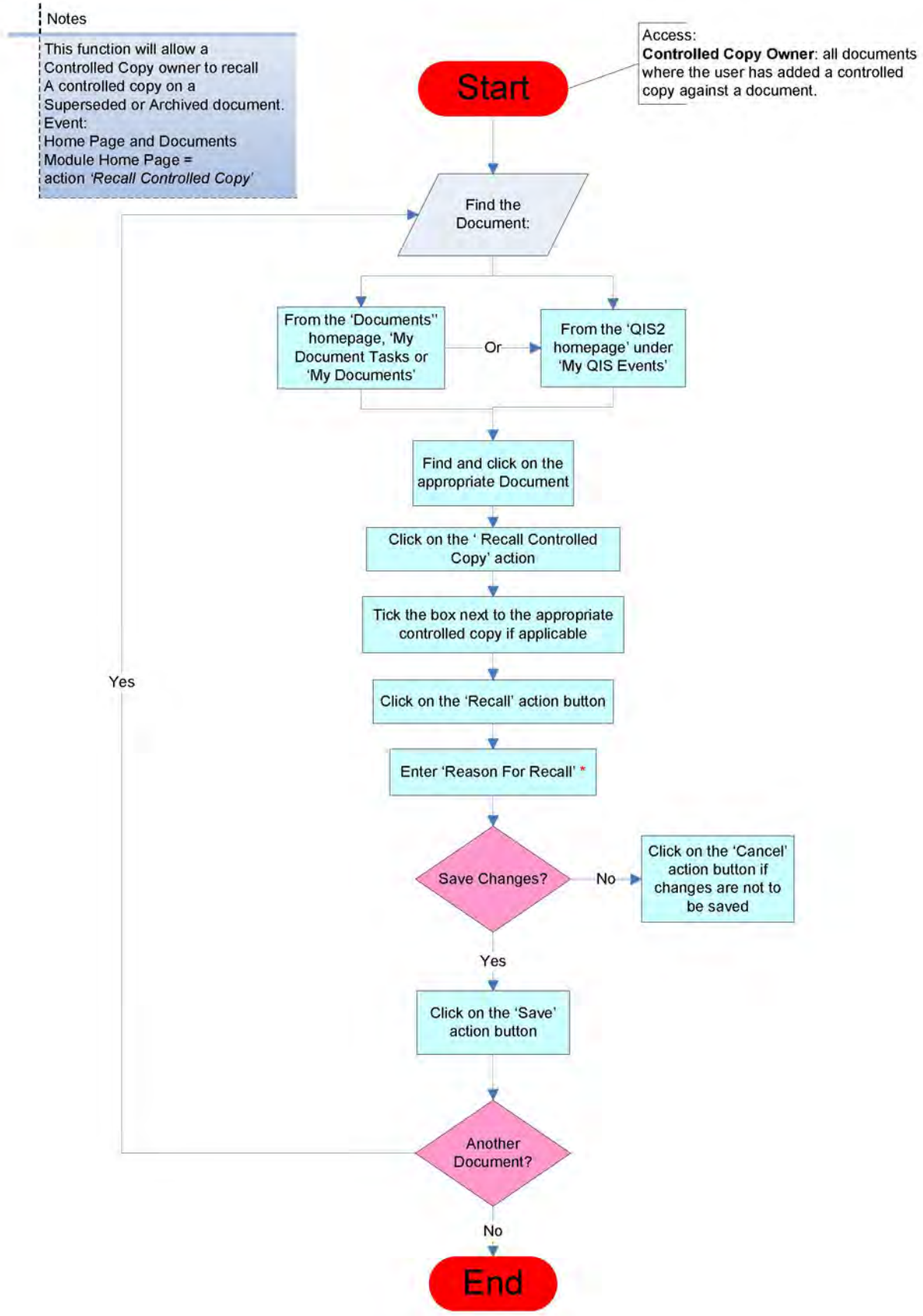
6.32 Print Controlled Copy Notice



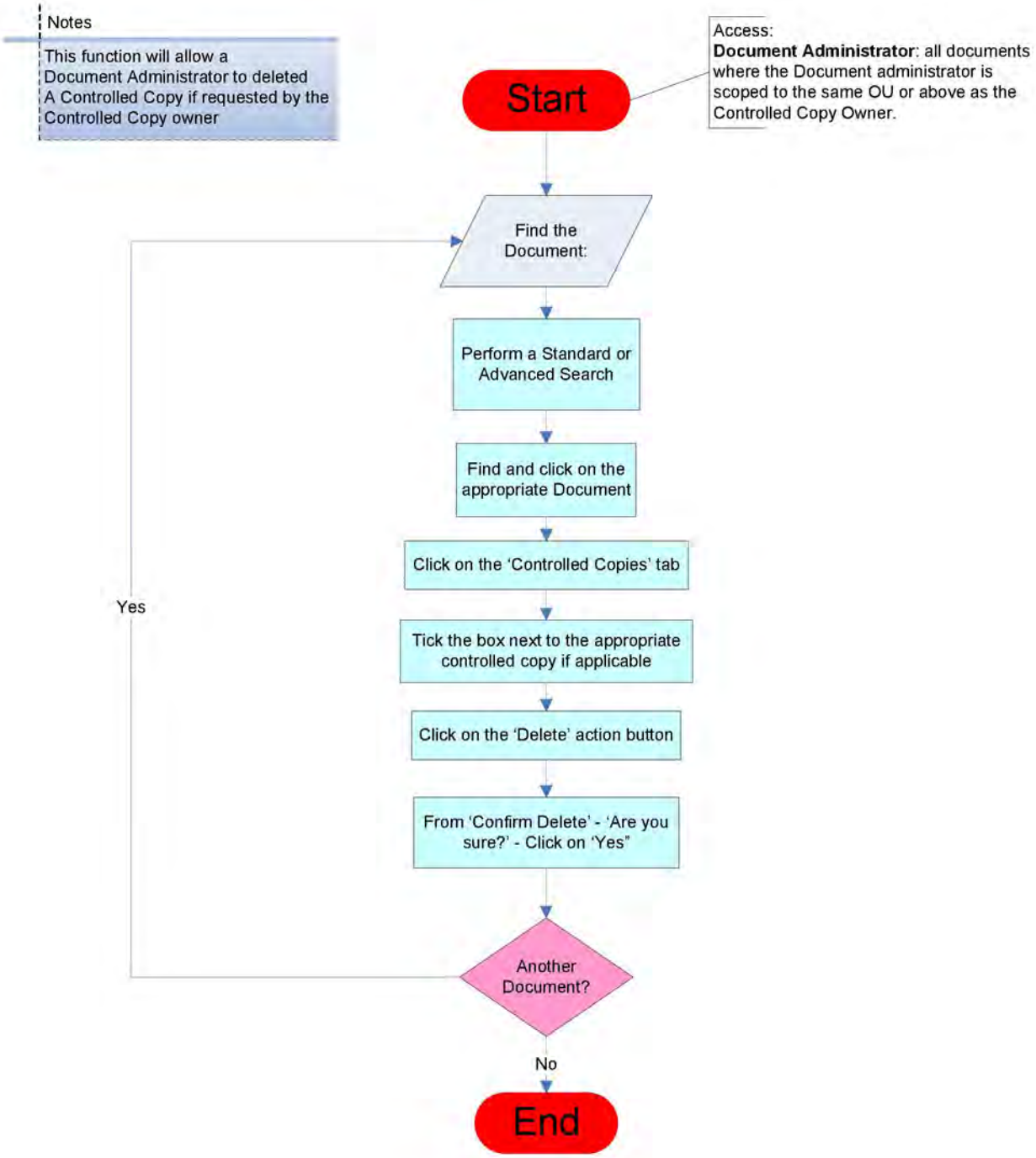
6.33 Recall Active Controlled Copy



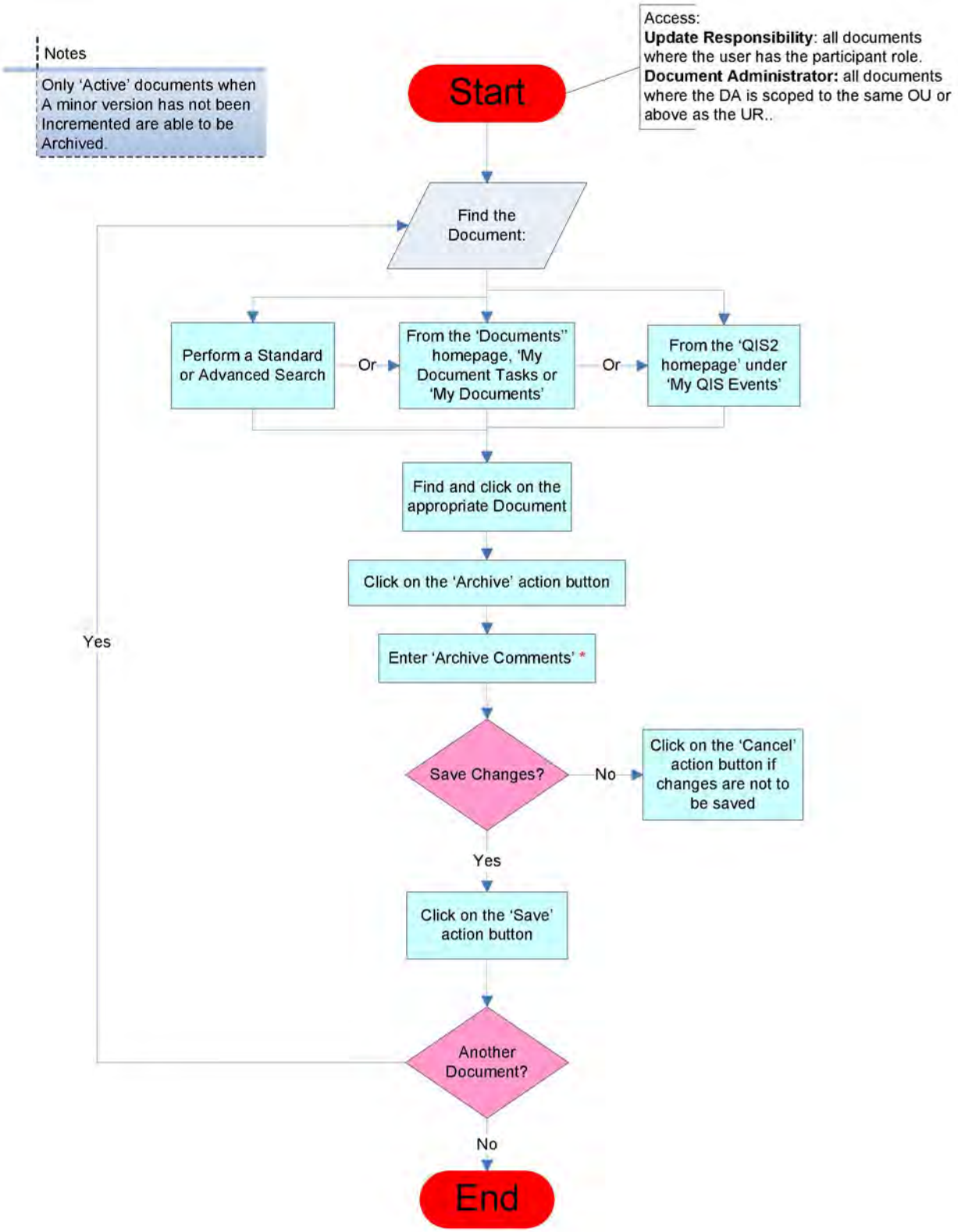
6.34 Recall Archived/Superseded Controlled Copies



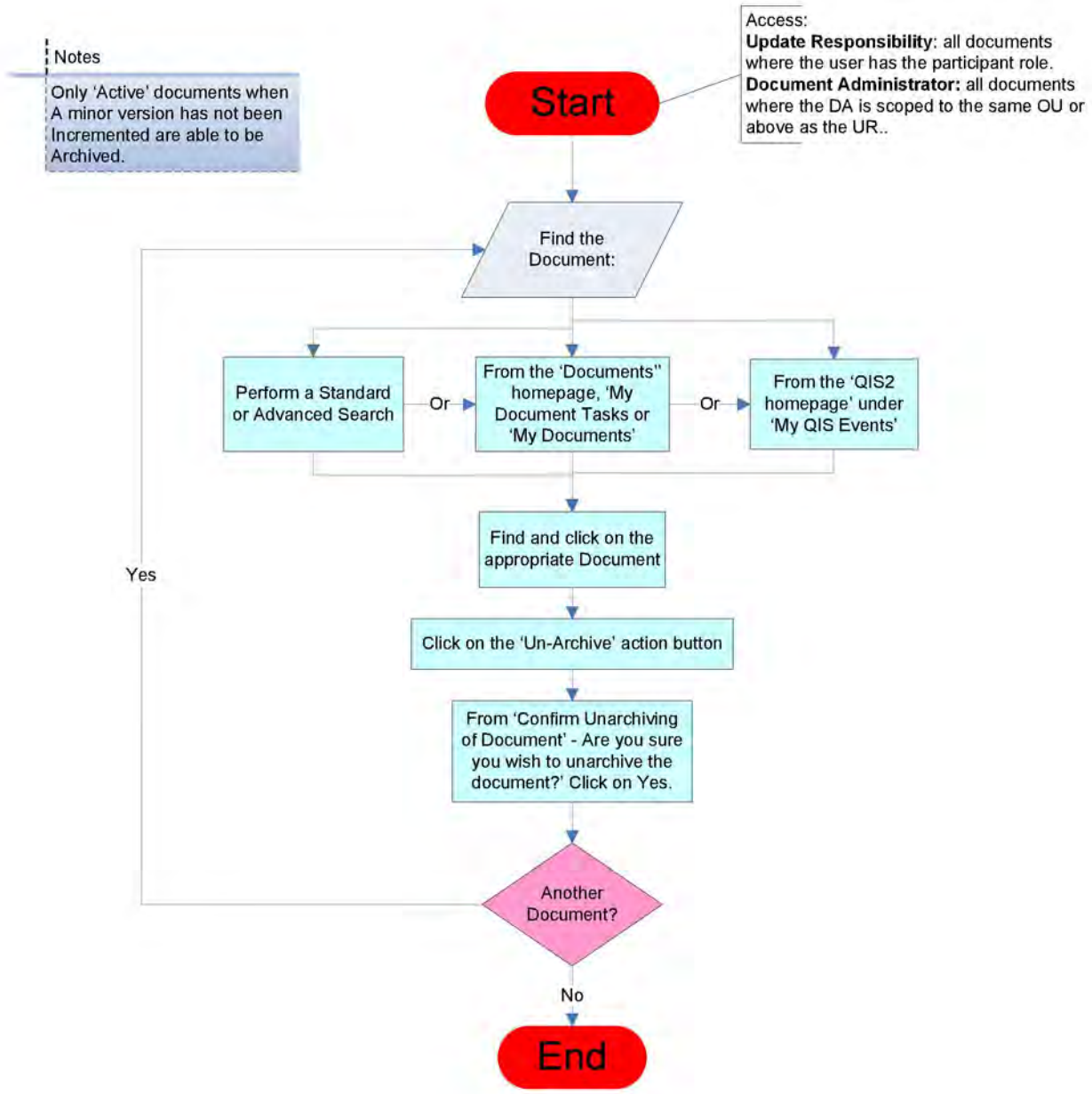
6.35 Delete Controlled Copies



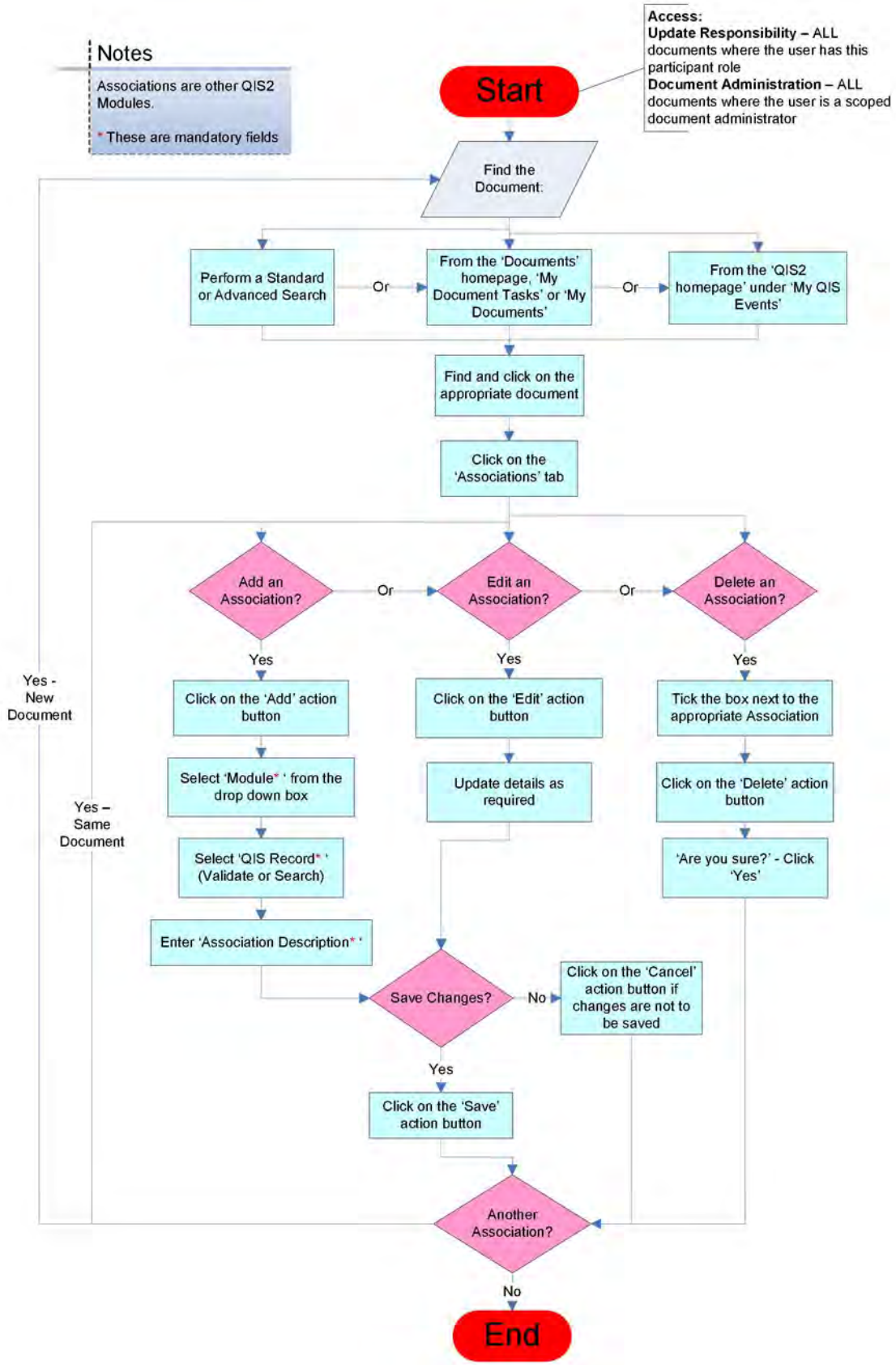
6.36 Archive a Document



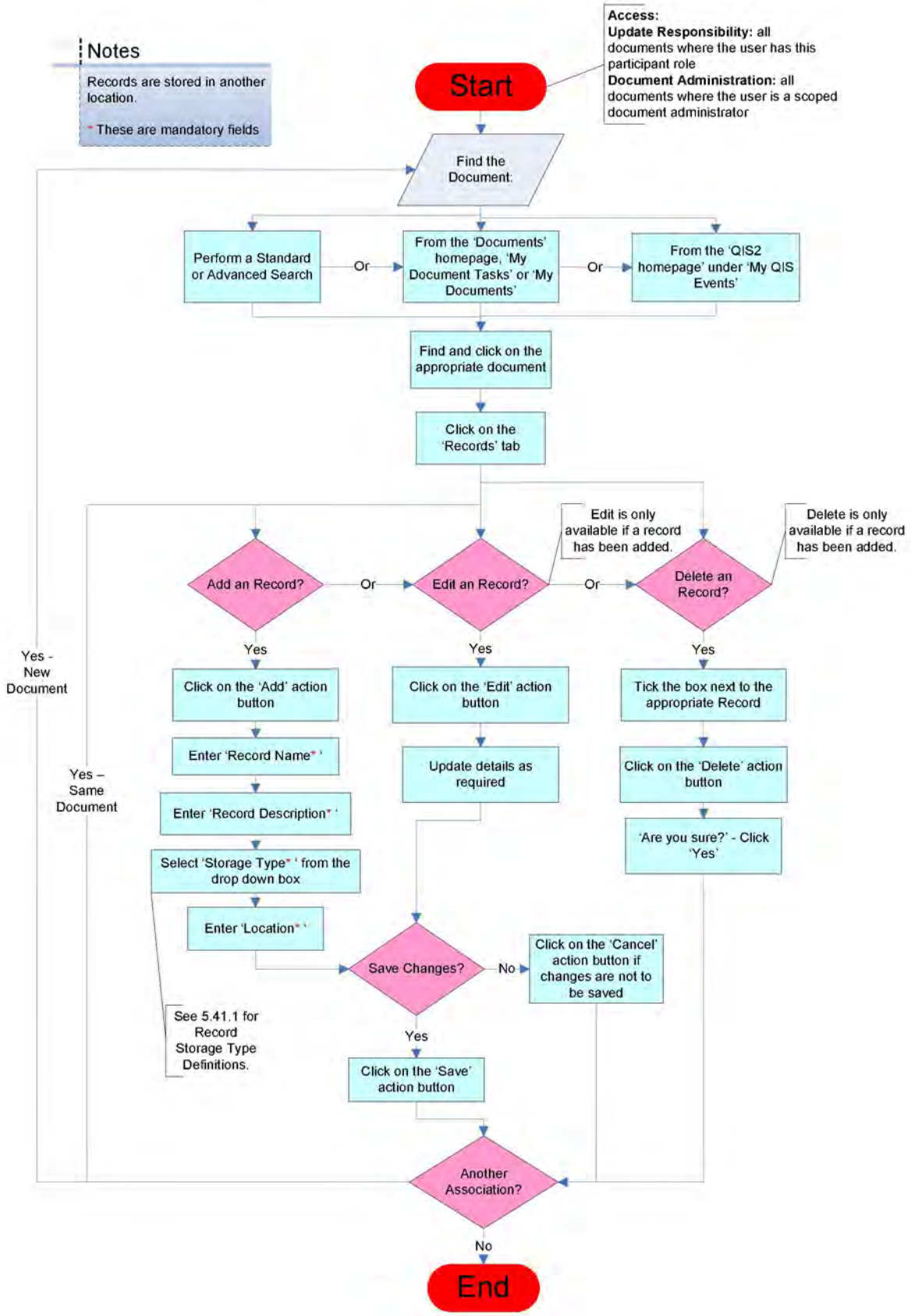
6.37 Un-archive a Document



6.38 Associations



6.39 Records


Notes
Records are stored in another location.
* These are mandatory fields
Access:
Update Responsibility: all documents where the user has this participant role
Document Administration: all documents where the user is a scoped document administrator
Start
Find the Document:
Perform a Standard or Advanced Search
Or
From the 'Documents' homepage, 'My Document Tasks' or 'My Documents'
Or
From the 'QIS2 homepage' under 'My QIS Events'
Find and click on the appropriate document
Click on the 'Records' tab
Add an Record?
Or
Edit an Record?
Or
Delete an Record?
Edit is only available if a record has been added.
Delete is only available if a record has been added.
Yes
Yes
Yes
Yes - New Document
Click on the 'Add' action button
Click on the 'Edit' action button
Tick the box next to the appropriate Record
Enter 'Record Name* '
Update details as required
Click on the 'Delete' action button
Yes – Same Document
Enter 'Record Description* '
'Are you sure?' - Click 'Yes'
Select 'Storage Type* ' from the drop down box
Enter 'Location* '
Save Changes?
No
Click on the 'Cancel' action button if changes are not to be saved
See 5.41.1 for Record Storage Type Definitions.
Yes
Click on the 'Save' action button
Another Association?
No
End

7 References

Nil

8 Associated Documents

10003 – Document Management Procedure
26213 – QIS2 User Manual – General (Home Page, My QIS & Support) Module
28179 – QIS2 User Manual – List Management
26214 – QIS2 User Manual – Reports

9 Amendment History

Version	Date	Author/s	Amendment
1	27 Feb 2009	Renee Corney & Roslyn Williams	First Issue
2	20 Mar 2009	Roslyn Williams	Minor addition page 25, 5.24
3	13 May 2009	Roslyn Williams	Minor addition to 5.24 & 5.31, correction to document footer; addition of 5.27 and 5.28 and respective workflows 6.26 & 6.27; minor addition to user matrix
4	May 2011	F Stewart	Major document updated. Document updated to included 2011 Quarter 1 release items.
Version	**Date**	**Updated By**	**Amendments**
5	Oct 2012	F Stewart	Update to document due to QIS2 September Release 2012 Updated to HSSA Template. Valid Date updated to Valid From. Advanced Search (including No Login) screen shot updated Advanced Search Workflow Notify Author/Update Responsibility updated – author removed (including workflow) Added 'Delete User' from Notification list
6	Oct 2014	F Stewart	Updated to HSQ template. 5.19.2 screen shot updated 5.37.2 screen shot updated Minor updates through out.
7	Jul 2020	F Stewart	Reviewed and updated, minor updates throughout. Updated HSQ logo Added reports section. Added reports manual to associations. Updated Definitions.

CA-66

HealthSupport Queensland
Forensic and Scientific Services

Processing DNA Exhibits/Samples

1 Purpose

The purpose of this procedure is to detail the process to be followed for processing DNA crime scene, reference and coronial exhibits in the Forensic Property Point. Processing includes:

- Receival of exhibits in AUSLAB and the FR
- Storage and handling
- Allocation and internal transfer
- Return and destruction

Exhibits are to be received in accordance with legal standards and requirements to ensure security and continuity of handling is maintained.

2 Scope

This procedure applies to all samples delivered to the FPP for testing in Forensic DNA Analysis by the Queensland Police Service. It applies to Property Officers, delegated administration officers and scientists who may receive DNA samples.

Work from private individuals, companies or other government departments will only be accepted if approved by the Managing Scientist – Police Services Stream.

3 Definitions

CRISP: Numbering system for QPS cases prior to 2007. Crisp number format is 2 digits for the year a slash then seven digits for the case number e.g. [redacted]

CSSE: Crime Scene Sample Envelope, these are envelopes used by the QPS labelled with all relevant case and exhibit information that contain small items or subsamples of items.

CCC: Crime and Corruption Commission

DVI: Disaster victim identification

Evidence Reference Samples: Reference samples taken for comparison to a particular case. Evidence samples may be included on the database if advised by the police.

Exhibits: collective term used in this SOP to refer to both items and tubes

FR: Forensic Register

FPP: Forensic Property Point

FSS: Forensic and Scientific Services

FTA: This is the acronym for Flinders Technology Australia. This is the company that produces the cards that preserve the DNA from a buccal (or cheek) swab. The standard FTA card packaging is a sealed envelope with the details of the person sampled on the front, inside the sealed envelope will be the FTA card. Each envelope should have a unique barcode attached.

HSPB: Heat sealed plastic bag

Intelligence Reference Samples: Reference samples taken for the purpose of inclusion on the database. These are not linked to a particular case.

Items: exhibits not subsampled by a Scenes of Crime or Scientific Officer. These items include swabs, cigarette butts, clothing, weapons, Sexual Assault Investigation Kits (SAIKs) etc.

JTC: John Tonge Centre

Kit D: Post mortem samples submitted for DNA analysis

Major crime: crimes against a person including murder, rape and assault

Occurrence Number: Numbering system for QPS cases from 2007 onwards. Number is prefixed with QP followed by 2 digits for the year then 8 digits for case number e.g. [redacted] Also known as QP Number

PHPP: Public Health Property Point

PM samples: post-mortem or coronial samples

QPRIME: Queensland Police information management system.

QPS: Queensland Police Service

QP127 Form used by the Queensland Police Service when submitting articles for forensic examination

SAIK: Sexual Assault Investigation Kit

SMU: Sample Management Unit

SSLU: Scientific Services Liaison Unit

SOCO: QPS Scenes of Crime Officer

Tubes: Eppendorf tubes that contain subsamples of crime scene exhibits

Volume crime: high occurrence, mainly property related crimes

4 Access

4.1 Conditions of Access to the Forensic Register

Access to and use of the QPS FR system is for authorised users only. Unauthorised access and use is strictly prohibited. By accessing or using this system you are acknowledging that you are an authorised user. You are NOT authorised to access information for personal reasons including curiosity or personal interest.

The information contained on this computer system is confidential and must not be disclosed to unauthorised persons. Improper disclosure of information is an offence, as outlined in section 10.1 of the Police Service Administration Act 1990 and the Code of Conduct for the Queensland Public Service 2011.

Misuse of information stored in the FR is serious. If you use QPS computer systems to access information not for a purpose connected with your duty, your conduct will be considered misconduct. The QPS will consider criminal charges being applied.

Malicious entry of false information is strictly prohibited. Any member who maliciously enters false information may be liable for misconduct.

Details of all transactions, including User-IDs, are automatically recorded by the computer system and will be regularly audited to ensure compliance. By accessing and using this computer system you are consenting to security monitoring.

All notations in the FR form part of the Queensland Health case file records and should be professional in manner. Note: All records within the FR may need to become available under Right to Information.

If you are ever uncertain about accessing information, ask a supervisor for advice before undertaking the activity. If you inadvertently enter an area that you shouldn't, it is a requirement for you to make a case note explaining the reasoning for accessing the data.

5 Procedure

5.1 General Requirements

Receiving exhibits shall be the responsibility of a Property Officer. Scientists may fulfil this function in the absence of or to assist a Property Officer.

When items are delivered to the FPP, the standard procedure must be followed. If any part of the procedure cannot be followed, all relevant information should be noted in the Forensic Register and brought to the attention of the Supervisor or delegate. It may be necessary to raise an OQI.

5.2 Safety and Contamination

To reduce the risk of contamination, primary packaging is not to be opened in the FPP. The only exceptions are Sexual Assault Investigation Kits (SAIKs; are to be opened to retrieve medical notes and any samples for toxicology only) and Kit Ds containing coronial samples, in these instances items from different cases must not be handled at the same time.

Property Officers are to wear gloves when handling the items and the bench is to be washed down with alcohol solution and gloves changed between handling different exhibits.

Appropriate gloves, safety glasses and personal protective equipment (PPE) should be used if necessary when handling items. If knives, syringes or other sharps are received, ensure they are safely packaged in accordance with Australian Standards and labelled with appropriate stickers to warn others.

The FPP is equipped with a biohazard cabinet and a spill kit that can be used if necessary. Any exhibit for submission to FSS that is not packaged correctly according to NATA standards and Workplace Health and Safety guidelines will be refused.

5.3 Receiving Crime Scene Exhibits from the Queensland Police Service

5.3.1 Methods of Delivery

Crime scene exhibits from the QPS can be delivered to the FPP one of two ways:

1. Delivered personally to the FPP front counter by the Investigating officer or designated delivering officer, including Scenes of Crime Officers or Scientific Officers.
2. Sent via Registered Australia Post from Scenes of Crime Offices. These are delivered to FSS on the regular Australia Post mail.

NOTE: *Property Officers will endeavour to receive DNA exhibits delivered by Australia Post as soon as practicable; however in some circumstances DNA exhibits may be stored in a secure location to await registration and receipt at a later time.*

5.3.2 Case Requirements

All cases submitted to FSS by the QPS must have an occurrence (QP) number or CRISP number when old cases are resubmitted. This includes internal investigations, whilst no case information need be put on the QPRIME system an entry is to be made to create a valid QP number. Cases without a QP number will not be accepted under any circumstances unless first approved by the Managing Scientist – Police Services Stream.

5.3.3 Standard Packaging Requirements

QPS sub-sampling procedures apply to any crime scene exhibits and hair samples requiring DNA testing. The requirements are that all whole items, including hair samples must be submitted / screened prior to being lodged at FSS. Sub-sampled exhibits must be packaged in CSSE by SOCO or Scientific Officer. FSS will not accept whole exhibits or unscreened hair samples without the prior authorisation of the Inspector of the QPS DNA Management Section, the Inspector of the QPS Scientific Section or a delegate with the following exceptions:

- SAIKs
- Syringes
- Washed items for semen confirmation.

Smaller whole items such as chewing gum, cigarette butts, condoms, tampons and sanitary pads will still be accepted provided that they are packaged in a CSSE.

5.3.4 The Forensic Register and Barcoding Requirements

All exhibits must be received at FSS labelled with a grey Forensic Register barcode. This barcode is allocated and affixed to the exhibit/packaging by a SOCO or Scientific Officer. The exhibit should have been entered onto the QPS Forensic Register prior to arriving at FSS.

Upon scanning the FR barcode if no data is available in the Forensic Register the delivering officer is to contact the relevant SOCO and confirm that that the FSS DNA Analysis examination section box has been ticked, or the NTR (No Testing Required) box has been unticked. In the case of exhibits sent via Australia Post, FPP property officers can contact the relevant Scenes of Crime Office or the QPS Sample Management Unit prior to receival.

5.3.5 QP127 Submission of Articles Form

Exhibits requiring Forensic DNA analysis do not require an accompanying QP127 Submission of Articles Form. FSS is directly using the Forensic register and information contained within; the quality of the data in the Forensic Register rests with the QPS.

NOTE: *If the packaging of a crime scene exhibit is not correct according to NATA or Workplace Health and Safety standards FSS Property Officers can reject the item and insist on having a QP127 completed and signed off by a police forensic 'Scenes of Crime' officer to indicate that the exhibits have been checked for correct packaging, labelling and appropriate case information.*

At times QP127 forms are completed by QPS officers, these forms are to be scanned and added to FR as a Case File Notation.

5.3.6 Dual Analysis

If an exhibit needs to be examined by two or more laboratories (eg. Forensic Chemistry and Forensic DNA Analysis) refer to 25459 Dual Analysis of Forensic Exhibits.

5.3.7 Handling Exhibits Pre-Receipt

Primary Packaging – exhibits delivered by Australia Post

Primary packaging (i.e. the packaging containing the actual exhibit) of exhibits delivered by Australia Post must be visually inspected to ensure that the exhibit packaging is intact if it is identified that packaging is not intact, primary packaging must be resealed and a note must be added as a casefile notation in the Forensic Register

Primary Packaging – exhibits hand delivered

Primary packaging (i.e. the packaging containing the actual exhibit) must be visually inspected to ensure that the exhibit packaging is intact. If it is identified that packaging is not intact it is to be handed back to the delivery officer to be repackaged appropriately.

Primary packaging (i.e. the packaging containing the actual exhibit) must not be opened unless absolutely unavoidable. Any packages where the primary packaging is opened and sealed upon receipt are to be signed "opened by ….. time & date".

The only exhibits opened by Property Officers as a standard are SAIKs. This is done to retrieve the examination notes which are forwarded to Forensic DNA Analysis for the casefile and remove any blood and urine samples which may have been included in the kit.

Blood and/or urine samples contained within a SAIK requiring analysis by Forensic Toxicology must be removed and received in accordance with 21118 Receiving samples for analysis by Forensic Toxicology.

If a blood and/or urine sample is removed from a SAIK at time of receipt a notation is to be entered into the Forensic Register stating: SAIK opened at time of receipt and blood and or urine sample contained within was removed and receipted for analysis by Toxicology.

DNA reference blood samples collected at time of SAIK examination are to be removed from the SAIK at time of receival. The FPP Property Officer is to check with the QPS DNA Sample Management Unit (SMU) if the sample is required for analysis. In most instances an FTA Reference sample has been collected and is the preferred option for analysis. In this case the blood sample is to be returned to the delivery officer and a case file notation is to be entered into the Forensic Register stating: "Blood sample/s obtained for DNA analysis removed from SAIK and returned to Delivery Officer (Insert name) as FTA Reference Sample obtained for this purpose".

If the QPS DNA SMU advise the blood is required for analysis it must be registered as a separate exhibit in the Forensic Register as per ***Appendix 3***.

5.3.8 Pre- Receipt Checks

1. Ensure all items requiring Forensic DNA Analysis have been labelled with the QPS Forensic Register barcode.
2. Check all items are dry. Items are only received wet after consultation with a Scientist, they are to be wrapped in plastic and placed immediately into the FPP Vault Freezer for transfer to the Forensic DNA Analysis Exhibit Freezer as soon as practical.
3. All exhibits must be packaged according to Workplace Health and Safety guidelines and NATA standards.

If any of these requirements have not been met FSS Property Officers can reject the items until the acceptance criteria are appropriately met. If items are rejected, the reasons must be communicated to the delivery officer and recorded as a casefile notation in the Forensic Register.

Cases with urgent priorities may be accepted even if they have not met the criteria after consultation with the QPS DNA Management Unit and/or Forensic DNA Analysis.

If QPS exhibits not meeting the requirements are received a Case Management task can be created in the Forensic Register and assigned to the collecting SOC officer.

5.3.9 DNA receival process.

FSS now use the Queensland Police Service Forensic Register to receive all DNA samples. In most instances all exhibits will be pre-registered prior to arriving at FSS.

See **Appendix 1** for DNA exhibit receival process.

5.3.10 LIMS Downtime

During Forensic Register down-time or extreme system slowness a manual receipting system is employed in accordance with 23263 FPP Laboratory Information Management Downtime Procedure. When the Forensic Register is available the exhibits are to be received and stored, the manual receipt is to be scanned into to the Forensic Register and attached to a CM request. Detailed notes are to be added to the CM request.

If an error is made during the manual receival / receipting process a manual forensic receipt is issued with incorrect information an amended receipt is to be issued in accordance with 26040 Procedure for Amended Receipts. This can be done either by the Property Officer who issued the original receipt or the person who discovered the error.

5.3.11 Environmental Samples

Environmental samples are sent by Scenes of Crime Officers and are swabs from their laboratories to ensure cleaning and contamination control measures are effective. See **Appendix 1** for receival process.

5.3.12 Storage of Exhibits Post-Receival

All items and tubes are stored individually by the Forensic Register barcode within the Forensic Register. Some exhibits require freezing after receipt, they are:

- Sexual Assault Investigation Kits (SAIK's)
- Food stuffs of any kind
- Tissue samples including flesh
- Used condoms, sanitary pads or tampons
- Wet items

These exhibits are to be heat sealed in plastic and Forensic Register barcode written on the exterior of HSPB prior to being placed in the freezer. All other exhibits are stored at room temperature in the packaging they are delivered in.

Exhibits for room temperature storage are separated and stored according to the type of exhibit (either item or tube). Plastic boxes are available for storage and are labelled for the two different types of exhibit:

- In-tubes storage box
- Items storage box

All boxes used for exhibit storage are to be stored to the FPP storage bench (mnemonic FPPB-DNAT-0001) when in use. See **Appendix 6** for storage process. If an item is received that is too large to be placed in an items box it is to be stored directly to the FPP storage bench.

All secondary packaging (envelopes, paper bags etc) must be ripped completely open before disposal to ensure no samples are still contained within and then shredded.

5.4 Manually Receiving NON QPS DNA crime scene exhibits

On occasion DNA exhibits may need to be manually registered and received in the FR. Exhibits that will require manual registration in the FR may be lodged by private clients or the Crime and Corruption Commission. See **Appendix 6**.

5.4.1 Submission of Coronial Samples

Coronial samples are submitted for DNA testing in relation to a homicide / suspicious death investigations, identification of unknown deceased or Disaster Victim Identification (DVI) investigations.

5.4.2 Methods of Delivery

Coronial samples (otherwise known as Post-mortem/PM samples) are delivered to the FPP in one of two ways:

a. Samples from autopsies conducted at QHSS Forensic Pathology are delivered to the FPP by a staff member of Forensic Pathology.

b. Samples from autopsies conducted at external mortuaries are sent via courier and initially received at Public Health Property Point (PHPP), The samples are then transferred via esky tracking to the FPP for receival.

NOTE: *ALL Samples delivered via esky tracking, needs a notation added in the "Exhibit Note & FSS Advise" with esky tracking number, who delivered, and what sections they are from*

5.4.3 Receiving Coronial Samples from QHSS Forensic Pathology

Coronial Samples delivered from QHSS Forensic Pathology are to be packaged in a HSPB with the seals signed and dated by a Morgue Attendant. FTA cards and Reference Bloods are to be separated and each registered as its own exhibit in FR as per **Appendix 4.**

Each item delivered is to be received on the FBTRAN page in AUSLAB prior to being registered in the FR. **See Appendix 14.** Once the FBTRAN page has been completed samples are to be registered in FR as per **Appendix 4** 10.4.1 and **Appendix 5** 10.5.1

Coronial cases are typically recorded in FR under the Occurrence (QP) Number. In some cases, a Case File may not have yet been created as there have been no previous

Forensic Samples registered. If a search for the Case File in FR under the occurrence number fails, the Property Officer can contact QPS DNA Unit to determine if a Case File exists or to send the recipient a CM request that allows FSS access to the Case File. If no Case File exists, the Property Officer is to create a Case File as per **Appendix 6.**

PM Samples from external / regional mortuaries can be registered directly into FR as per **Appendix 4** 10.4.2 and **Appendix 5** 10.5.2. If no Case File exists, the Property Officer is to create a Case File as per **Appendix 6.**

5.4.4 Packaging Post-Receipt

Coronial samples receipted for DNA Analysis are to be packaged in a HSPB and seals signed and dated by Receiving Property Officer. The exhibit barcode is to be positioned on the packaging where it can be scanned, and the exhibit number written on the HSPB with a black marking pen. The samples are to be stored immediately to the FPP vault freezer and transferred to the DNA Analysis Exhibit Freezer as soon as possible. Reference samples are kept separate and stored to the FPP storage bench (mnemonic [redacted] and transferred directly to DNA Analysis for profiling as soon as possible.

5.5 Receiving DNA Reference Samples

5.5.1 General Information and Requirements

1 Reference Samples from the QPS DNA Management Unit:

Most DNA Reference Samples are delivered or posted from members of the QPS around the state directly to the QPS DNA Sample Management Unit (i.e. not to Queensland Health). Reference samples must be submitted through the QPS DNA SMU for quality checking and are then delivered by the DNA SMU to the FPP for processing. These samples are received as per **Appendix 2**.

The DNA Management Unit delivers Intelligence and Evidence samples to the FPP on a standard schedule. Deliveries outside this schedule are to be negotiated between the parties.

Reference samples are labelled with a unique barcode number and all sample information is available in the Forensic Register.

Reference sample types may include:

- Blood samples
- Hair
- FTA cards with buccal cells
- FTA cards with blood
- Swabs

Intelligence and Evidence Reference samples are often received together in bulk and can be a mixture of FTA cards containing buccal cells, swabs, hair samples or blood samples.

NOTE: *Any FTA sample that transfer as **RED** need to be given back to the delivery person.*

2 Crime and Corruption Commission (CMC) and Ethical Standard Command Samples (exception1):

Reference samples being delivered by the CCC or QPS Ethical Standards Command are an exception in that they are not processed through the QPS DNA Management Unit. These samples delivered directly to the FPP and are received manually in a similar fashion to reference blood samples in accordance with **Appendix 3**. This is an uncommon event and advice should be provided regarding these samples prior to delivery.

3 Post Mortem Reference Samples (exception 2):

Post mortem reference samples are received directly from the Coronial Support Unit or Forensic Pathology in accordance with **Appendix 4**. PM reference samples are not handled by the QPS DNA Sample Management Unit.

5.5.2 Packaging

1 FTA DNA Kits: Return any attached property tags or documentation to the QPS DNA Sample Management Unit. FTA DNA Kits do not require any further packaging.

5.5.3 Storage

1 Each sample needs to be stored with in the Forensic Register to a barcoded FTA storage box.

2 These boxes are stored on the FPP Storage Bench [redacted] to await transfer to Forensic DNA Analysis.

3 Blood samples are tracked and stored to the FPP fridge [redacted] in the vault to await transfer to Forensic DNA Analysis.

5.6 Transfer to Forensic DNA Analysis – The DNA Run

Morning Run 9:30am and 3pm daily all samples received for DNA testing during that day are transferred to Forensic DNA Analysis on "The DNA Run".

During the DNA Run the following jobs are performed by the rostered Property Officer:

- Boxes of DNA Crime Scene Samples and whole items (eg. SAIKs) received on that day are transported to Forensic DNA Analysis.
- Boxes of DNA Reference Samples received on that day are transported to Forensic DNA Analysis.
- DNA Scientist will create an exam request task to request items be retrieved from main storage areas and transferred to DNA Analysis. Exhibits requested by scientists via an exam request task are to be retrieved and allocated daily.
- Exhibits returned from scientists' post-analysis are collected and returned to general storage in either the exhibit room or the FPP Block 8 Undercroft Freezer.
- Empty Crime Scene or Reference sample boxes are returned to the FPP for re-use. These must be transferred in the FR to location (Returned FPP)

NOTE: *All DNA samples delivered after 3pm is to be stored in DNA cupboard for next day's delivery. A notification/message is to be sent via DNA TEAMS chats.*

5.6.1 Preparing for the DNA Run

1 DNA analysis will create an exam request task and tick the request radio button in the FPP Allocation field in the FR. This request will appear on the Allocation – DNA list in the FR. The FPP staff member rostered to complete the DNA run must check the Allocation – DNA list and action if required.

2 The Worklist can be printed and retained with FPP (only if any items for DNA Analysis have been requested). Items requested are to be collected if they are in PP storage (either the Block 8 Undercroft or Vault freezers).

3 The Exhibit Room Returns (FDNA-EXRT-0001) and Freezer Returns (FDNA-RTFZ-0001) shelves can be printed to provide a hard copy of samples being returned from testing.

5.6.2 The DNA Run

1 Rostered Property Officer escorts the DNA samples to Forensic DNA Analysis entering through the second door so as not to take samples through the administration area of the section.

2 In the Exhibit Room the Property Officer logs onto the Forensic Register using one of the available computers to complete storage transfers as they occur. See **Appendix 8** for instructions on how to store storage boxes and items to a fixed location.

3 Allocating in Exhibit Room:

a. Crime Scene Sample boxes and whole items for room temperature storage are transferred to daily shelves in the exhibit room compactus. All shelves are barcoded with the storage location, use this mnemonic for storage.

b. SAIKs, requested coronial samples and other frozen items are transferred to one of the drawers in the DNA Analysis exhibit freezer. All freezer storage locations are barcoded with the storage location, use this barcode for storage.

4 Return to PP Controlled Storage:

Items received after 1st July 2008 that were subsampled by QPS will only be returned to general storage if no testing was required or part of a subsampled item (eg, fabric, hair etc) still remains.

If the sample has not been consumed in analysis the Scientist will repackage the exhibit for return to general storage or processing for return to the originating QPS establishment.

Scenario 1: Exhibits lodged and managed in Auslab lodged prior to FR implementation

See 17116 Processing DNA Exhibits / Samples in the Forensic Sciences Property Point.

Scenario 2: Exhibits managed in the Forensic Register post FR implementation

The scientist will store the exhibit or item into the [redacted] storage shelf (Forensic DNA Analysis Exhibits Returns shelf) or storage boxes located on the returns shelf in the Forensic DNA Analysis Exhibit room. Freezer returns will be located in the DNA Analysis exhibit freezer in location [redacted] (Forensic DNA Analysis Freezer Returns) location in the Freezer.

NOTE*: Only Sexual Assault Kits, food, tissue samples, coronial samples etc. require continued freezing and there should be the only items returned to* [redacted] *post analysis.*

Room temperature items (i.e. those that were in [redacted]) are physically transferred to storage shelves, storage boxes within the Exhibit Room or are processed for return to the originating QPS establishment. This action must be accompanied with the transfer of the storage location in the Forensic Register. Frozen items are to be taken back down to the FPP for storage in the FPP Block 8 Undercroft Freezer.

5.6.3 Completing the DNA Run

Scenario 1: Exhibits lodged and managed in Auslab prior to FR implementation

See 17116 Processing DNA Exhibits / Samples in the Forensic Sciences Property Point.

Scenario 2: Exhibits managed in the Forensic Register post FR implementation

1 The Property Officer is to return to the FPP with the empty storage boxes and any items requiring ongoing freezing. These items are then physically transferred to storage shelves or boxes in the Block 8 Undercroft Freezer. This action must be accompanied with the transfer of the storage location in FR as per **Appendix 7**.

2 Empty storage boxes are then transferred in the Forensic Register back to FPP by listing the location as "Returned FPP".

3 Any hard copy returns lists are then initialled and dated by the rostered Property Officer and scanned to be stored electronically in the FPP if required in the future. Hardcopy

returns lists are to be shredded once scanned. (Electronic retention of these lists is required as per ISO9001.)

5.7 Storage Post-Analysis

All items are kept in the Exhibit room or Block 8 Undercroft Freezer storage until returned to the investigating or delegated officer.

5.8 Return and Destruction of DNA Crime Scene Exhibits

Most crime scene items submitted after 1st July 2008 have been sub-sampled by the QPS under their procedures. Sub-sampled items that have been tested in Forensic DNA Analysis are either consumed during analysis or, if some sample remains, retained in Forensic DNA Analysis. All associated packaging is routinely destroyed by Forensic DNA Analysis for these samples (see Forensic DNA Analysis SOP 17142 Examination of Items). In this case FSS Property Officers never regain possession of the item.

Items requiring return to the QPS are:

- Whole items (fabric samples, SAIKs etc)
- Subsampled items that were not tested
- Items submitted pre-July 2008

NOTE: *To process exhibits received and analysed in AUSLAB for return see QIS document QIS 17116 Processing DNA Samples / Exhibits in the Forensic Sciences Property Point.*

Any exhibits that have been received and analysed in the Forensic Register that is required to be returned after analysis will be stored to a returns location within the DNA Analysis exhibit room (i.e [redacted]) Once these samples are stored to a returns location the property officers are then required to process these samples for return to the originating station. See **Appendix 12**.

FPP do not store exhibits for an extended period of time unless the Managing Scientist or delegate of Forensic DNA Analysis approves long term storage due to investigative needs.

Once advised items are ready for collection it is the responsibility of QPS Property Officers to make arrangements to have exhibits picked up from FSS. Ideally, exhibits should be collected from FSS within 30 days of analysis being completed.

DNA exhibits for the return to originating QPS Station

Upon completion of DNA examination exhibits will be stored to returns shelves within DNA Analysis; these shelves are cleared by property officers as soon as practical and processed for return.

DNA sub-samples can be requested to be returned to the client for examination by external agencies. The transfer of these sub-samples is the responsibility of the DNA Analysis Laboratory and FPP staff are not required to be involved in this process.

5.8.1 Preparation for Return

All property officers are required to process samples for return. Delegated Property Officers can at any time prepare lists of exhibits for return. These exhibits are then pulled from storage, bagged together according to return station / district and stored in the FPP Vault awaiting collection by the QPS. Property Officers are to generate a Property Returns Manifest which lists being returned to QPS. See **Appendix 12**

5.8.2 Returning DNA Crime Scene Exhibits to the QPS

When an officer arrives at the FPP to collect a Crime Scene exhibit the exhibit must be signed out in the Forensic Register, in accordance with **Appendix 13**.

NOTE: *This process can be used for returning Coronial Samples also. This is not a common occurrence but is sometimes required.*

5.9 Destroying Coronial Samples

The Coronial Services stream does not use the Forensic Register, all coronial sample destructions are handled in AUSLAB.

Coronial samples are destroyed only with the authorisation of a Coroner. This authorisation is received in the form of a Coroner's Form 6 – Order for Disposal of Tissue Kept for Testing. Form 6's can be scanned onto a PM report in Auslab, or sent to the PP from either staff of Forensic Pathology or Forensic DNA Analysis and is processed as per **Appendix 11** in QIS document QIS 17116 Processing DNA Exhibits / Samples in the Forensic Sciences Property Point.

When ready to destroy coronial samples, it is preferable to process between 10 and 20 cases at a time. Pull samples from storage locations and prepare for destruction by setting up a heat seal plastic bag for destroyed items and dressing in personal protective equipment including a lab coat and gloves. Proceed to open external packaging of one case at a time and view items. There is no need to open primary packaging if sample can be viewed through packaging (eg. Clip seal plastic bag, clear jar etc). At no point are Property Officers to put themselves in danger when handling coronial samples. The biohazard cabinet is available for use when opening samples if they are particularly malodorous or messy. Auslab entry and preparation of a Coroners Form 7 is then done as per **Appendix 11** in QIS document QIS 17116 Processing DNA Exhibits / Samples in the Forensic Sciences Property Point

Once destructions are complete the Government Undertaker is to be contacted via Fax using template on **Appendix 12** in QIS document QIS 17116 Processing DNA Exhibits / Samples in the Forensic Sciences Property Point. An FPP staff member is to deliver the coronial samples to the Government Undertaker at the mortuary. FPP staff are not required to enter the mortuary, press the buzzer and ask for the Government Undertaker/New Haven to meet you outside and sign the Form7's and then hand over the coronial samples.

6 Records

Nil

7 Associated Documentation

28286	Objectives of the FSPP
25459	Dual Analysis of Forensic Exhibits at FSS
23263	FSPP Laboratory Information Management System Downtime Procedure
26040	FSPP – Procedure for Amended Receipts
23762	Forensic Sciences Exhibit Freezer General Us Safety and Security
23793	FSPP DNA Training Module
33744	Forensic Register Training Manual
17116	Processing DNA Exhibits / Samples in the Forensic Sciences Property Point

8 References

Nil

9 Amendment History

Version	Date	Author/s	Amendments
1	June 2017	S Lemon	First Issue
2	May 2021	T Dawson	Revised document to include process of receiving coronial samples using revised FBTRAN page in AUSLAB (appendix 14). Update packaging requirements of coronial samples. Added FPP do not enter mortuary in 5.9. Update process for SAIK bloods (5.3.7). Reformatted and updated appendices to reflect current processes. Added paragraph re return of DNA sub-samples. Amended appendix 11 to include using QP127 bulk loader & manual attachments. Name changes to FPP and Forensic DNA Analysis

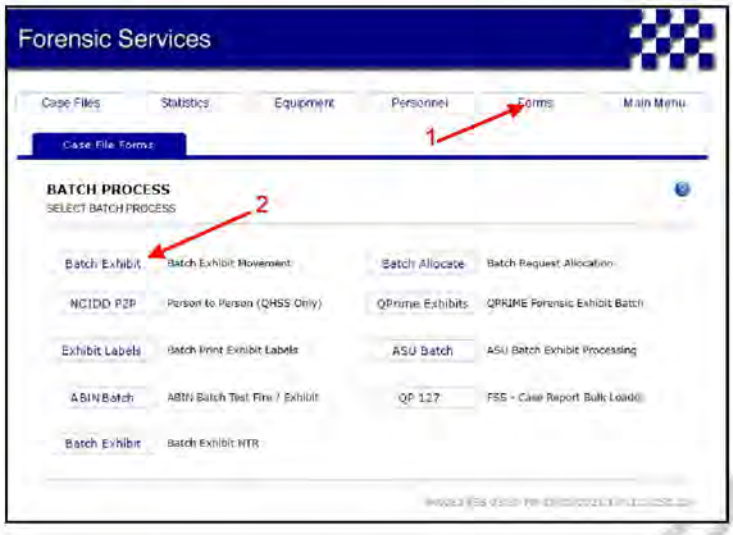
10 Appendices

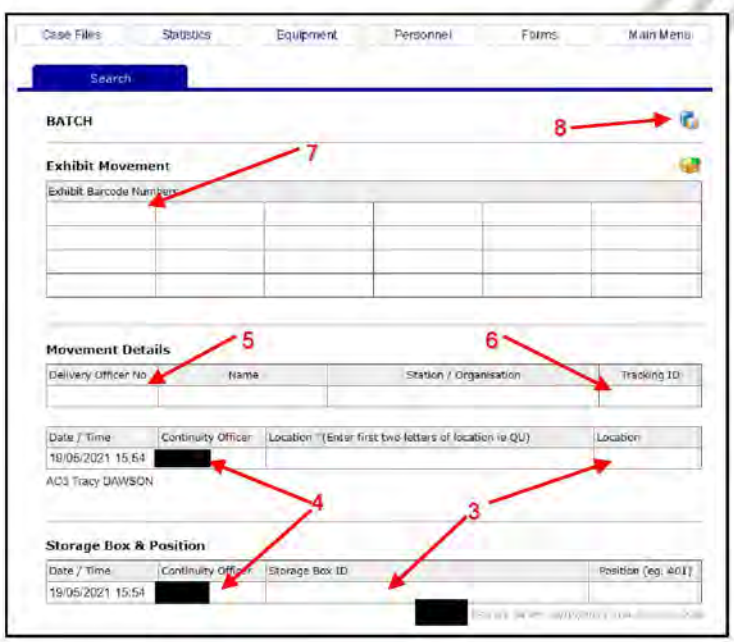
10.1 **Appendix 1:** Receiving DNA Crime Scene Exhibits in FR
10.2 **Appendix 2:** Receiving DNA Reference Samples in FR
10.3 **Appendix 3:** Receiving SAIK Bloods in FR
10.4 **Appendix 4:** Receival of Coronial Reference Samples
10.5 **Appendix 5:** Receival of Coronial Autopsy Samples
10.6 **Appendix 6:** Manual Registration of DNA Exhibits
10.7 **Appendix 7:** Storage box search and adding exhibits to a box
10.8 **Appendix 8:** Storage of exhibit boxes to a fixed location
10.9 **Appendix 9:** Creating a CM Request task
10.10 **Appendix 10:** Adding Case Notations in the FR
10.11 **Appendix 11:** Scanning paper based documentation into the FR
10.12 **Appendix 12:** Processing DNA exhibits for return in the Forensic Register
10.13 **Appendix 13:** Returning DNA exhibits to client
10.14 **Appendix 14:** Processing coronial samples in AUSLAB.

10.1 Appendix 1: Receiving DNA Crime Scene Exhibits in FR

Note: *As the receival and storage process is completed in one step all DNA exhibits will need to be separated by exhibit type ie: whole items, in-tube exhibits prior to being received and stored in the FR.*

- Ensure all exhibits are packaged in accordance with sections 4.2.3, 4.2.6 and 4.2.7





1. From the FR main menu click the 'Forms' tab
2. Click on the 'Batch Exhibit' button

   This displays the Batch Exhibit movement page
3. If storing item to a storage box scan storage box location barcode and click save

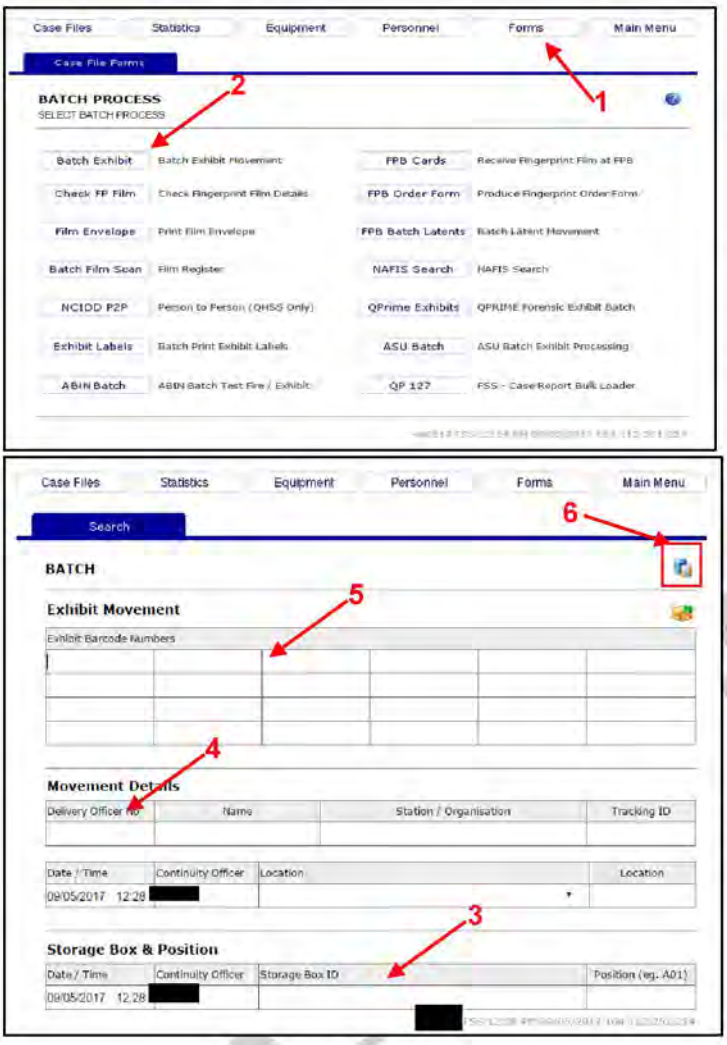
   If storing item to a fixed location, enter fixed storage location by typing "dna" into the location field, a drop-down box will appear displaying commonly used FPP storage locations
4. Ensure continuity officer is populated with receiving persons registration number
5. If personally delivered, enter delivery officer's registration number, this will populate the 'Name' and 'Station / Organisation' fields
6. If delivered via Australia Post, scan the tracking no into the 'Tracking ID' field, this with auto populate the 'Station / Organisation' field to 'Australia Post'
7. Scan each exhibit barcode into the exhibit movement table
8. Click the save icon

NOTE: *All items received via registered post must be grouped by the registered post number and systematically received. Exhibits tracked by various registered post numbers cannot be received in the FR at the same time.*

All items of the same exhibit type ie: whole items, in-tube exhibits are to be grouped together for processing.

10.2 **Appendix 2:** Receiving DNA Reference Samples in FR

NOTE: *Only 24 person reference samples can be received and stored in a single transaction.*



1. From the FR main menu click the 'Forms' tab
2. Click on the 'Batch Exhibit' button

   This displays the Batch Exhibit movement page
3. Scan the exhibit storage box location barcode into the 'Storage Box ID' field
4. Enter the delivery officer QPS registration number into the 'Delivery Officer No' field
5. Scan each reference sample barcode into the exhibit movement table
6. Scan each reference sample barcode into the exhibit movement table
7. Click the save icon

Once saved electronically and physically store exhibit storage box to fixed location as per **Appendix 7**

10.3 Appendix 3: Receiving SAIK Bloods in the FR

Any blood samples contained within a SAIK must be removed at time of receival. The Property Officer is to determine what type of analysis the sample requires by checking the medical notes or questioning the Investigating Officer. If the sample requires toxicology analysis refer to QIS 21118 **Appendix 5.** If medical notes state blood sample is for DNA analysis, consult with QPS DNA Sample Management Unit to authorise exhibit for analysis. Prior to registering the blood sample in the FR it must be labelled with a new FSS exhibit barcode and manually registered in the FR.

Follow steps below to manually register SAIK blood samples.



1. Scan in the SAIK barcode in the FR global search field and click the search button

   The FR will then open the exhibit record for the SAIK click the 'Exhibit' register tab

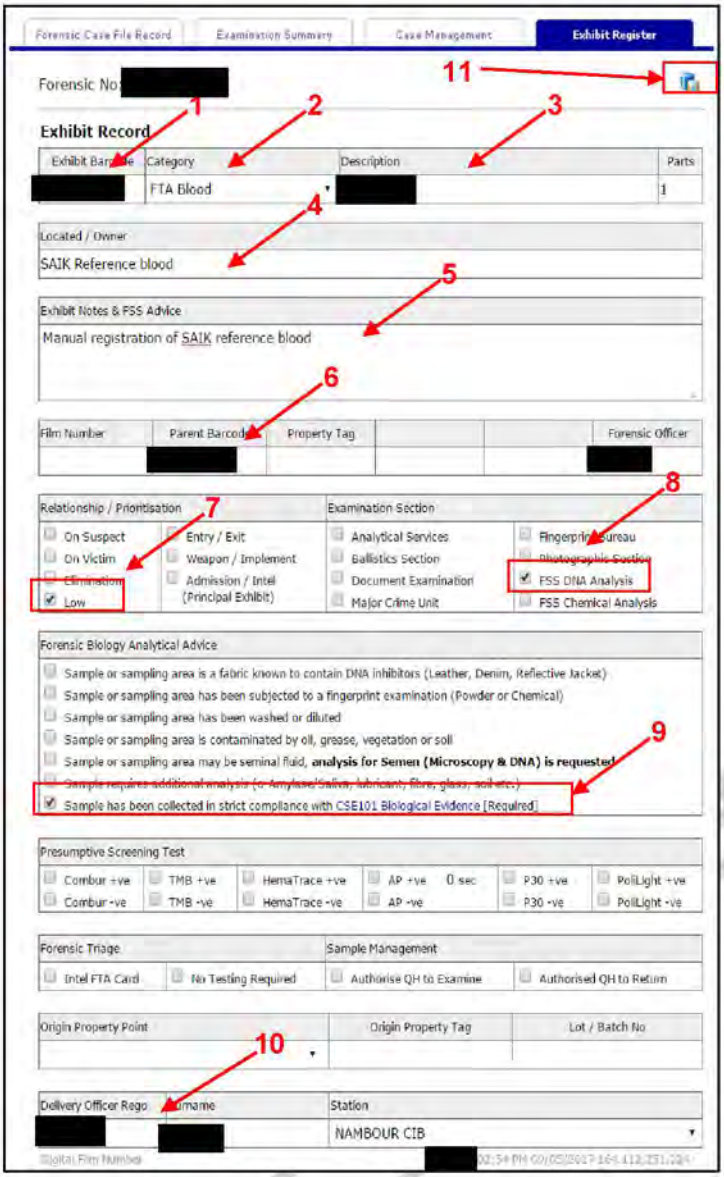
2. Click the 'Exhibit Register tab and the exhibit register list will appear



3. Click on the add button



Once the exhibit record page appears follow below steps 1 to 11 to manually receive the reference blood sample



1. Scan FSS exhibit barcode
2. Click on the 'Category' drop down list and select 'FTA Blood'
3. Enter the person's name nominated on the blood sample
4. In the Located / Owner field enter "SAIK Reference Blood"
5. Enter "Manual registration of SAIK reference blood" into the 'Exhibit Notes and FSS Advice' field
6. In the 'Parent Barcode' field enter the SAIK barcode
7. Select 'Low' priority
8. Select FSS DNA Analysis
9. Select CSE101 Biological Evidence
10. Enter delivery officer's registration number
11. Click the save button

Once saved, electronically and physically store SAIK blood sample as per **Appendix 7**

10.4 **Appendix 4:** Receival of Coronial Reference Samples

10.4.1 Receival of Reference Samples from QHSS Forensic Pathology

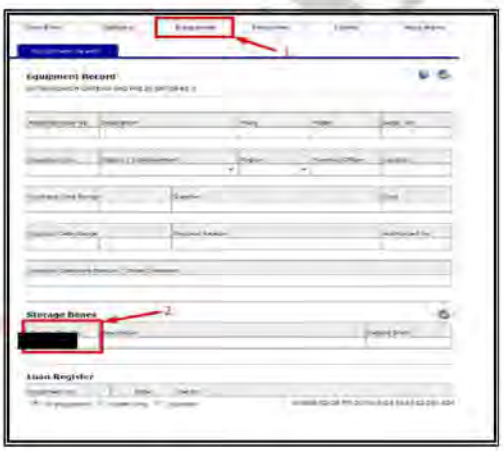
PM Samples delivered from Forensic Pathology for DNA testing and are pre-registered in the FR can be received as per **Appendix 1.** PM samples transferred to FPP for storage pending analysis (if required) are to be added manually and therefore received in AUSLAB prior to registration in FR as per **Appendix 14.**

Note: *PM samples for storage pending are to be stored electronically prior to registration in FR. This is only due to a workaround until enhancements are made to eliminate the exhibits from populating the DNA received list.*

Reference Samples such as FTA cards and Blood samples are to be separated from the other Autopsy Samples and registered as follows:

i. Assign a barcode to each sample and store to the appropriate location as follows:

1. Select the 'equipment tab from the main menu
2. Enter the storage box number in the 'storage box' field and press enter



3. Select the Contents tab
4. Click on the button

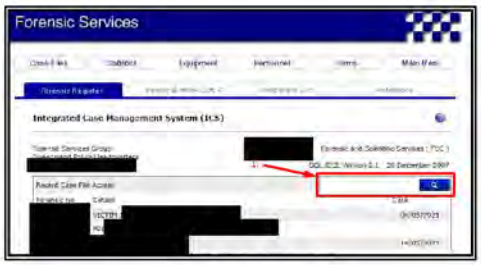


5. Scan in barcode number
6. Save record

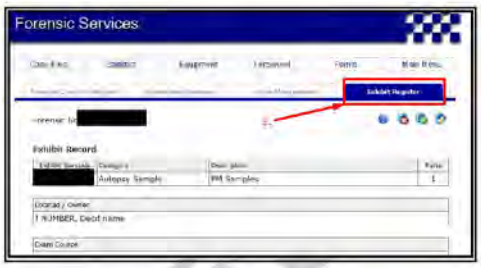


ii. You can then add the exhibit to FR as follows:

1. Scan in the PM Samples barcode (body barcode) in the FR global search field and click the search button.



2. Click the 'Exhibit Register' tab and the exhibit register list will appear

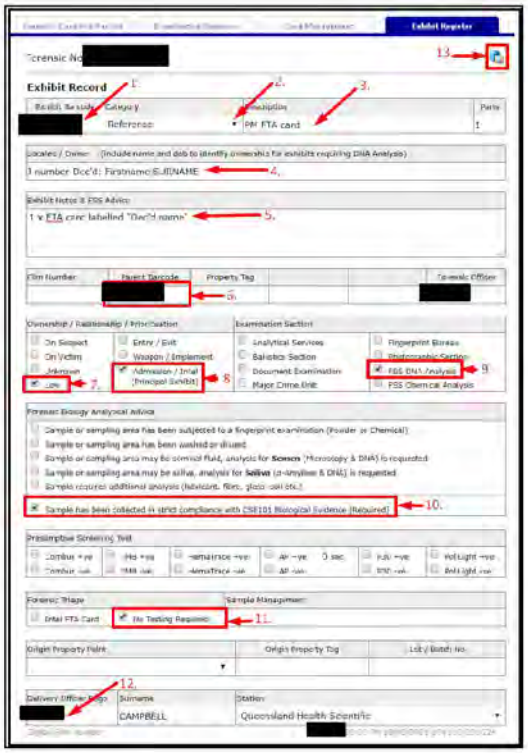


3. Click on the 'add' icon to add an exhibit.



iii. Once the exhibit record page appears follow below steps 1 to 12 to manually receive the PM reference sample

1. Scan FSS exhibit barcode
2. Click on the 'Category' drop down list and select 'Reference'
3. Enter 'PM FTA card' into the description field
4. Type in the J number and deceased name into the 'Located / Owner' field
5. Type in the description of items into the 'Exhibit Notes and FSS Advice' field
6. In the 'Parent Barcode' field enter the PM sample barcode (body barcode)
7. Select 'Low' priority
8. Select 'Admission/Intel'
9. Select 'FSS DNA Analysis'
10. Select 'CSE101 Biological Evidence'
11. Select 'No Testing Required'
12. Enter delivery officers FR number
13. Click on 'Save' icon

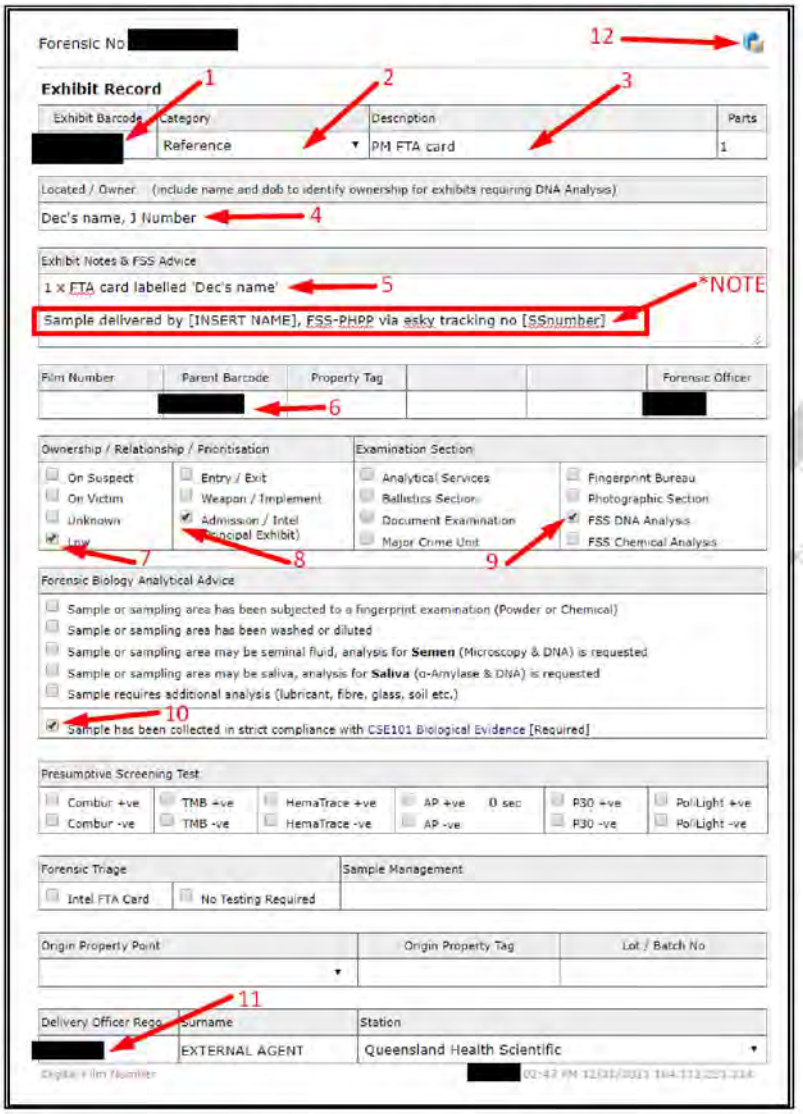


iv. Physically place sample in nominated storage location.

10.4.2 Receival of Coronial Reference Samples from External Mortuaries

Coronial Samples from external mortuaries (other than QHSS) can be registered directly into FR. The body barcode may or may not be registered in FR, a search of the QPS occurrence number (which can be located on the Form 1 image in AUSLAB) should find the relevant Case File. If there is no Case File, follow instruction as 5.4.3.

The sample can then be registered as follows:



1. Scan FSS exhibit barcode
2. Click on the 'Category' drop down list and select 'Reference'
3. Enter PM FTA card into the 'Description' field
4. In the 'Located / Owner' field enter the PM Dec'd name and J number
5. Enter the description of items into the 'Exhibit notes and FSS Advice' field *NOTE If samples are delivered via PHPP enter delivery officer details and esky tracking no as shown
6. In the 'Parent Barcode' field enter the PM sample barcode (body barcode)
7. Select 'Low' priority
8. Select 'Admission / Intel'
9. Select 'FSS DNA Analysis'
10. Select CSE101 Biological Evidence
11. Enter delivery officers QPS registration no or [redacted] for PHPP
12. Click the save button

Once saved, electronically and physically store the PM reference sample as per **Appendix 7**

10.5 Appendix 5: Receival of Coronial Autopsy Samples

10.5.1 Receival of Coronial Autopsy Samples from QHSS Forensic Pathology

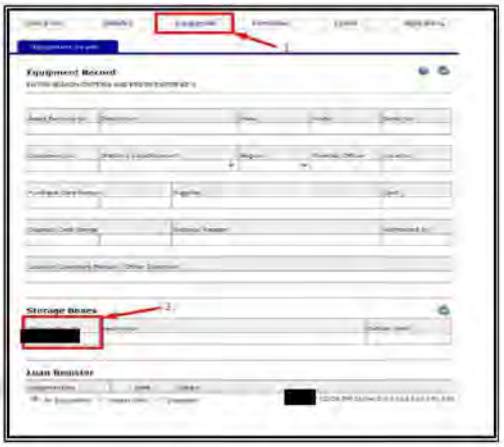
PM Samples delivered from Forensic Pathology for DNA testing and are pre-registered in the FR can be received as per **Appendix 1.** PM samples transferred to FPP for storage pending analysis (if required) are to be added manually and therefore received in AUSLAB prior to registration in FR as per **Appendix 14.**

Note: *PM samples for storage pending are to be stored electronically prior to registration in FR. This is only due to a workaround until enhancements are made to eliminate the exhibits from populating the DNA received list.*

PM Samples are to be registered as a collection of exhibits and are not required to be registered as individual items.

ii. Assign a barcode to each sample and store to the appropriate location as follows:

1. Select the 'equipment' tab from the main menu
2. Enter the storage box number in the 'storage box' field and press enter



3. Select the Contents tab
4. Click on the button

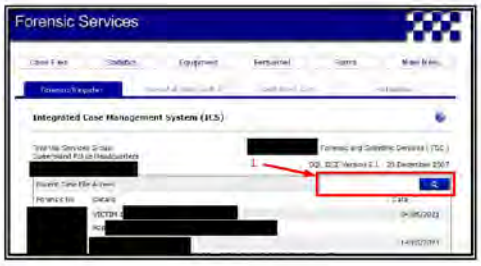


5. Scan in barcode number
6. Save record

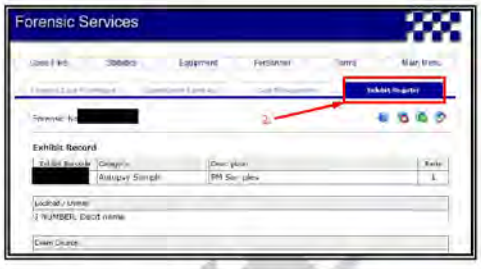


ii. You can then add the exhibit to FR as follows:

1. Scan in the PM Samples barcode (body barcode) in the FR global search field and click the search button.



2. Click the 'Exhibit Register' tab and the exhibit register list will appear

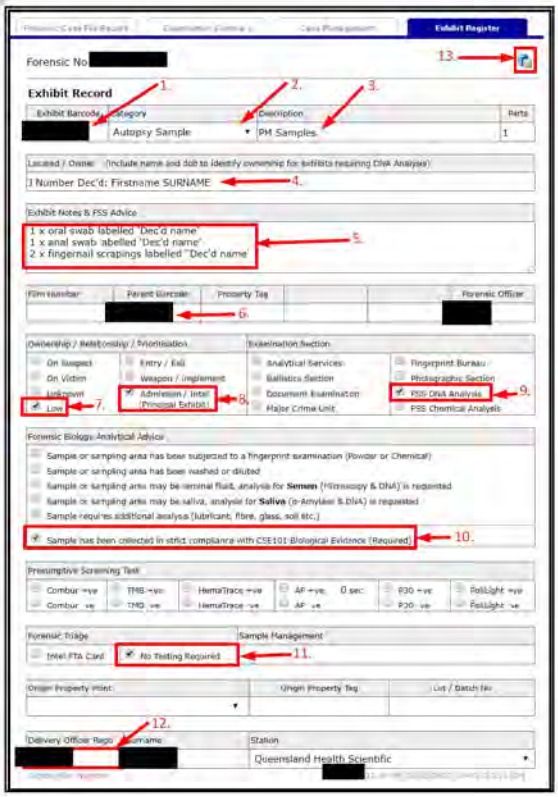


3. Click on the 'add' icon to add an exhibit.



iii. Once the exhibit record page appears follow below steps 1 to 13 to manually register the PM samples.

1. Scan FSS exhibit barcode
2. Click on the 'Category' drop down list and select 'Autopsy Sample'
3. Enter 'PM Samples' into the description field
4. Type in the J number and deceased name into the 'Located / Owner' field
5. Enter a detailed description of the PM exhibits delivered to FPP into the 'Exhibit Notes and FSS Advice' field
6. In the 'Parent Barcode' field enter the PM sample barcode (body barcode)
7. Select 'Low' priority
8. Select 'Admission/Intel'
9. Select 'FSS DNA Analysis'
10. Select 'CSE101 Biological Evidence'
11. Select 'No Testing Required'
12. Enter delivery officers FR number
13. Click on 'Save' icon



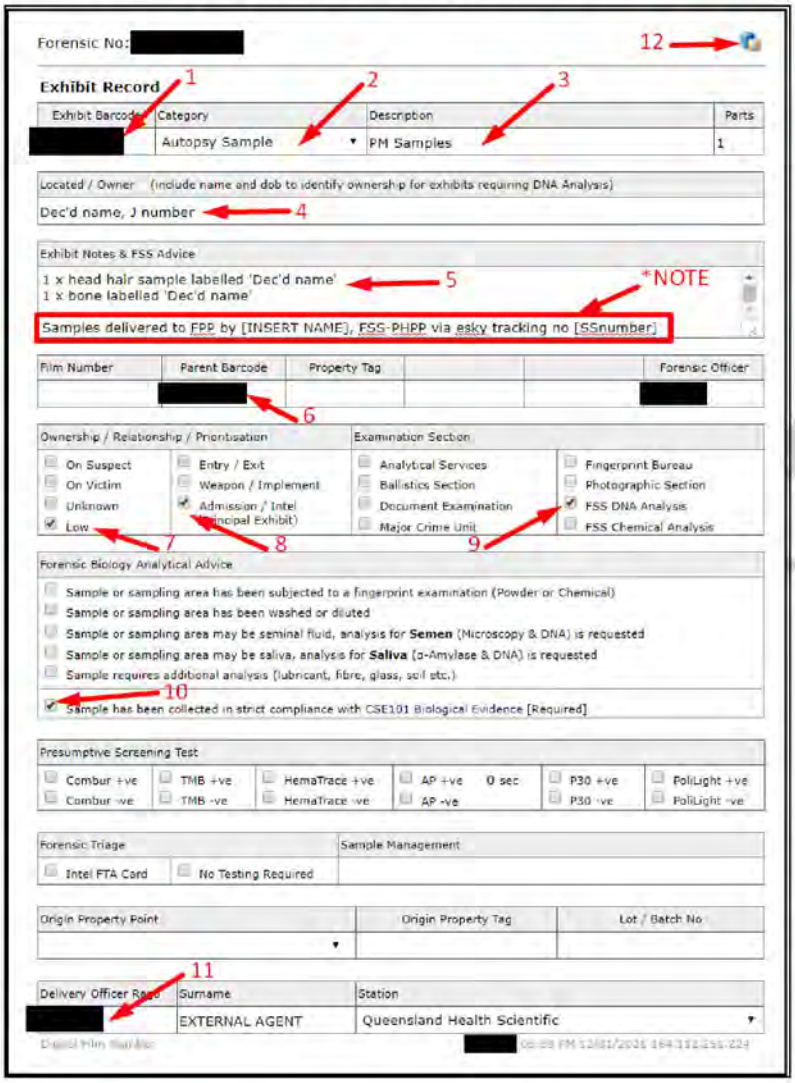
iv. Physically place sample in nominated storage location.

Note: *PM samples are to be sealed into a HSPB with the exhibits barcode affixed a being placed in the freezer for storage. Ensure all seals are signed and dated.*

10.5.1 Receival of Coronial Autopsy Samples from External Mortuaries

Coronial Samples from external mortuaries (other than QHSS) can be registered directly into FR. The body barcode may or may not be registered in FR, a search of the QPS occurrence number (which can be located on the Form 1 image in AUSLAB) should find the relevant Case File. If there is no Case File, follow instruction as 5.4.3.

The sample/s can then be registered as follows



1. Scan FSS exhibit barcode
2. Click on the 'Category' drop down list and select 'Autopsy Sample'
3. Enter PM Samples into the 'Description' field
4. In the Located / Owner field enter the PM "Dec'd name and J Number"
5. Enter detailed description of Description of items" into the 'Exhibit Notes and FSS Advice' field.

   *NOTE If samples are delivered via PHPP enter delivery officer details and esky tracking no as shown
6. In the 'Parent Barcode' field enter the PM sample barcode (body barcode)
7. Select 'Low' priority
8. Select 'Admission / Intel'
9. Select 'FSS DNA Analysis'
10. Select 'CSE101 Biological Evidence'
11. Enter delivery officers QPS registration no or [redacted] for PHHP
12. Click the save button

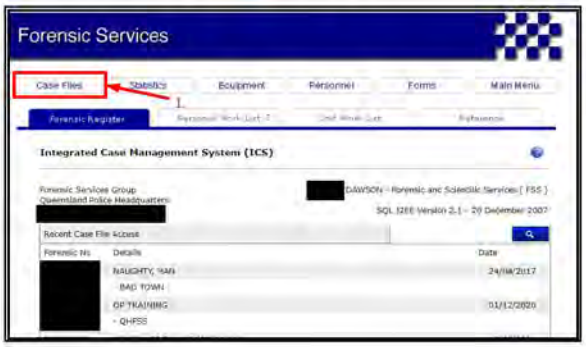
Once saved, electronically and physically store the PM reference sample as per **Appendix 7**

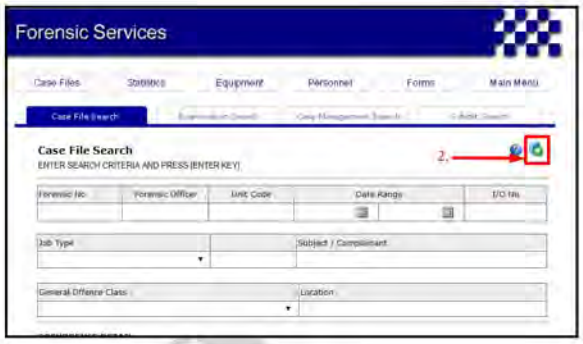
10.6 Appendix 6: Manual Registration of DNA Exhibits

Most DNA exhibits from QPS will be entered onto the Forensic Register by SOC prior to delivery to QHSS. In some instances however, Property Officers are required to create a Case File in the Forensic Register for the registration and receival of DNA exhibits from external agencies and clients

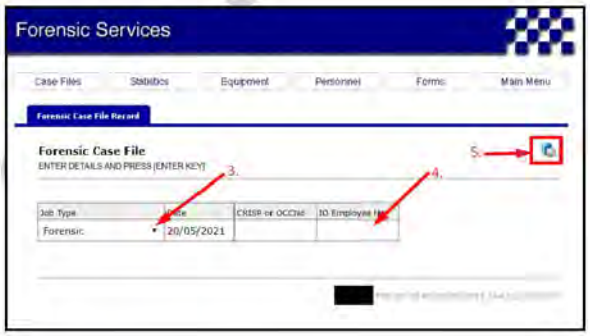
i. To manually create a Case File, Open the Forensic Register as follow the steps as shown:

1. From the Main Menu, click on the 'Case File' button
2. Then click the 'add' icon

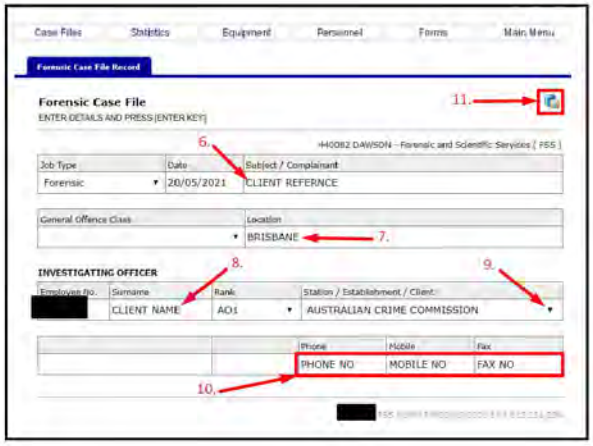




3. Select Job type from drop down list
4. Add the generic user number [redacted] for external clients Delivery Officers Registration no. to the 'IO Employee No' field
5. Click on the 'save' icon

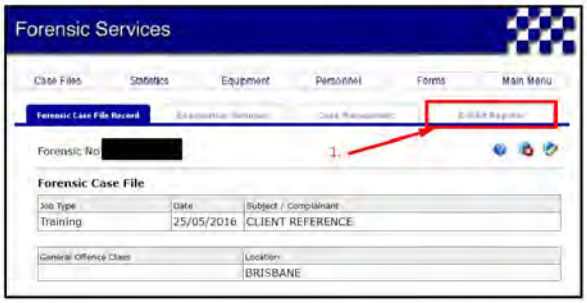


6. Enter relevant information into each field.Click on the 'save' icon



ii. You can then add exhibit to FR as follows:

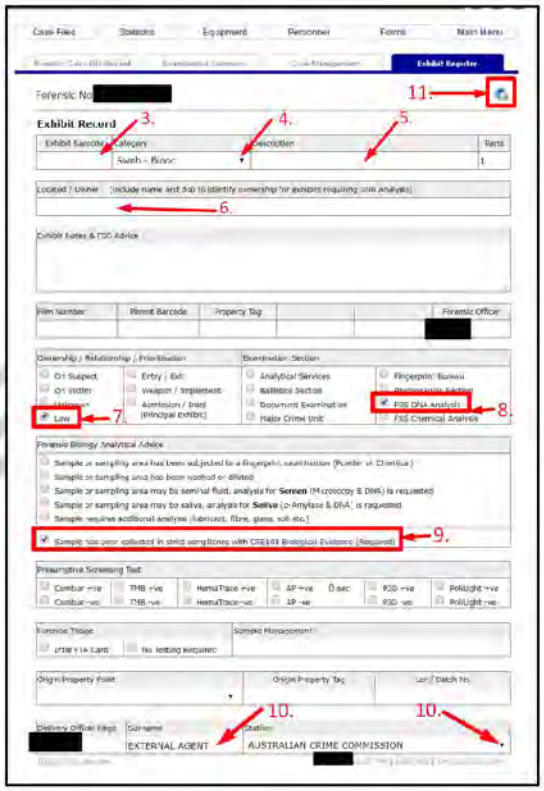
1. Click on the Exhibit Register Tab



2. Click on the add button

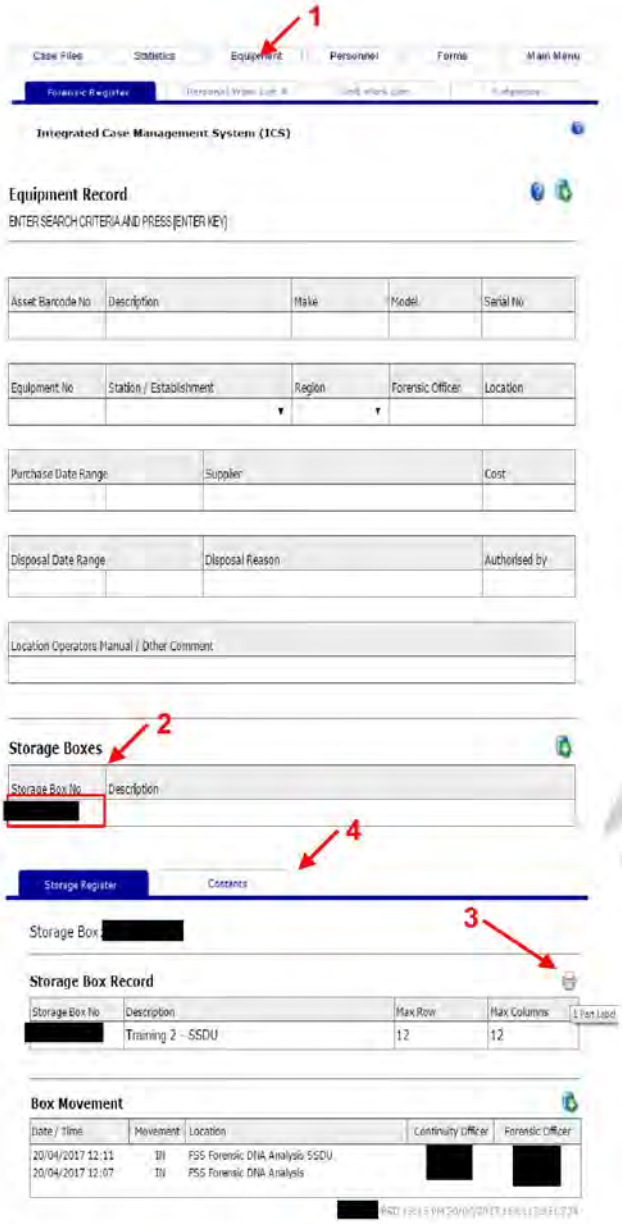


3. Scan in a new barcode and affix a copy of the barcode to the item.
4. Select the category from the drop-down list
5. Tab to 'Description' field and type in a brief description of the item
6. Tab to the 'Located / Owner' field and type in a general location where item / items were located.
7. Tick the Low 'Relationship / Prioritisation' box
8. Ensure the FSS DNA Analysis checkbox is ticked.
9. Tick the CSE101 Biological Evidence box
10. Type in Delivery Officers name and select their station from the drop-down list
11. When all relevant fields are complete, click on the 'save' icon



See **Appendices 5** and **6** for exhibit storage processes.

10.7 **Appendix 7:** Storage box search and adding exhibits to a box



1. From the main menu, click on the Equipment Tab

   The Equipment Record screen will appear

2. Enter the storage box number into the 'Storage Box No' field

   Press Enter to return the search

   The Storage Register tab open detailing the details of registration and box movement

3. To print a storage box label click on the 'Printer' icon

4. Click on the 'Contents' tab to view exhibits stored within.

Scenario 1



Adding Exhibits to a storage box:

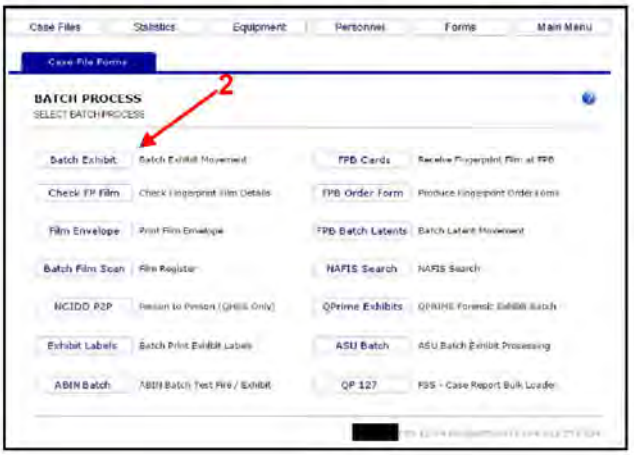
1. On the searched Storage box, click on the contents tab
2. Click on the add symbol

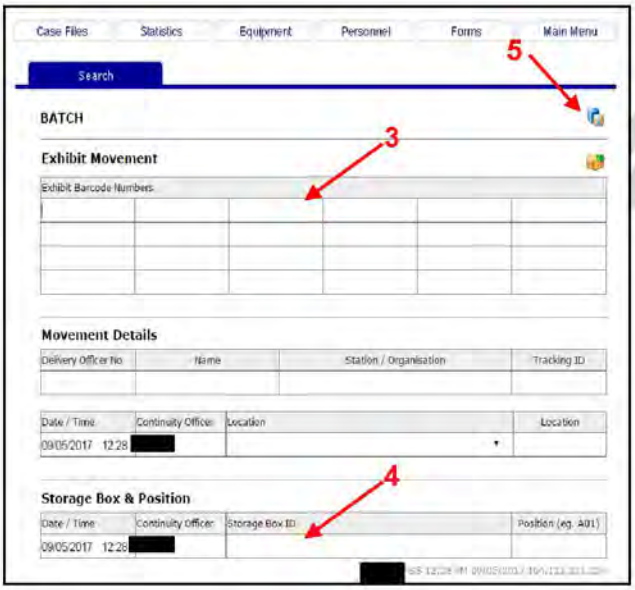
Scan or type the Barcode Number of the exhibit as each barcode is scanned or entered it will clear the 'Barcode No' field allowing the next barcode to be entered

3. Click on the 'save' icon or press enter to store

Scenario 2:







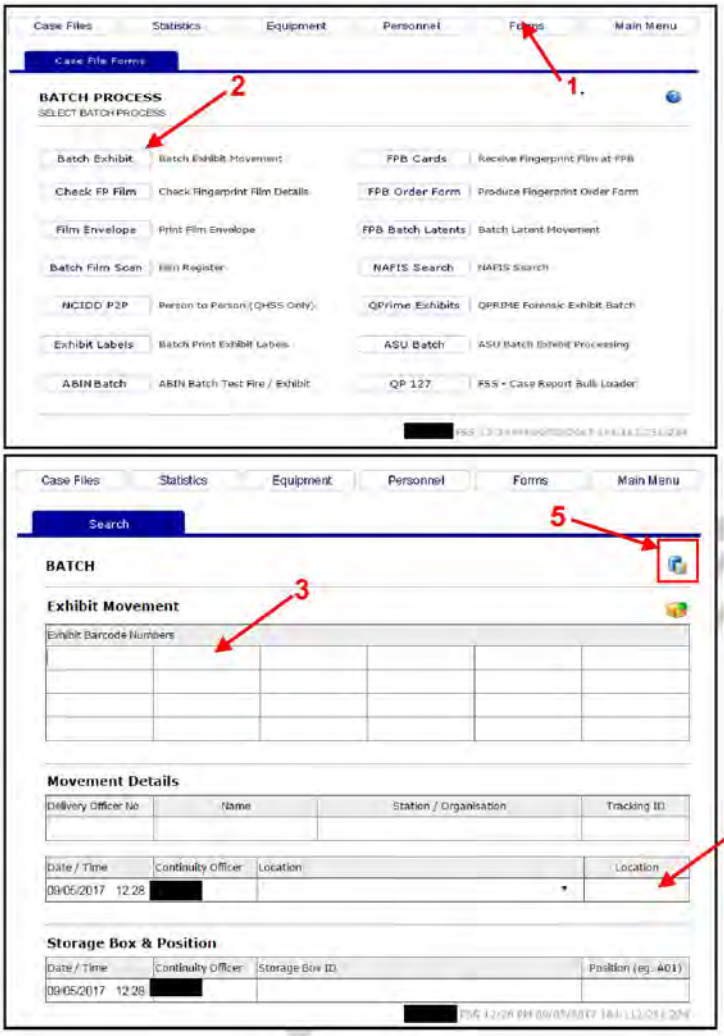
1. From the FR Main menu click on the 'Forms' tab
2. Click on the 'Batch Exhibit' button

   The 'Batch Exhibit Movement' page will appear
3. Scan exhibit barcodes into the exhibit movement table
4. Scan the exhibit storage box barcode into the 'Storage Box ID' field
5. Click the 'save' icon

10.8 **Appendix 8:** Storage of exhibit boxes and exhibits to a fixed location

Note: *Storing both large exhibits and storage boxes to fixed locations follows the same process*

- Open the Forensic Register and click on the 'forms' tab and click the batch exhibit movement.



1. From the FR main menu click the 'Forms tab'
2. Click on the 'Batch Exhibit' button

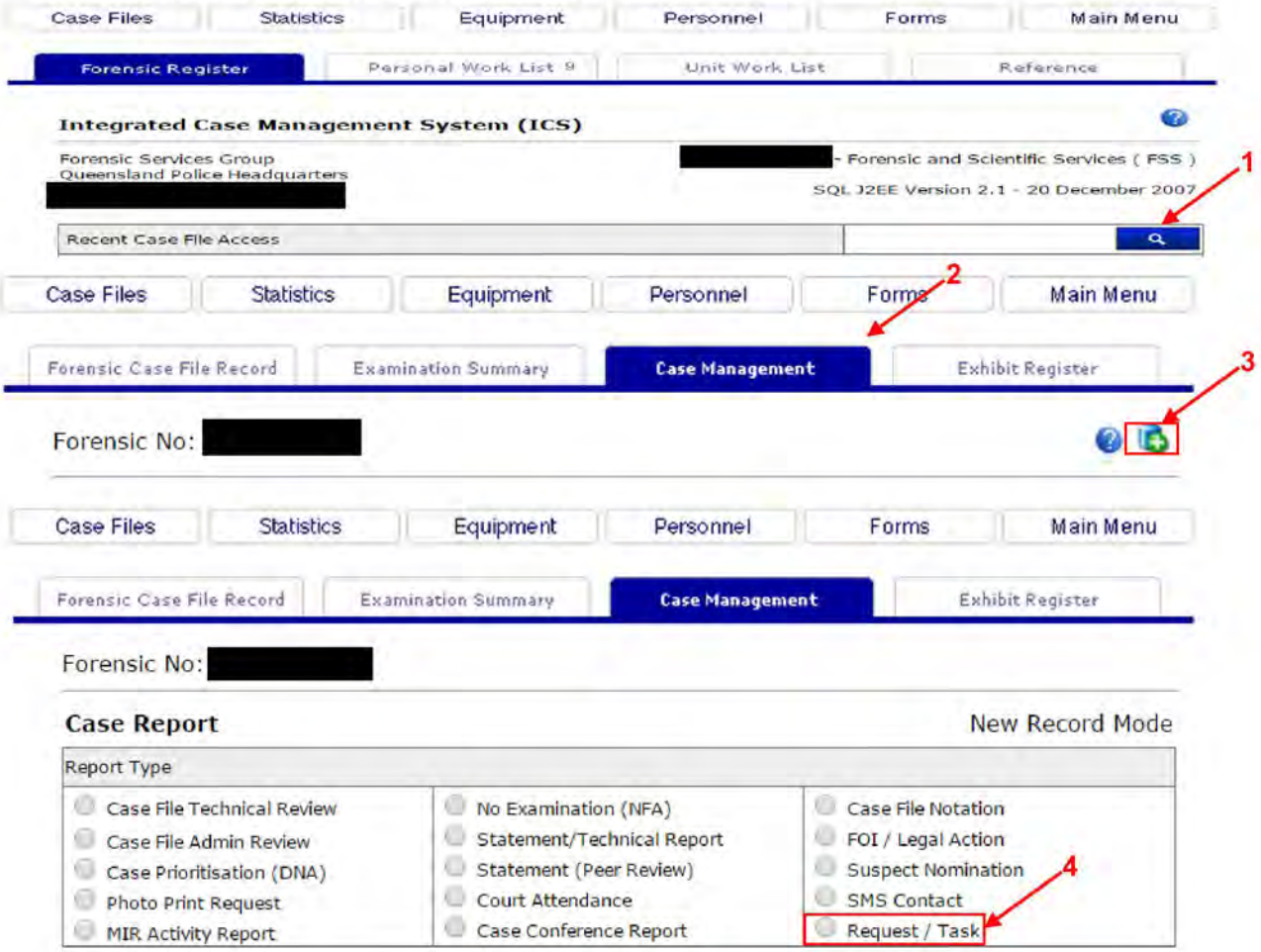
   This displays the Batch Exhibit movement page
3. Scan each of the storage box barcodes into the exhibit movement table
4. Input the fixed storage location

   Fixed storage locations can be selected by typing "prop" into the location field.
   A dropdown box will appear displaying commonly used FPP storage locations
5. Click the save icon

10.9 Appendix 9: Creating a CM Request task

- A CM request is created when a case officer is to do anything; generally, CM requests are used for notations that need to be noted by a person for actioning.

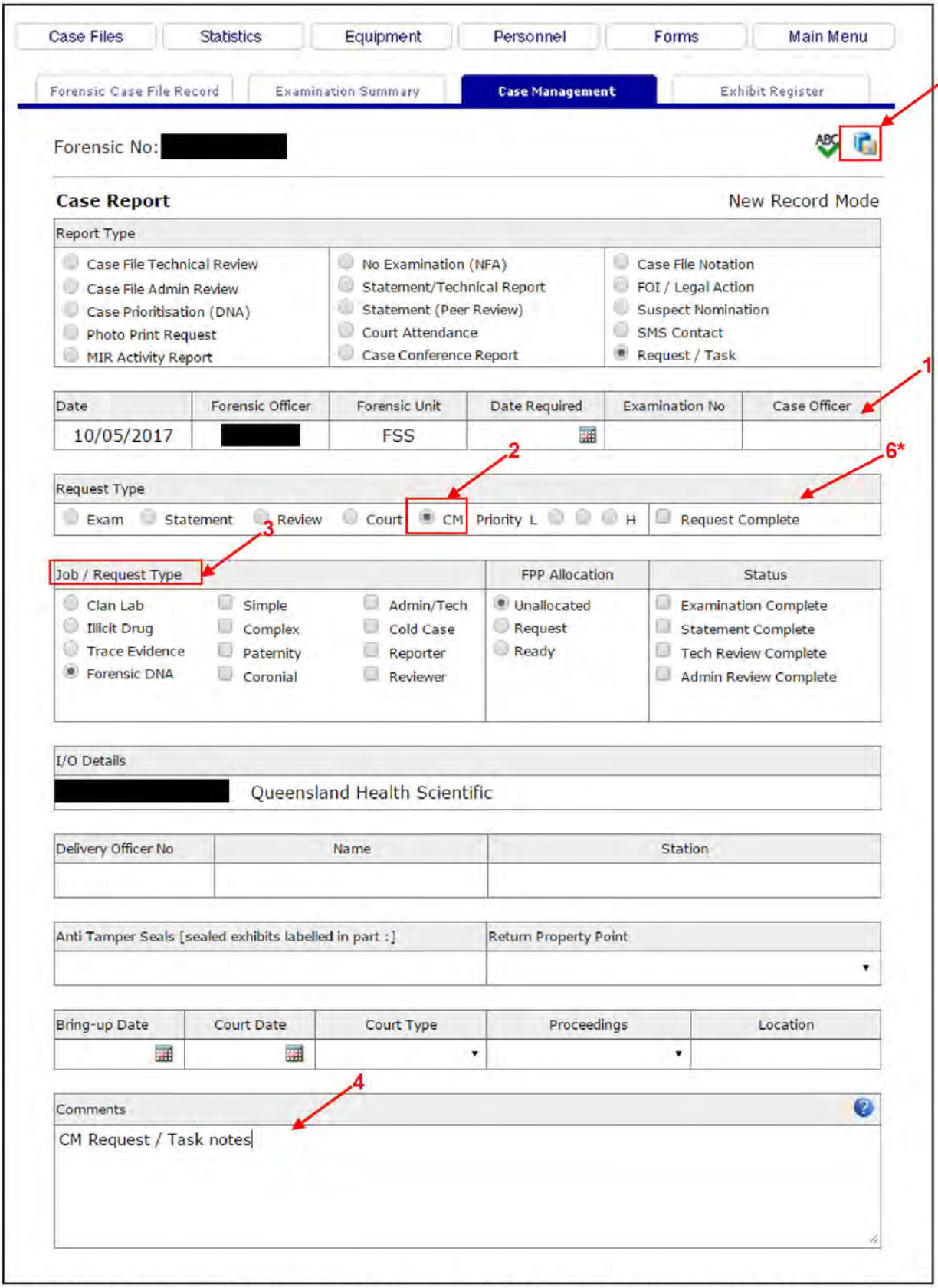
1. From the FR main menu page search for relevant case by entering a report, exhibit or occurrence number into the global search field and press the search button
2. Once the case opens click on the 'Case Management' tab
3. Click on the add button the 'New Record Mode' page will appear
4. Click on the Request / Task radio button



Select Report Type Above

Once the Case Report page appears follow steps 1 to 5 below.

1. Insert the case officer (who task will be sent to)
2. Select the 'CM' radio button
3. Select the Job / Request Type radio button ie: Forensic DNA
4. Enter task notes into the comments field
5. Click the save button

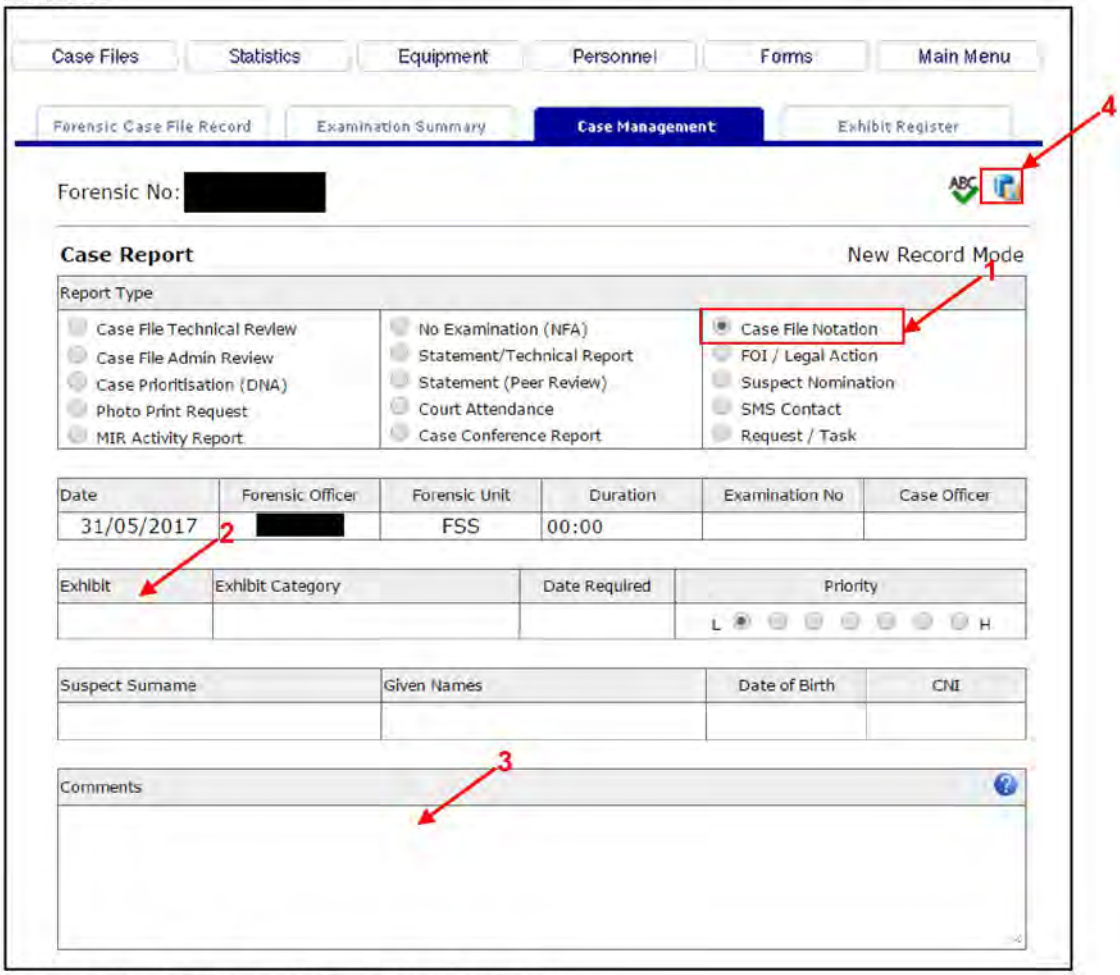


6. *The Request Complete radio button should only ever be marked once the task has been completed and no further action is required. ***Note:*** *This step should not be undertaken at time of task creation.*

10.10 **Appendix 10:** Adding Case Notations in the FR

- All case notations are to be made contemporaneously by adding a case file notation in FR.

1. From the FR main menu page search for relevant case by entering a report, exhibit or occurrence number into the global search field and press the search button
2. Once the case opens click on the 'Case Management' tab
3. Click on the add button the 'New Record Mode' page will appear
   Once the "New Record Mode" page appears follow steps 1- 4 below to add a Case File Notation



1. Click on the 'Case File Notation' radio button
2. Add exhibit barcode of relevant exhibit
3. Add notation
4. Click the save icon

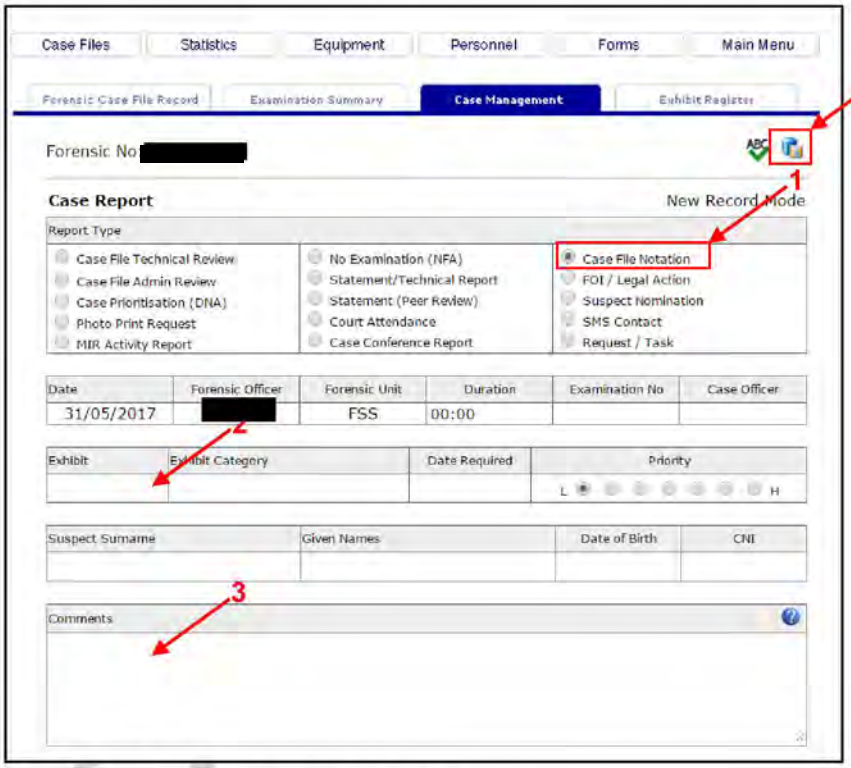
10.11 **Appendix 11:** Scanning Paper based documentation into the FR

i. From the FR main menu page search for relevant case by entering a report, exhibit or occurrence number into the global search field and press the search button

ii. Once the case opens click on the 'Case Management' tab

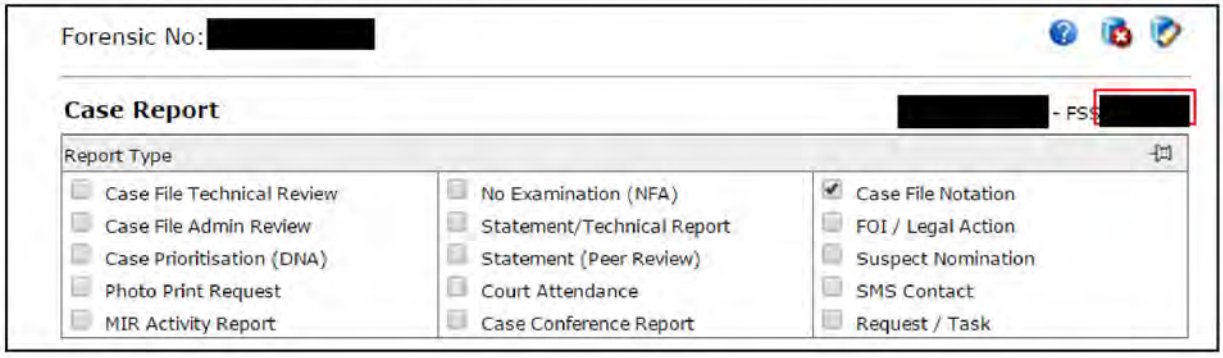
iii. Click on the add button the 'New Record Mode' page will appear

Once the "New Record Mode" page appears follow steps 1- 4 below to add a Case File Notation

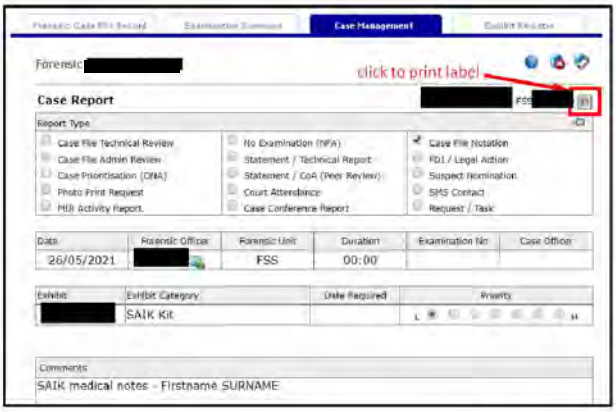


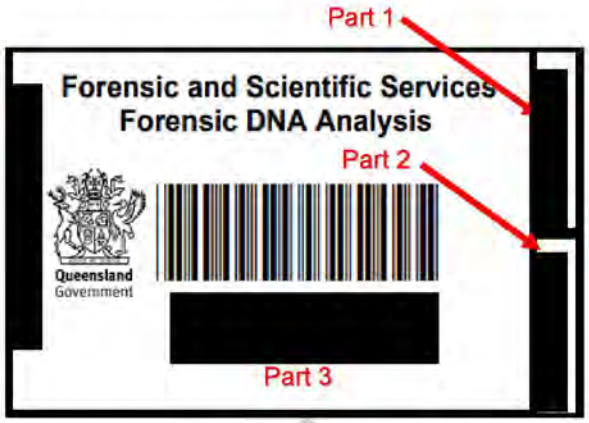
1. Click on the 'Case File Notation' radio button
2. Add exhibit barcode of relevant exhibit, add the SAIK barcode when scanning SAIK medical notes
3. Add relevant notes
4. Click the save icon.

iv. Once the casefile notation has been saved, record the 'Report' number on the paperwork being scanned, example below.



v. If the notation is to add medical notes for a SAIK, the record will produce a 3-part barcoded label of the report number as shown below. Click on the label icon to print and affix part 1 to the top left or right hand corner of the paperwork.



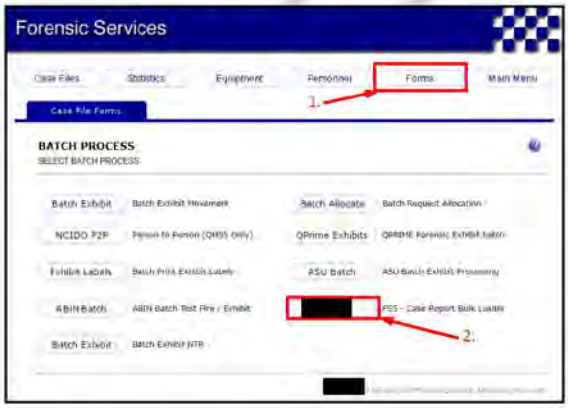


vi. Scan the documents using the Multi Function Device (MFD) and email as pdf to selected recipent as follows:

1. From the main menu of the MFD select the scanner function
2. Load the paperwork into the feeding tray on the top of the MFD.
3. Select the recipients name from the email tab on the MFD display and hit the start button.
4. The MFD will email the scanned documents in pdf format to the selected recipient.
5. The recipient can then drag the pdf to their desktop and then drag and drop into the QP127 bulk loader or manually add to a report number in FR as follows:

a. [redacted] Bulk loader to attach paperwork in FR:

1. From the main menu, select 'forms'
2. Select [redacted]



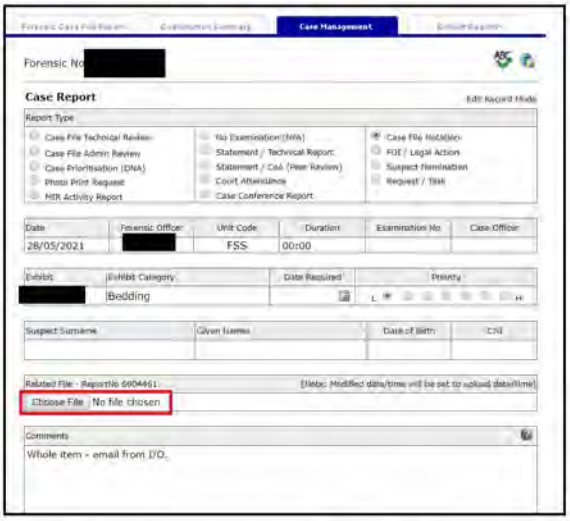
3. Drag pdf into space provided
4. Click 'Start Upload'

*Note: When the file status icon button turn green the page can then be saved

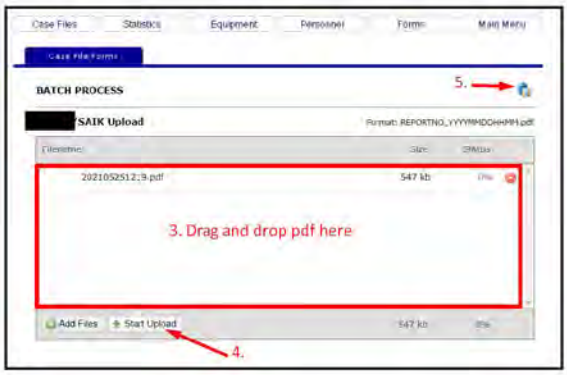
5. Click on 'save' icon

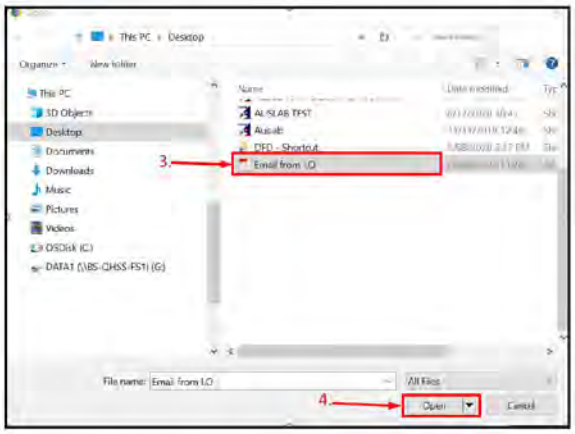
b. Manually attaching scanned paperwork in FR:

1. Access the 'Case File Notation' previously created and click on the edit icon
2. Click on 'Choose file'



This will then open up another window displaying the network map (as per below image)



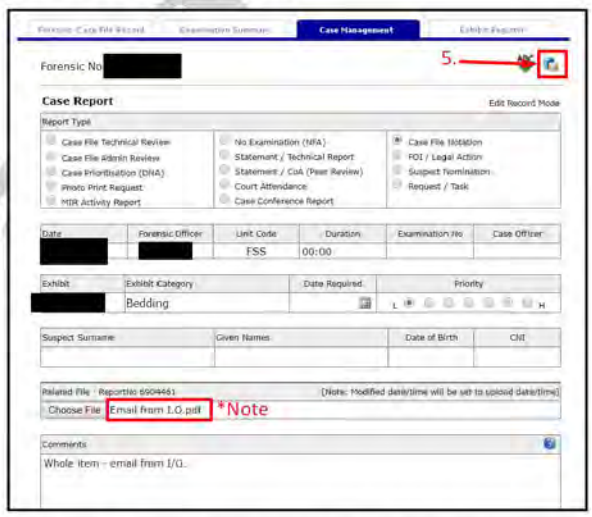


3. Select PDF document from desktop

4. Click the 'open' button

* NoteThe document will then appear on the Case file notation page

5. Click the save icon

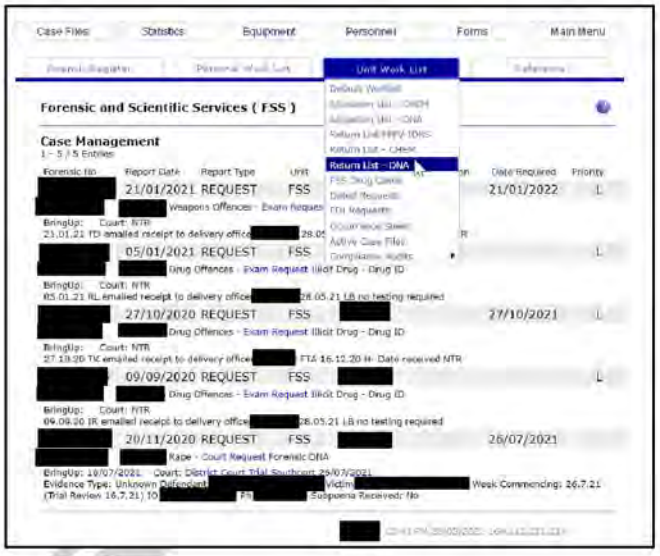


The PDF file will now be attached to the case file notation.

10.12 **Appendix 12:** Processing DNA Exhibits for return in the Forensic Register

At the completion of analysis exhibits requiring return to the QPS are stored to various returns locations within the DNA Analysis laboratory. When exhibits are stored to these returns locations they populate onto the 'Return List – DNA' in the Forensic Register. Property Officers are to work through this list to package items for return.

1. To view the returns list from the Main menu, click on the:
   - 'Unit Work List' this will open the Case Management list window,
   - Click again on the 'Unit worklist tab' the drop down will appear
   - Click on 'Return List – DNA' the DNA returns list will then open.



Note: *The DNA returns list is populated when items are stored to various DNA return storage locations ie:*

- *FDNA-EXRT – DNA Exhibit Room Returns*
- *FDNA-RTFZ - DNA Freezer Returns*
- *FDNA-RTFR – DNA Fridge Returns*
- *FPPU-EXFZ – FPP Under croft Freezer*
- *FPPV-DNAR – Vault DNA Returns Shelves*

2. DNA exhibits appearing on the 'DNA Returns List' will appear on sorted by Occurrence number and by IO station. These exhibits are to be pulled from the various storage locations and returned to the Forensic Sciences Property Point for processing and packaging for return.



Note: *Exhibits that are nominated for return to the same 'IO Station' are to be packaged together see steps below to generate returns manifest.*

3. Packaging DNA Exhibits for Return:

   Once DNA exhibits have been sorted by return location, they are to be placed into a heat-sealed plastic bag. Each seal of the heat-sealed plastic bag is to have a bag seal number ie: [redacted] sealed within. The AA number will then become the storage location for the package of exhibits awaiting return.

a. From the FR Main Menu, click on the 'Forms' button

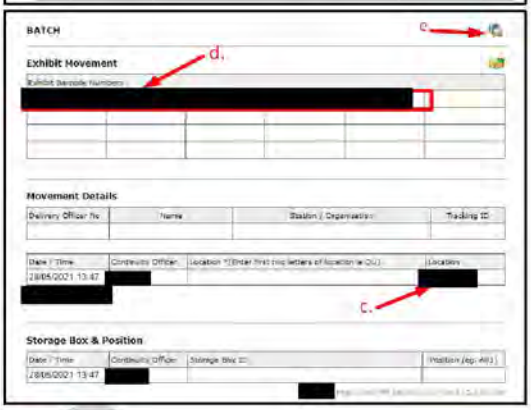
b. Click on the 'Batch Exhibit movement' button.

c. Once the 'Batch Exhibit Movement' table appears, input the AA bag seal number with the prefix of D into the 'Location field' e.g. [redacted]

d. Scan in each exhibit barcode for the exhibits being processed for return

e. Click on the 'save icon'





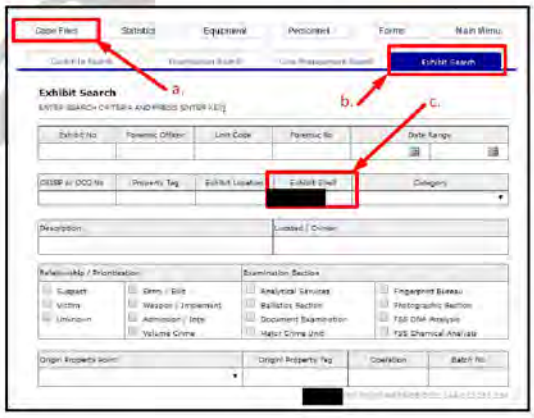
The exhibits are now stored to [redacted] storage location.

4. Creating the DNA Returns manifest:

a. From the FR Main Menu screen click on 'Case Files'

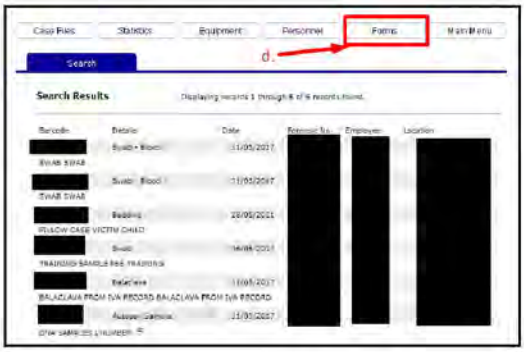
b. Click on the 'Exhibit Search' tab, the exhibit search screen will then open

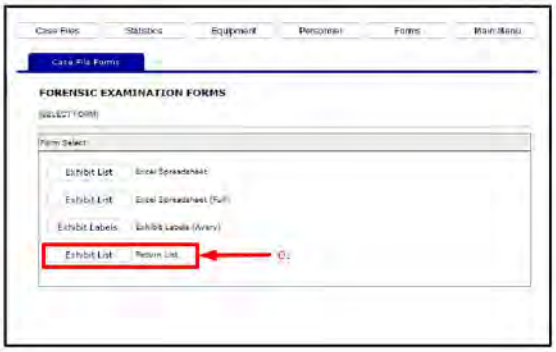
c. In the 'Exhibit Shelf' field enter the bag location number including the prefix ie: [redacted] then press 'enter' this will then display each of the exhibits previously stored in the steps above.



d. Once the search results appear, click on the 'Forms' button, the 'Forensic Examination Forms' window will appear.

e. Click on the 'Exhibit List' button next to 'Return List' this will then generate the returns manifest





5. Print the returns manifest, write the name of the return location on the top of the bag and affix to the heat-sealed plastic bag

Example of DNA Returns manifest:



Queensland Government

Forensic and Scientific Services
HealthSupport

Write return location here

RETURN LIST

FSS [redacted] 28 May 2021

QP

PropertyTag	ExhibitNo	Item	Station	I/O
[redacted]	[redacted]	Autopsy Sample	Queensland Health	[redacted]
		Balaclava	INNISFAIL STATION	
		Swab	INNISFAIL STATION	
		Bedding	INNISFAIL STATION	
		Swab - Blood	INNISFAIL STATION	
		Swab - Blood	INNISFAIL STATION	

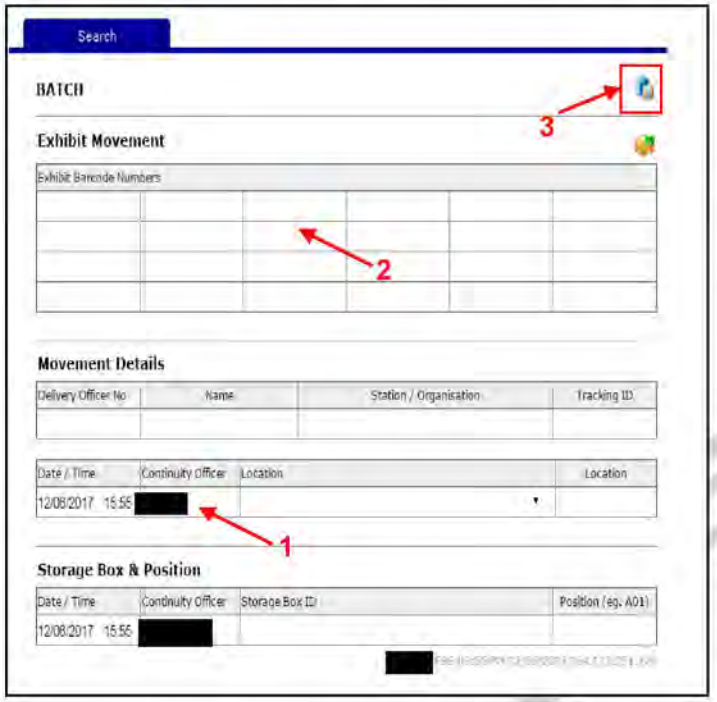
[redacted] [redacted] Phone Fax Email [redacted]

Page 1 of 1

10.13 Appendix 13: Returning DNA exhibits to client

- When returning DNA exhibits to the client the FR records must be updated and exhibits must be transferred to the collecting person possession.

1. From the Main Menu screen click on the 'Forms' button and then click on the 'Batch Exhibit' button
2. The 'Batch Exhibit Movement' table will appear



1. Enter the collecting officer's registration number into the 'Continuity officer' field then press 'tab'
2. Scan each exhibit barcode
3. Click the 'save' icon to generate and save the exhibit movement.

Note: *Generally only QPS registration numbers are accepted in the 'Continuity Officer' field.*

If returning a sample to a NON QPS client enter [redacted] *into the "Continuity Officer' field and then the collecting officers first initial and last name into the 'Location field' appropriate notes must be made against a casefile notation when moving an exhibit to a NON QPS client.*

10.14 **Appendix 14:** Processing coronial samples in AUSLAB

1. When a member of Forensic Pathology delivers a coronial sample, note down their name FR number and time of delivery.
2. Open AUSLAB and go to Patient enquiry (3) Enter barcode number into Lab Number field or search using J number e.g. [redacted]
3. Page down to FBTRAN page as shown in below image.
4. Enter delivery officers name and location in the 'Transferred By' field
5. Enter receiving officers name and location in the ''Transferred To' field
6. Enter Time and Date of delivery in the relevant field
7. Check items against the samples entered in the 'Sent' column
8. Type number of items received in the 'Received' column
9. A comment will need to be added as a form of continuity of where samples have come from. E.g. "Autopsy sample/s transferred to FPP in relation to QP "Insert number" and "FR Number" under the barcode that will be registered in the FR.
10. Register exhibits to FR as per **Appendix 4** 10.4.1 and **Appendix 5** 10.5.1

AUSLAB Clinical and Scientific Information System

1/1 Page 1/ 1

Lab Number : [redacted] Received : 07:15 18-Sep-20
UR/Case No : DOB :
Name : AUSLAB CCR Client : ASU - Forensic

INTERDEPARTMENTAL TRANSFER
Transferred By: Sally SMITH
From Location: QHSS-Forensic Pathology

	Sent	Received
FTA Paper	1	1
Bone	2	2
Nail Scrapings	1	1
High Vaginal Swab	1	1
Low Vaginal Swab	1	1
Anal Swab	1	1
Oral Swab	1	1
Hair	4	4
Additional Items:		
Scrapings	1	1
Fragments of skin	2	2
Clothing	4	4

FPP FR Number:
Transferred To: John SMIDT
Receiving person location: QHSS-Forensic Property Point
Transferred Time and Date: 09:48 18-Sep-2020
Comments:
Autopsy samples transferred to FPP in relation to
under barcode

F6 Validate F8 Notes SF8 Audit

CA-67

Queensland Health

Forensic and Scientific Services

Examination of Items

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1 Purpose

The purpose of this procedure is to describe the processes used for the examination of evidentiary items by Evidence Recovery Scientists and Technicians in Forensic DNA Analysis using the Forensic Register.

2 Scope

This procedure applies to all Forensic DNA Analysis staff that examine or interpret examinations of evidentiary items. This standard operating procedure is an adjunct to individual methods for relevant screening tests. Interpretations and limitations of reporting are to be found in each method.

3 Definitions

ERT:	Evidence Recovery Team
CSSE:	Crime Scene Sample Envelope (packaging used by QPS to store items collected at a scene
PPE:	Personal Protective Equipment
SSLU:	Scientific Services Liaison Unit
SMU:	Sample Management Unit
QPS:	Queensland Police Services
WATB:	What appears to be
FR:	Forensic Register
FPP:	Forensic Property Point
Dual analysis:	The term used for the examination of an exhibit by two or more forensic sections (e.g. Forensic DNA Analysis and Forensic Chemistry).

4 General Principles

4.1 Anti-contamination procedures

QIS document 22857 describes the anti-contamination procedures for the examination of items, which must be adhered to at all times.

4.2 Safety

Full PPE including hair net, safety goggles/glasses, face mask, gown and gloves must be worn in the laboratory for all examinations.

Refer to QIS document 14576 for Forensic and Scientific Services exposure procedures.

4.3 Continuity

Continuity is the ability to demonstrate and account for the movements and ownership of an item, meaning that at any point between when the exhibit is seized through to when the exhibit is produced in court or destroyed, its location and all persons who have been in contact with the exhibit can be determined. This provides evidence that the exhibit has not had the opportunity to be tampered with or has not come in direct contact with other exhibits. Refer to QIS document 14077 (FSS- Legal Analysis).

When moving an exhibit or case file, the physical movement must be recorded electronically in the Forensic Register using the exhibit movement function. Depending on the process, this can be done by moving the item from location to location or the storage

rack or box that the item is contained in. The exhibit movement function must accurately reflect all the locations within the laboratory that the sample has been.

In addition to recording the physical location of exhibits and case files, continuity also includes:

- Recording exhibit packaging details, including seals
- Examination notes
- Use of unique identifying numbers or barcodes for exhibits and subsamples
- Maintaining custody and security of exhibits always. Only items which are drying should be left in the laboratory overnight, all other items must be returned (tracked) to the exhibit room or freezer

4.4 Priority

The QPS will designate a priority for a case and for exhibits, which may differ, case / sample may be given the following priorities:

- Priority 1 (Urgent): Samples specifically approved by the QPS for processing in 3-5 day turn around. Samples may only be processed as Priority 1 with the approval of the Senior Scientist, Team Leader or Managing Scientist. Samples identified as needing to be processed before routine samples, due to an identified specific issue e.g. pending court date for case.
- Priority 2 (High): Allocated based on crime code and generally used for crimes against a person.
- Priority 3 (Medium): Allocated based on crime code and generally used for crimes not against a person i.e. property crime.

The priority of a sample/case may change at any stage and should be reviewed when determining testing or re-testing requirements.

4.5 Exhibit notes

The QPS can enter examination strategies or other information to guide the examination by Forensic DNA Analysis in the Exhibit Notes and Analysis Advice field in the Forensic Register.

4.6 Dual Analysis

Dual analyses must be completed in the Evidence Recovery laboratory as this location has the optimal environmental conditions for DNA sampling.

Exhibits which are to be transferred to the custody of Forensic DNA Analysis must be receipted as per normal receipting arrangements through FPP. Where the item is maintained in the custody of another section (e.g. when samples are suspected of containing prohibited substances), the chemist will track the exhibit to a Forensic DNA Analysis location but will physically remain with the exhibit.

Where the dual analysis involves hazardous chemicals or other substances (i.e. drugs, explosives etc.) the relevant forensic section is responsible for making a hazard assessment and documenting this as a case file notation. This assessment must include personal risk to staff during examination, storage, subsequent analysis as well as potential risks to equipment.

Refer to QIS 33798 for lubricant procedures.

4.7 Sample Selection

The case history, presumptive/screening test results and the staining present on the item are all used to determine which samples are to be submitted. The following elements should be considered when selecting samples for submission:

- Case history – offence type and the modus operandi.
- Number of offenders – if there are multiple offenders/complainants then an increased number of samples may be required to identify as many involved persons as possible.
- Presumptive/screening test results – samples of each biological fluid type should be considered for submission.
- Size, location and distribution of staining.

4.8 Sampling techniques

Forensic DNA Analysis uses the following sampling techniques:

- Swabbing
- Tape-lifting
- Scraping
- Excision
- Submission of whole item

Note: If the area to be sampled is large, it may be necessary to adopt a checkerboard style of sampling in consultation with the Evidence Recovery Senior Scientist.

Note: Invasive/damaging techniques such as excision or scraping should only be used when it is the most appropriate method of recovering DNA and care should be taken as to not cause unnecessary damage to an item/exhibit.

4.8.1 Swabbing – used for non-porous surfaces

Swabs moistened with nanopure water or 70% v/v Ethanol are used to sample the area of interest and the entire swab head is submitted for analysis. In some cases, a dry swab may be used after a wet swab and both swabs combined in one tube for submission.

4.8.2 Tape-lifting – used for porous surfaces

The sticky surface of commercial tape is pressed against the area of interest until the tape's adhesive properties are exhausted. Always ensure that a newly exposed section of the tape is used to reduce the chance of contamination. The tape must be rolled with adhesive side in the middle and submitted for analysis in 2mL tubes only.

4.8.3 Scraping

This method is used for fabrics or surfaces where tape-lifting or swabbing are not appropriate and the area of interest is too large to excise. A scalpel handle and blade are used to scrape the top layer of the exhibit.

4.8.4 Excision

A scalpel handle and blade are used to excise an entire area of interest that is small enough to fit into a 1.5 or 2mL tube (e.g. ~5mm x ~5mm marked area).

4.8.5 Submission of whole item

This method is used where the entire item as received is small enough to fit into a 1.5 or 2mL tube.

5 Pre-examination preparation

Before commencing the examination of an item, all available case details should be reviewed to determine the type of examination and the testing required. This information may also be used to prioritise examinations. The following items should be reviewed:

- Exhibit notes & Analysis Advice field
- Medical notes including SAIK paperwork
- [redacted] (if available)
- Relationship/Prioritisation information
- Exhibit description

Information on the parent item may also be viewed if QPS have ticked the FSS DNA Analysis box.
Where the above information does not provide sufficient information to determine testing requirements the following additional strategies may be employed:

- Contacting the Investigating Officer, SOCO or Scientific Officer either directly or through SSLU (refer to QIS 33771 to create and complete a request/task).
- Contacting the QPS DNA Sample Management Unit
- Contacting FMOs or FNEs

All communications must be recorded electronically by a case file notation or request/task.

Note: Specific details relating to the examination of sexual cases are outlined in QIS 33798.

Note: Specific details relating to the examination of post mortem and associated samples from deceased persons are outlined in QIS 34300.

Note: If an adverse event occurs during any examination refer to QIS 30800.

6 Examination

6.1 Specific examination strategies

Refer to appendices 10.2 to 10.6 for the workflow of items with different scenarios.

6.1.1 Examination of clothing/footwear for epithelial cells

Generally, only a small number of epithelial cells are deposited by touching or wearing items. It is best to use one side of a swab or a piece of tape no more than 2cm long to collect for submission, thereby concentrating cellular material into one sample.

High friction areas, including armpits, collars, inside collarbone, waist bands, hat bands and other parts of clothing that are in constant contact with the wearer are ideal areas to sample.

6.1.2 Swabs

Record the amount of the swab that is stained, the colour, the stain intensity, the result of any screening tests and the amount of the swab that is submitted for DNA analysis. The entire swab head material can be cut off and submitted for testing.

6.1.3 Cigarette Butts

When examining cigarette butts, use the cigarette but notes table to select the appropriate check boxes to indicate whether the cigarette appears to have been smoked, whether there

is burnt tobacco or paper, whether it has been stubbed/flattened and any brand names visible on the butt. Select the appropriate check boxes to identify if the cigarette butt is hand rolled (with or without a filter) or a manufactured type. See Figure 10 for automatic lines that are used for cigarette butt examinations. When sampling cigarette butts, any tobacco and/or filters present are not submitted for testing.

- Smoked manufactured cigarettes: Excise a 0.5cm circumference of the filter paper from the butt using a scalpel blade and submit for testing.
- Smoked hand rolled cigarettes: Submit entire cigarette paper for testing.

For manufactured cigarette butts, once sampling has been completed, any remaining portion of the filter paper and exposed tip of the filter is retained as a subsample in the item retention box. For hand-rolled cigarette butts, any tobacco and/or entire filter is to be retained as a subsample, no part of a hand-rolled cigarette is to be discarded.

If multiple cigarette butts are contained within one CSSE, complete an item exam for the packaging only, in the notes field state how many cigarette butts are present. Each individual cigarette butt is registered as a subsample and converted to a child exhibit see sections 6.8 & 6.11, alternatively an Examination Record may be created. Refer to QIS 33798 for specific information on creating an examination record.

Submit the entire cigarette paper and filter paper for testing for unsmoked manufactured and hand-rolled cigarettes. If there is too much substrate for one tube, the sample must be submitted for extraction in multiple tubes to be pooled (refer to appendix 10.7 for the pooling process).

If a cigarette butt has a TMB positive stain, two subsamples need to be created and converted to child exhibits. One subsample will consist of any unstained filter paper as would routinely be submitted and the other subsample will consist of the stained portion of filter paper. The presumptive test must be recorded against the parent barcode.

6.1.4 Syringes, Needles and other sharps

Packaging and labelling
Syringes should be appropriately contained in a sharps container and labelled prior to receipt. Syringes that are not correctly contained are to be reported by the examining Scientist to the Evidence Recovery Senior Scientist for action. This action should include identifying the non-conformance in a Case file Notation in the FR and possibly raising an OQI.

Safety
Safety is important when examining these items as they pose a sharps risk. Syringe and needle analysis must not to be performed by untrained staff unless under the direct supervision of trained senior staff. If there are any concerns about the sampling of a syringe (e.g. feeling unwell) discuss with the Evidence Recovery Senior Scientist prior to commencing examination.

Re-capping of syringes may be required to preserve exhibit integrity post sampling. This is due to the nature of Forensic testing, whereby those areas of interest (inside of cap and outside of needle) are in a contained environment due to the syringe being capped. Preservation of that contained environment post sampling to maintain sampling integrity and limit possible environmental contamination is required. Considerable care and caution should be taken when re-capping syringes. If the recapping of a syringe is not necessary (e.g. when received uncapped) then it should not be carried out.

Procedure

1. Carefully remove the syringe from the sharps container using forceps and place onto a large petri dish.

Note: Even if the syringe needle is capped, exercise extreme caution. Always maintain control of the syringe and needle, keep the exhibit low on the bench and close to the petri dish with the sharp facing downward.

2. The hierarchy of syringe sampling is governed by the case circumstances. If sampling of both the external and internal surfaces of the syringe are required, then the following order should be adhered to:
    a. Place a clamp on a section of the syringe that is secure (refer to Figure 1), recommended locations are the tip (circled in orange), barrel flange (circled in blue) and the plunger end (circled in red). Hold the clamp to safely manoeuvre the syringe during sampling.
    b. Moisten a swab with nanopure water and swab the entire outside surface of the syringe (barrel and plunger) and cap if present.
    c. If the needle is covered with a plastic cap it will need to be removed for sampling. Face the needle toward the petri dish, hold the clamp on the syringe and place a secondary clamp on the cap. Apply light pressure with a twisting motion to slowly remove the cap. Always use the clamp to manoeuvre cap when sampling.
    d. Moisten a swab with nanopure water and swab the entire needle and inside of the cap if present. The needle and inner cap can be sampled together.

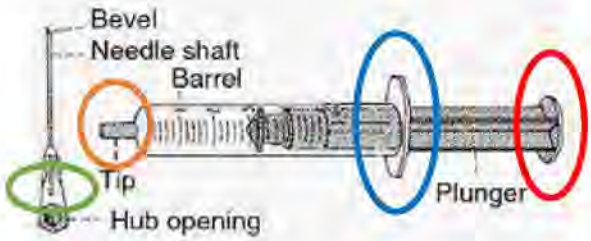


Figure 1 – Parts of a syringe and needle
(**Note:** There are various configurations of syringes that may be received including syringes with non-removable needles)

3. If the syringe contains suspected blood, hold onto the clamp and carefully remove the plunger to sample the contents of the barrel using a swab moistened in nanopure water.
4. If there is suspected dried blood in the needle, clamp the hub of the needle (see Figure 1 circled in green) and hold both clamps on the needle and syringe to slowly remove the needle. A swab moistened with nanopure water is then used to collect a sample from the needle, needle/syringe junction or syringe tip. Ensure the needle is secured with a clamp during sampling.
5. Note: Step 4 may not be required depending on the syringe/needle type, some needles are unable to be separated from the syringe.
6. If a needle is received with no syringe it must be adequately contained upon receipt. A clamp must be used to secure the needle during sampling.

7. Upon completion of the examination, safely reapply the cap using the same technique as step 2c.
8. Return the syringe/needle to the original packaging. If the item cannot be returned to the original packaging, consider using a larger sharps container to return the contents. Consult the Evidence Recovery Senior Scientist if required.

6.1.5 Possible hairs

If a possible hair is located on an item, the examiner must create a subsample on the exhibit that is being examined. Follow section 6.12 and manually add the result line "HAIRNFA - Hair located – not examined at this time" to the parent barcode. Transfer the possible hair to a clip seal plastic bag, label appropriately and return the item with the original packaging of the parent exhibit.

6.1.6 Examination of large volume fluid samples

If a fluid sample is received for testing for cells (e.g. Urine), the following procedure should be followed.

1. Transfer the fluid from the original container to a 1.5mL tube.

Note: Depending on the volume received, multiple 1.5mL tubes or 50mL falcon tubes may be necessary.

2. Create a balance tube and centrifuge the sample for 3 minutes. If a falcon tube is used it must be transferred and centrifuged in the Analytical laboratory.
3. Carefully remove the supernatant from the tube without disrupting the pellet and return to the original container.
4. If a falcon tube is used, transfer the pellet using a single use pipette to a 1.5mL tube. Alternatively the pellet can be collected using a swab.
5. Submit the tube containing the pellet.

6.2 Tracking of Storage Boxes

1. Check shelves [redacted] – [redacted]) in the Exhibit Room [redacted]) for item boxes; these are delivered by FPP on a daily basis, Monday to Friday.
2. Click the equipment and supplies  icon and select "Storage Box Search".



Figure 2 – Equipment and Supplies icon, Storage Box Search

3. In the Storage Box No field scan the barcode of the box and press enter or click submit.



Figure 3 – Storage Box table

4. In the Box Movement table click the add storage box movement plus icon.



Figure 4 – Box Movement table

5. In the Storage Location field, scan the room location from a location sheet or enter "EVI" and from the dropdown list and select "DNA Evidence Recovery Evidence Recovery").

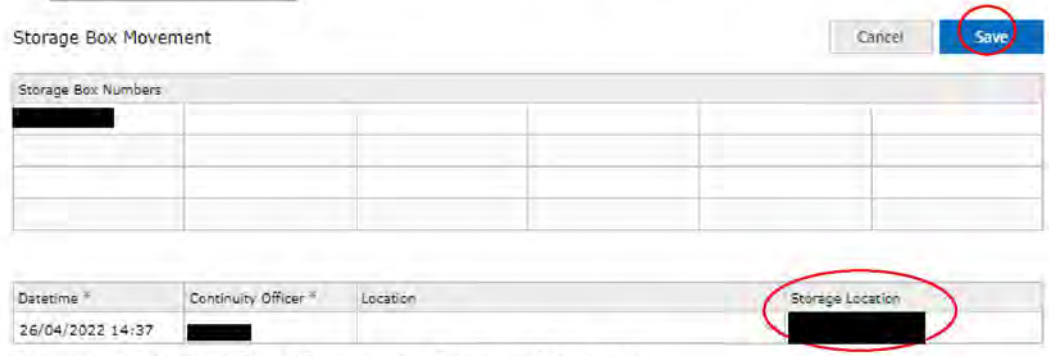


Figure 5 – Storage Box Movement, Storage Location

6. Click on the save button and place the storage box into the pass-through hatch.
7. Complete a new Exhibit Movement following the above steps and track an ERT-AS box to a relevant bench location ( ) before tracking samples.
8. Item boxes must be tracked back to the Exhibit Room Returns ( ) when they have no contents remaining. Follow the above steps to track the box and ensure the contents show as "0/0" on the Storage Box Record page.
9. Item boxes must be tracked back to a shelf ( ) in the Exhibit Room) at the end of each day if they still contain exhibits. Follow the above steps to track the box to a shelf.

6.3 Assessment of testing requirements

1. On any page, click the key identifier search icon and scan the exhibit barcode and press enter or click search.

Note: If the exhibit record is not visible, check the description on the CSSE to ensure that the exhibit is for Forensic DNA Analysis. Contact the QPS Forensic Reception Centre on (0) 3364 6208, identify yourself and explain that you have a sample that is not visible in the FR that requires the Forensic DNA Analysis box to be ticked. If the sample is not for FDNA, then it should be returned to QPS untested (refer to section 6.14).

2. In the Exhibit Record screen, scroll down and click on the thumbnail image of the CSSE, a larger image will open in a new window. Check the image and item description ensuring all details match the packaging. Check the image quality, ensuring barcodes affixed to the exhibit and other labelling are legible and that the entire CSSE is visible in the image. If the image does not meet requirements, a new photo will need to be taken and uploaded – refer to QIS 33771 for details.

3. Close the window containing the image.

4. Check the testing requirements (see Figure 6) and assess the item to see if biological fluid screening is required before submitting for DNA analysis.

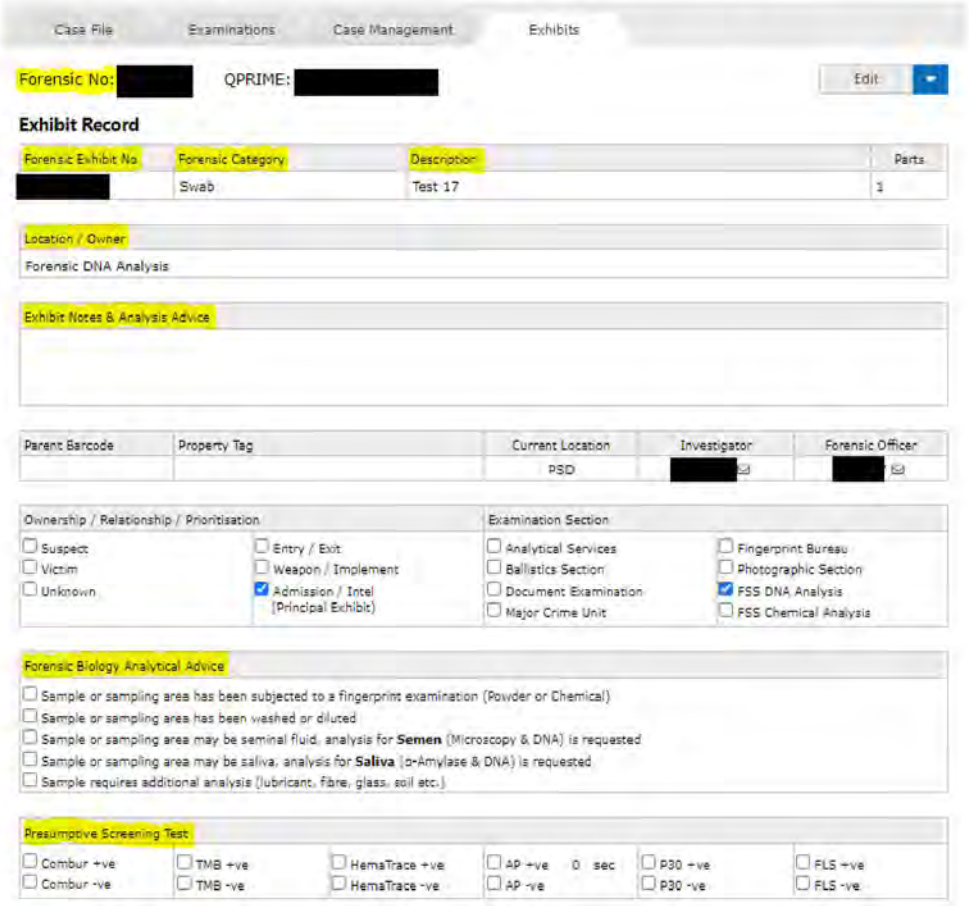


Figure 6 – Exhibit Record page

6.4 Digital Imaging

Photos must be taken for exhibits which are complex and/or difficult to accurately describe in typed notes. Smaller, uniform items (i.e. cigarette butts, fingernails, straws etc.) do not require photos, except where there is unusual staining, damage or other features which are difficult to describe. A scale and exhibit barcode must be included in every image. When photographing items with two sides that are designated side A and side B by the examiner, the side that is being photographed (e.g. side A or side B) must be specified and visible in each image. **Note:** Multiple images can be uploaded to an item exam.

If the packaging is damaged in any way, it must be re-photographed. If additional images are required, a new photo will need to be taken and uploaded – refer to QIS 33771 for details. **Note:** All images are stored on the network for 12 months.

6.4.1 Annotating images

If images need to be annotated this can be done using the FR annotation application or the windows paint program. Always ensure that the original image and the annotated image are both uploaded to FR.

Annotating using the FR annotation application:

1. Upload the image to the item exam and press save.
2. Click on the image in the images table of the item exam and click the "Annotate" button, annotate the image.
3. Enter "Annotated image" into the Filename field and ensure a title and description are entered into the annotation details table for each numbered area marked (both can be the same e.g. area 1).
4. Press the save button. The annotated image will appear in the Files table field as a pdf.

Note: The file/annotated image cannot be edited after it is saved.

Annotating using paint:

5. Save a copy of the image in I:\FR Images.
6. Right click on the image > Open with > paint.
7. Use the Save As function to save as a JPEG with the original filename and "Annotated".
8. Use the functions in the paint program to annotate the image.
9. Save the image.
10. Upload the annotated image to the item exam.

6.5 Packaging

1. Packaging should be opened in such a way as to maintain the original seals. When packaging is opened, the staff member must write "Opened" followed by their initials and date.

2. Scroll down to the Exhibit Analytical/Testing table, click the create exhibit test icon.
3. In the Testing/Analysis table process field select item exam from dropdown menu.
4. In the Packaging and Sample Assessment Notes table, tick the relevant boxes to describe the nature of the packaging and the seals (refer Figure 7).

Note: The Sample meets requirements check box is specific to in-tubes and must not be used for an item exam.

5. If the seals are complex, the tick boxes do not need to be used, the notes field can be used to describe the packaging and seals.

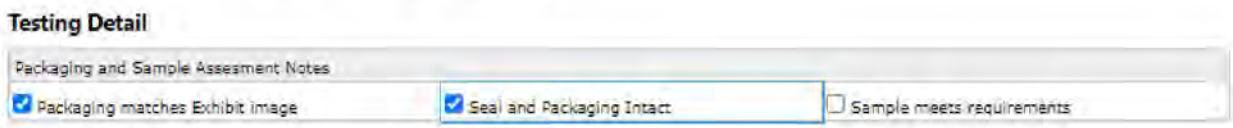


Figure 7 – Description of packaging tick boxes

Note: Packaging matches exhibit image check box expands to "The packaging matches the QPS exhibit image". This is to be used only when the entire packaging is visible in the QPS image and matches exactly what is received.

Note: If multiple exhibits are received in a single package, an Examination Record can be created to describe the packaging once. Refer to QIS 33798 for more details. Each of the exhibits contained within the packaging can then be added to the Exhibit/s Examined table.



Figure 8 – Exhibit/s Examined fields in Examination Record

6.6 Item descriptions

1. The Notes field is used to type the examination notes. If the exhibit is a swab or cigarette butt the text can be auto-generated by ticking the relevant boxes in the Swab or Cigarette Butt Notes tables.
2. Exhibits must be described according to the following minimum requirements:
   - What it is
   - Size (including measurements)
   - Labelling/brand
   - Colour
   - Staining (including any presumptive tests conducted)
   - Physical appearance of damage (without commenting on the cause of the damage)
   - Whole items must be further described to categorise the “inside/outside” surfaces and “left/right side” of the garment.

Note: When describing the I/S, O/S, right side or left side of a garment; examiners should be aware that these terms are used in relation to ‘as would be worn’.

3. Staining must be further described according to:

    - Shape
    - Distribution
    - Colour
    - Size (including measurements)
    - Intensity
    - Which side of the item the stain may have originated from
    - Any presumptive tests performed
    - Odour if applicable
    - Whole items should include where the stain is positioned i.e. left/right side of garment as would be worn

    Note: Images can be used if the physical appearance of stains are difficult to describe.

    Refer to appendices 5 and 6 in QIS 33798 for standardised wording when describing subsamples and sides of an exhibit.

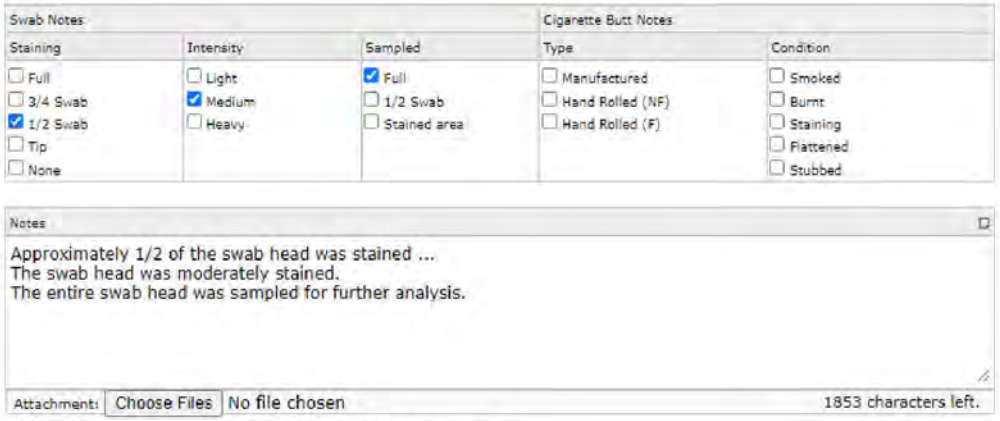


Figure 9 – Examination Notes for a swab

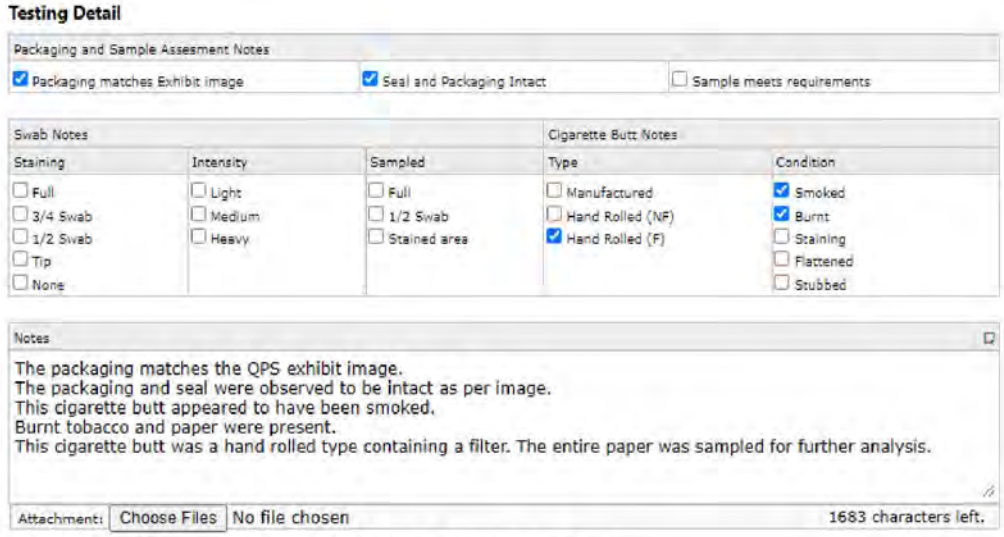


Figure 10 – Examination Notes for a cigarette butt

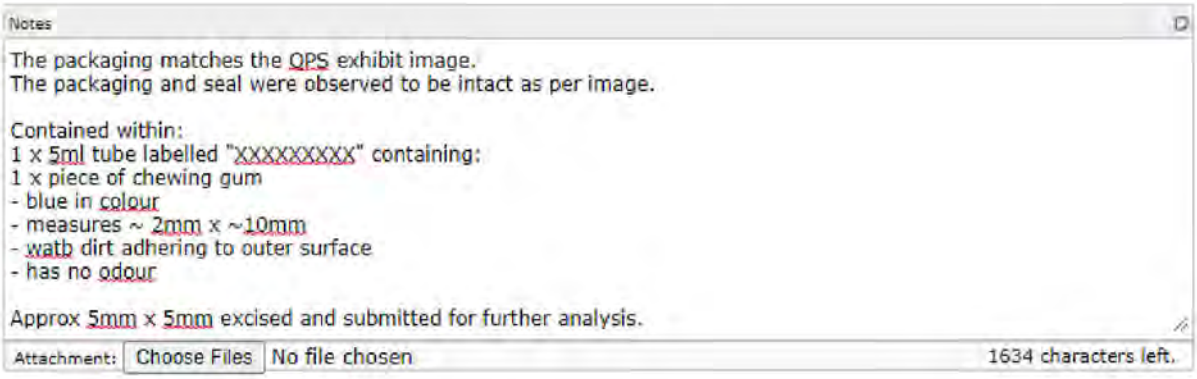


Figure 11 – Examination Notes for miscellaneous items

4. Scan the ERT-AS box barcode into the Storage Box ID field.

5. Scan the barcode affixed to the bag of tubes into the Tube Lot No field.



Figure 12 – Recording Storage Box ID and Tube Lot No

6. Click on the save button.

   Note: It is recommended that samples are stored when completing the item exam for each exhibit. Where this is not possible refer to section 6.13.

6.7 Presumptive or Screening tests

If no presumptive testing is required proceed to 6.8. If the examining Scientist elects not to perform a presumptive or screening test, a record of this must be recorded in the examination notes (e.g. if presumptive testing would consume the sample). Where an examination strategy has not been prepared, the examining Scientist is responsible for assessing the exhibit and selecting the appropriate presumptive and/or screening tests.

Forensic DNA Analysis uses the following screening tests:

- TMB test for blood – see QIS 17190
- AP test for seminal fluid – see QIS 17186
- Phadebas test for saliva – see QIS 33998
- P30 test for seminal fluid – see QIS 17185.
- Microscopy for spermatozoa – see QIS 17189

Note: Results of a presumptive test must only be recorded if a valid control has passed.

6.7.1 Recording details of presumptive testing

Record the details of a presumptive test against the parent exhibit (testing performed prior to sampling) or the child exhibit (testing performed on the subsample).

1. Click the create exhibit test icon in the exhibit analytical/testing table and select presumptive from the dropdown menu in the process field.

2. Record the results by checking the appropriate radio button and use the comments field to make any additional notes.

3. Enter the results and if necessary add an annotated image into the exhibit's initial Item Exam. If there is insufficient space, creation of a new Item Exam may be necessary.

4. Record details of reagent lot numbers in the Reagents field. The name of the reagent will auto-populate after saving.

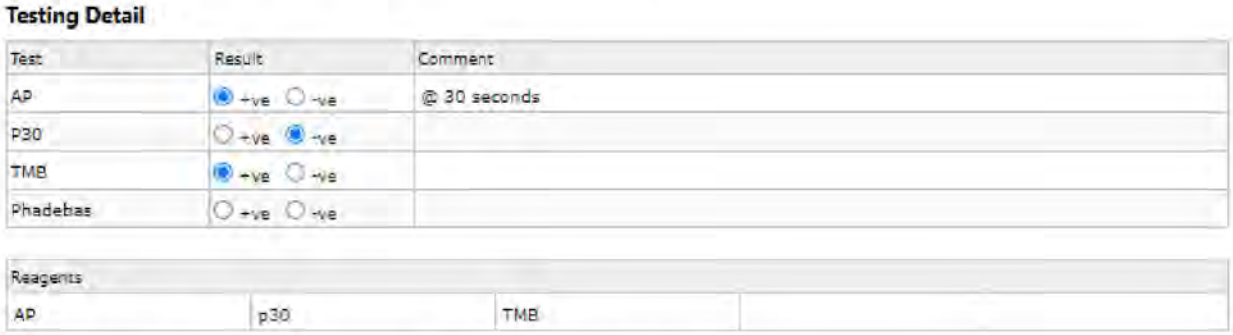


Figure 13 – Presumptive testing detail and reagents fields

5. Click on the save button.

6.8 Registration of subsamples

During an item examination, any samples that are created can be registered as a subsample or alternatively examiners can use the Examination Record process (refer to sections 4.12.4 and 4.12.5 in QIS 33798 to create an examination summary record and register related exhibits). Subsample's must be upgraded to an exhibit before being submitted to Analytical (see section 6.11). This upgrade will ensure that a profile analytical detail page is created and results can be reported back to QPS. See section 6.8.2 for exceptions.

1. Click the create exhibit test icon in the exhibit analytical/testing table and select subsample from the dropdown menu in the process field.

2. In the SubID field click the plus icon to auto assign a new barcode.

3. In the SubType dropdown list select MISC.

4. In the Notes field add a description of the subsample.

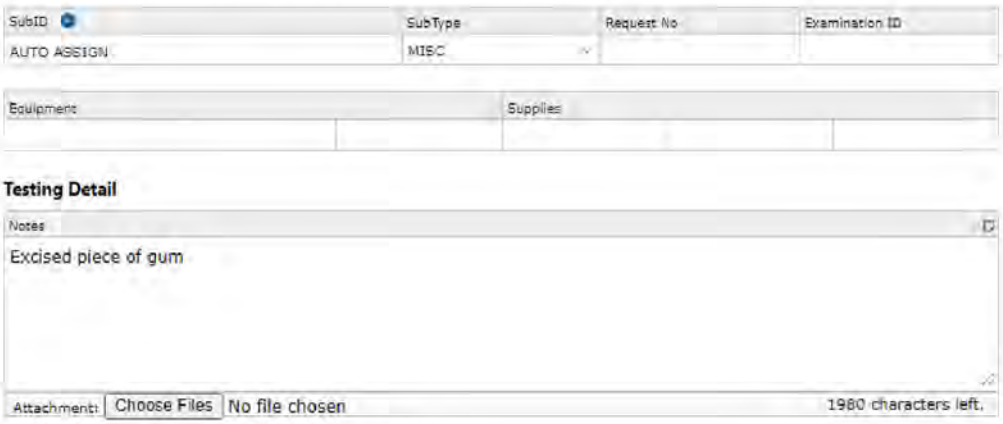


Figure 14 - Subsample registration

5. Click on the save button.
6. Repeat steps 1 – 5 for all subsamples as required.
7. For analytical processing, convert subsamples to child exhibits refer to section 6.11.

6.8.1 Subsamples for retained portions

For portions of a sample that are to be retained (e.g. remainder of filter paper and end of filter of a manufactured cigarette butt), the retained portion must also be registered as a subsample using the following steps.

Note: This subsample is for storage purposes only so will not require conversion to a child exhibit.

1. Click the create exhibit test icon in the exhibit analytical/testing table and select subsample from the dropdown menu in the process field.
2. In the SubID field click the plus icon to auto assign a new barcode.
3. In the SubType dropdown list select RETAIN.
4. In the Notes field add a description of the subsample.
5. Track the item retention box to the examination bench (see section 6.2) and scan the box barcode to the Storage Box ID field. Alternatively, a group of subsamples can be stored as per section 6.13.
6. Scan the label affixed to the relevant tubes into the Tube Lot No field.



Figure 15 – Registering retained portion of cigarette butt

7. Click on the save button.

6.8.2 Subsamples for ante-mortem exhibits

Ante mortem samples that are collected for the purposes of identification only, will remain registered as subsamples and not be upgraded to child exhibits. For example, tissue samples and toothbrushes etc.

6.9 Analytical Notes

1. Click the create exhibit test icon in the exhibit analytical/testing table and select Analytical Note from the dropdown menu in the process field.
2. Use the Notes field to type an appropriate comment for the Analytical team.
3. Click on the save button.

6.10 Printing tube labels

1. On the exhibit record page click the arrow 

icon next to the edit button and select "3 Part Tube Barcode".

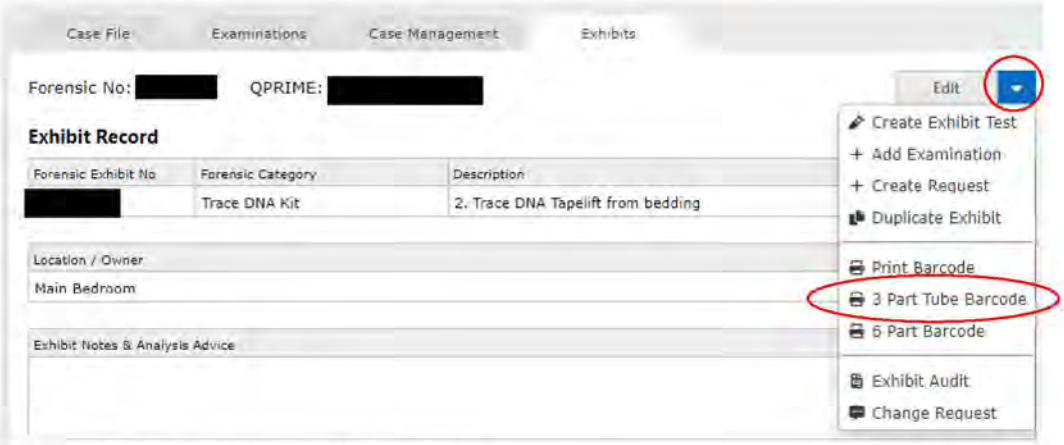


Figure 16 – Printing sample tube labels

2. A new window will open displaying the 3 part label, click the printer icon and select print.
3. To print a subsample barcode, click on the subsample hyperlink from the exhibit record page and follow the above steps.

6.11 Converting subsamples to child exhibits

1. Click on the Exhibits tab and click the add button.



Figure 17 – Exhibits tab and add exhibit button

2. Enter barcode of the subsample into the Forensic Exhibit No field.

Note: A warning will display when a barcode has already been used (e.g. when upgrading a subsample to an exhibit). The warning appears as:

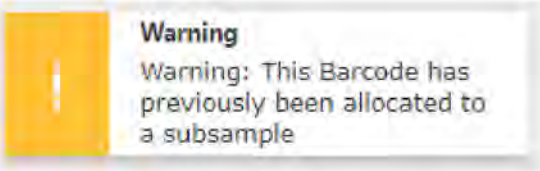
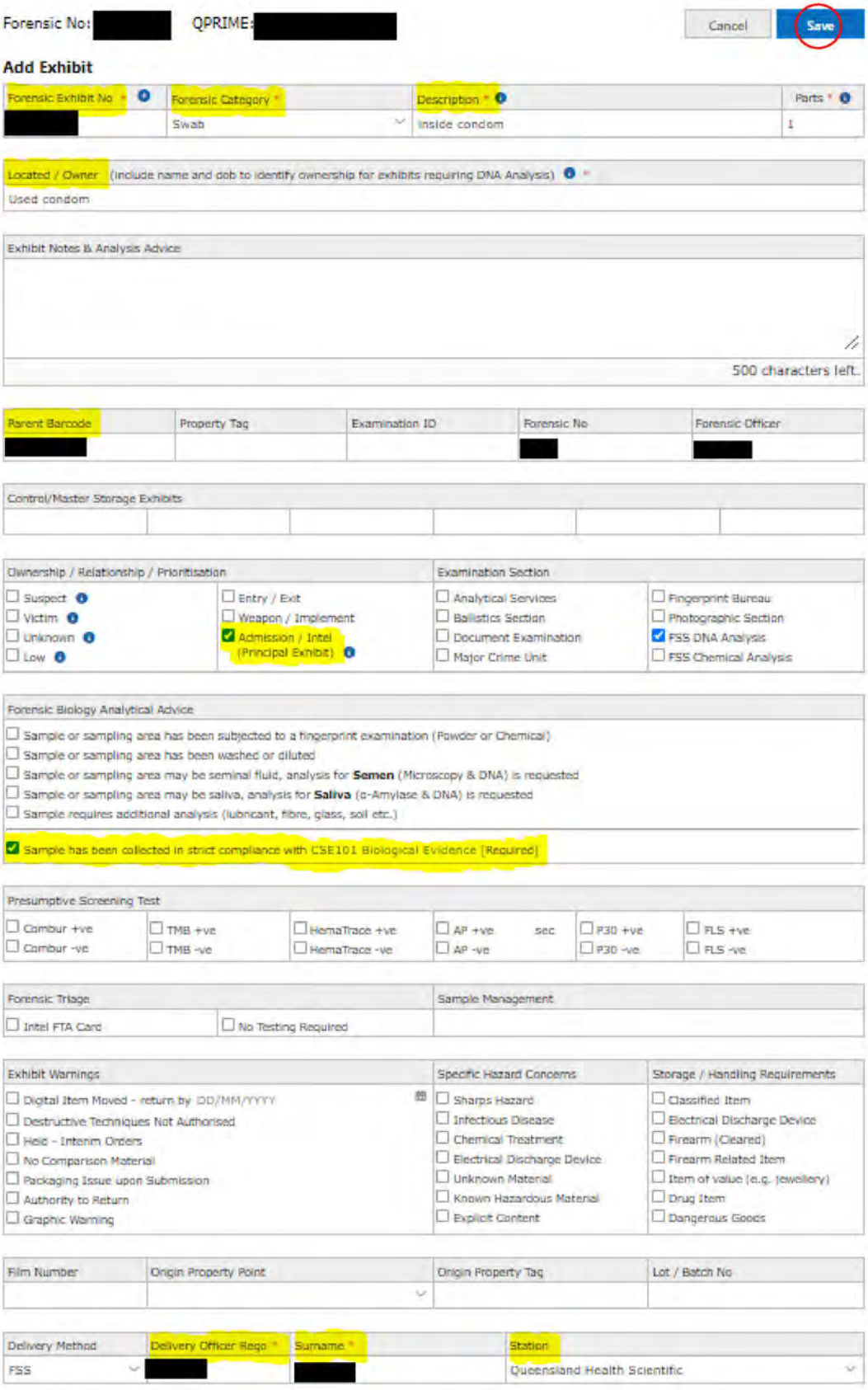


Figure 18 – Warning display

3. In the Forensic Category field select the relevant subsample type from the dropdown menu.
4. Add description of subsample.
5. In the Located/Owner field, copy the relevant description from the parent item. If there is additional information within the Located/Owner field of the parent item indicating ownership (e.g. a name) this must be added.
6. Add the parent barcode into the Parent Barcode field.
7. Tick the "Admission/Intel (Principal Exhibit)" and the "Sample has been collected in strict compliance with CSE101 Biological Evidence [Required]" boxes.
8. The examiner must enter their FR User ID in the Delivery Officer Rego field, press tab for the Surname field to auto-populate and select Queensland Health Scientific from the dropdown list in the Station field.
9. Click on the save button.
10. Repeat steps 1 – 9 for all subsamples if required.



Forensic No: [redacted] QPRIME: [redacted]

Cancel Save

Add Exhibit

Forensic Exhibit No *	Forensic Category *	Description *	Parts *
[redacted]	Swab	inside condom	1

Located / Owner (include name and dob to identify ownership for exhibits requiring DNA Analysis) *

Used condom

Exhibit Notes & Analysis Advice

500 characters left.

Parent Barcode	Property Tag	Examination ID	Forensic No	Forensic Officer
[redacted]			[redacted]	[redacted]

Control/Master Storage Exhibits

Ownership / Relationship / Prioritisation		Examination Section	
☐ Suspect	☐ Entry / Exit	☐ Analytical Services	☐ Fingerprint Bureau
☐ Victim	☐ Weapon / Implement	☐ Ballistics Section	☐ Photographic Section
☐ Unknown	☑ Admission / Intel (Principal Exhibit)	☐ Document Examination	☑ FSS DNA Analysis
☐ Low		☐ Major Crime Unit	☐ FSS Chemical Analysis

Forensic Biology Analytical Advice

- ☐ Sample or sampling area has been subjected to a fingerprint examination (Powder or Chemical)
- ☐ Sample or sampling area has been washed or diluted
- ☐ Sample or sampling area may be seminal fluid, analysis for **Semen** (Microscopy & DNA) is requested
- ☐ Sample or sampling area may be saliva, analysis for **Saliva** (α-Amylase & DNA) is requested
- ☐ Sample requires additional analysis (lubricant, fibre, glass, soil etc.)

☑ Sample has been collected in strict compliance with CSE101 Biological Evidence [Required]

Presumptive Screening Test

☐ Combur +ve ☐ Combur -ve	☐ TMB +ve ☐ TMB -ve	☐ HemaTrace +ve ☐ HemaTrace -ve	☐ AP +ve sec ☐ AP -ve	☐ P30 +ve ☐ P30 -ve	☐ FLS +ve ☐ FLS -ve

Forensic Triage		Sample Management
☐ Intel FTA Card	☐ No Testing Required	

Exhibit Warnings	Specific Hazard Concerns	Storage / Handling Requirements
☐ Digital Item Moved - return by DD/MM/YYYY	☐ Sharps Hazard	☐ Classified Item
☐ Destructive Techniques Not Authorised	☐ Infectious Disease	☐ Electrical Discharge Device
☐ Helc - Interim Orders	☐ Chemical Treatment	☐ Firearm (Cleared)
☐ No Comparison Material	☐ Electrical Discharge Device	☐ Firearm Related Item
☐ Packaging Issue upon Submission	☐ Unknown Material	☐ Item of value (e.g. jewellery)
☐ Authority to Return	☐ Known Hazardous Material	☐ Drug Item
☐ Graphic Warning	☐ Explicit Content	☐ Dangerous Goods

Film Number	Origin Property Point	Origin Property Tag	Lot / Batch No

Delivery Method	Delivery Officer Rego *	Surname *	Station
FSS	[redacted]	[redacted]	Queensland Health Scientific

Figure 19 – Exhibit Record

11. Any further testing carried out on the child exhibit (e.g. presumptive testing) is to be added to the Exhibit Analytical/Testing table on the child exhibit.

6.12 Entering exhibit result lines

Exhibit result lines are created to communicate results to the QPS electronically. Some results will automatically be generated by ticking various boxes or radio buttons; however, some results will need to be entered manually following the steps below:

Note: The result lines only appear in the Exhibit Analytical/Testing table (and are auto-validated) after the associated process has been validated. Refer to appendix 10.1 for manual and automatic result lines.

1. Click the create exhibit test icon in the exhibit analytical/testing table and select Result from the dropdown menu in the process field.
2. In the Police Report field select the appropriate result(s) from the dropdown menu (up to three results can be added at any one time).
3. Click on the save button.

6.13 Sample tracking

If samples have not been stored during the examination, they can be added to a storage box at the end.

1. Click the equipment and supplies icon and select "Storage Box Search". Scan the ERT-AS box barcode into the storage box no field and press enter or click submit.



Figure 20 – Storage Box search table

2. Check that the latest entry in the Box Movement table is the examination bench. If necessary, click the plus icon and enter "EVI" into the storage location field and select "FDNA-EREB- (DNA Evidence Recovery Bench) and enter the bench number, press the save button.

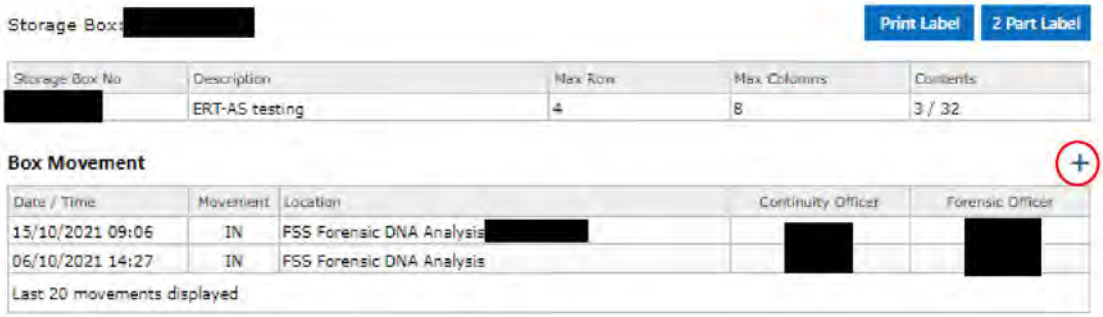


Figure 21 – Box Movement table

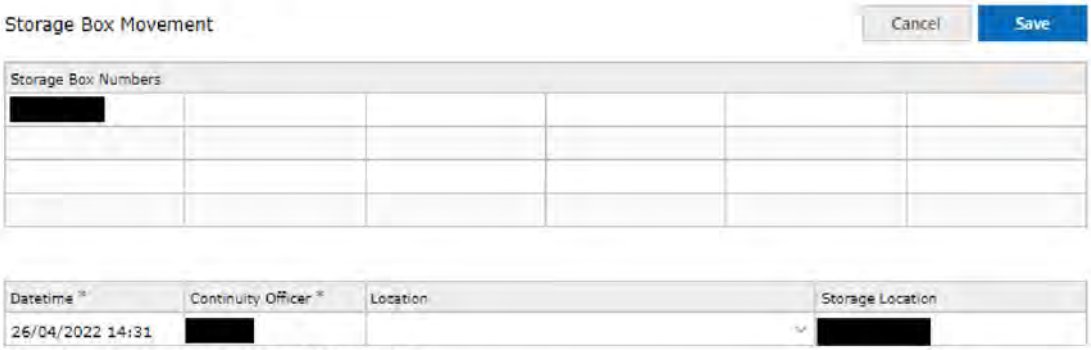


Figure 22 – Storage Box Movement

3. Click on the Storage Box Contents tab and click the Add to Storage Box button.

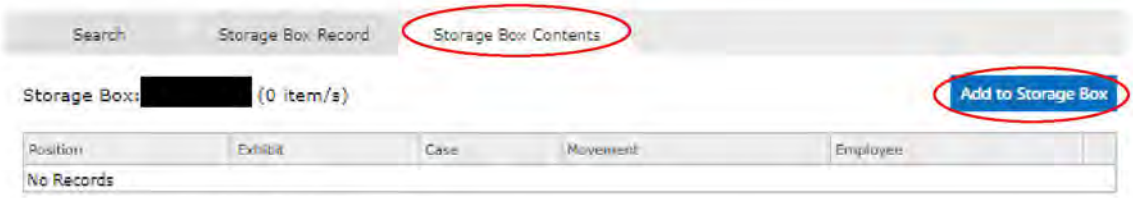


Figure 23 – Storage Box Contents

4. Scan the barcode of the tube into the Forensic Exhibit No field, note the position in the rack and place the tube into that position.

5. Click on the save button or press enter. Repeat the above steps for any further tube storage.

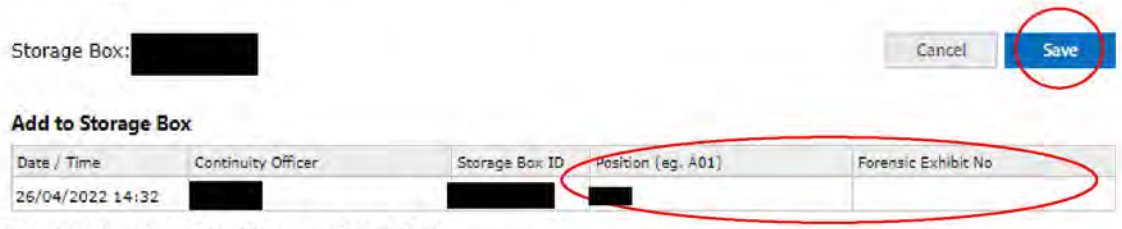


Figure 24 – Add to Storage Box table

6. Follow step 2 and track the ERT-AS box to the generic laboratory location ([redacted]), place the storage box in the pass-through hatch.

7. The pass-through hatch must be checked each afternoon and any ERT-AS boxes that have not been collected must be stored to freezer box 1 ([redacted]), following the procedure in section 6.2.

6.14 Exhibit repackaging and return

Exhibits should be repackaged in the same packaging if practical. Re-seal the openings with evidence tape, sticky tape or heat seal and initial and date the seal.

If an exhibit is wet as the result of examination, it can be placed on the drying rails overnight. Ensure that the rails are cleaned with bleach and ethanol before and after drying. Exhibits must have a piece of brown paper between the rail and the item and an additional piece of brown paper covering the item. Ensure that the brown paper is adequately labelled.

If examination of an exhibit is not complete, the item must be tracked back to freezer box 2 or a shelf in the exhibit room. Where the examination is complete, the exhibit must be tracked to the Exhibit Room return location for room temperature samples ([redacted]) or to the Freezer returns location for frozen samples ([redacted]). Exhibits should be stored in the same way they were received (room temperature or freezer).

6.15 Temporary storage of CSSE and destruction

Empty CSSE's are placed into a bundle according to the month they are examined, within the items destruction box, which is located in the Evidence Recovery laboratory.

A bundle of CSSE's that were processed 3 months prior must be discarded into a biohazard bin every month.

Note: CSSE's are not to be tracked electronically to the destruction box.

CSSE's that contained multiple cigarette butts require an exhibit movement on the parent barcode (the CSSE). In the location field select "DESTROYED" from the dropdown menu and click the save button.

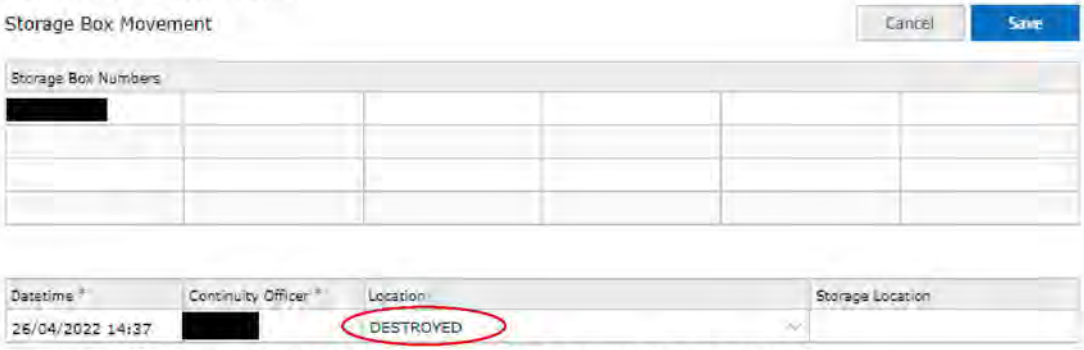


Figure 25 – Destruction of CSSE for multiple cig butts in one CSSE

6.16 Repackaging of multiple exhibits (subsamples and or child exhibits) into primary packaging

On rare occasions multiple exhibits (subsamples and or child exhibits) may be repackaged into one larger outer package for storage and/or return. In these instances, the individual exhibits cannot be left tracked to an examination bench or laboratory location, nor should they be marked as destroyed. As such these items are to be stored to "Stored in primary packaging" enter [redacted] in the Storage Box ID field.

6.17 Examination and sampling of manual reference samples

All manual reference samples (e.g. hair, swabs, Guthrie cards, fingernails etc.) are to be examined by the Evidence Recovery team and must be registered as "Reference" in the forensic category field to ensure that the sample is allocated to the correct Analytical batch. Inform the Quality and Projects team if this is not the case upon examination as the category will need to be changed. A notation will be added to the exhibit to state the reason for the change "Category changed to "Reference" to ensure correct reference processing". All samples that are designated as reference samples **must** be examined and sampled on Examination **Bench 15** ([redacted]).

Manual reference samples will be tracked to a storage box labelled "Evidence Sample – Manual" by the Quality and Projects team and placed on the daily shelves in the exhibit room ([redacted]). The sample will be visible on the Examination worklist.

The principles of examination and sampling of reference samples are the same as those for casework exhibits.

1. Click the create exhibit test icon in the exhibit analytical/testing table and select Item Exam from the dropdown menu in the process field.
2. In the Notes field, write a brief description of the sampling performed.
3. Click on the save button.
4. Click the create exhibit test icon in the exhibit analytical/testing table and select Subsample from the dropdown menu in the process field.
5. In the SubID field click the plus icon in the forensic exhibit no field to auto assign enter a new barcode; this barcode will go onto the sample tube. A printed barcode must also be attached to the outside of the reference packaging i.e. envelope, CSPB etc. for tracking purposes.
6. In the SubType dropdown menu select EREF.
7. Examine the reference sample appropriately. For FTA cards excise ~5mm x ~5mm section from each of the black circles on the FTA card and place into an appropriately labelled 2mL tube.
8. In the Storage Box ID field scan the barcode of the ERT-AS box.
9. Scan the barcode that is affixed to the bag of tubes in the Tube Lot No field.
10. Select DNA Extraction from the Technique field dropdown menu.
11. Select Maxwell 16 DNA IQ from the Method field dropdown menu and press the save button.

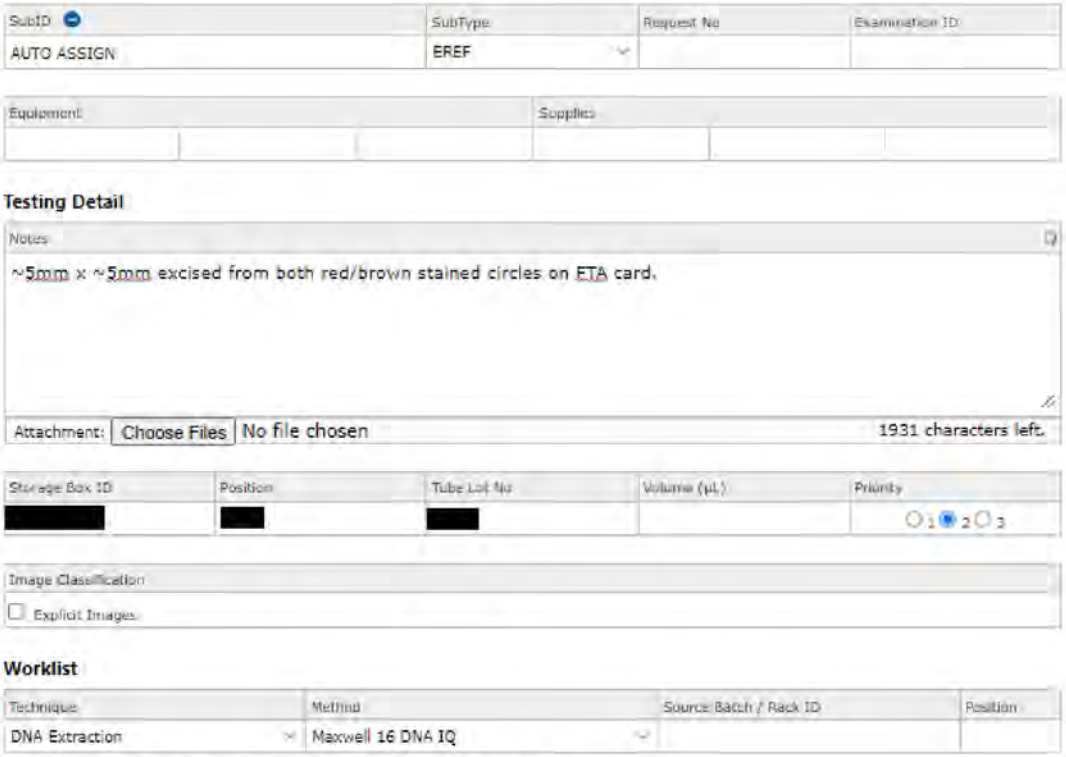


Figure 26 – Examination of reference samples

7 Associated Documentation

QIS: 14576 – Blood and Body Fluid Biological Exposure
QIS: 17185 – Detection of Azoospermic Semen in Casework Samples
QIS: 17186 – The Acid Phosphatase screening test for seminal stains
QIS: 17189 – Examination For & Of Spermatozoa
QIS: 17190 – Tetramethylbenzidine Screening Test for Blood
QIS: 22857 – Anti-contamination Procedure
QIS: 23849 – Common Forensic DNA Analysis Terms and Acronyms
QIS: 23959 – Storage Guidelines for Forensic DNA Analysis
QIS: 30800 – Investigating Adverse Events in Forensic DNA Analysis
QIS: 33771 – Examination of in-tube samples
QIS: 33798 – Examination of Sexual Cases
QIS: 33998 – Phadebas Test for Saliva
QIS: 34300 – Examination of post mortem and associated samples from deceased persons

8 References

AS2243.1:2005 Safety in Laboratories Part 1 - General

Workplace Health and Safety Act 2011

Workplace Health and Safety Regulation 2011

Workplace Health and Safety Advisory Standards – various

Health, safety and wellbeing | HSQ staff site

9 Amendment History

Version	Date	Updated By	Amendments
1	10/06/2016	A Houlding	First issue.
2	14/06/2017	A Ryan	Added storage procedure, reference sample examination, explanation of subsamples and destruction of packaging. Added subsample label printing. Added annotating images. Moved all the general principles for sample selection, sampling techniques and specific examination strategies to the beginning of the document. Added entering exhibit result lines. Added workflow appendices
3	12/12/2017	A McNevin	Minor edits to reflect FR updates/enhancements and procedure changes, inclusion of pooling, return to primary packaging and multiples items in one package, inclusion of contents of archived SOP 17135.
4	02/11/2018	N Roselt	Minor edits to reflect current FR processes/enhancements. Updated screenshots to reflect FR enhancements. Added information to description of exhibits section (6.6). Updated process for lubricant testing. Added information regarding invasive sampling techniques. Updated pooling appendix and reference sample workflow. Inclusion of workflow for submitting retained portions of cig butts (appendix 6). Added standardised wording for request/tasks
5	05/09/2019	S Byrne	Changes to reflect new equipment and usage for examination of syringes, needles and similar sharps – safety and procedure. Amend typo's and some wording, add exhibit testing procedure with changes: Worklist and Method now added at validation.
6	30/07/2021	K Morton A McNevin	Added new standard wording for request/tasks. Added procedure for handling large fluid samples. Updated referenced and associated documents. Updated and added INT result line to appendix. Added new hair process for items and removed hair associated document. Removed lubricant testing procedure. Updated pooling process. Added additional information on syringes Removed

Version	Date	Updated By	Amendments
			Forensic Register from document title, new template.
7	26/04/2022	K Morton	New template, updated screenshots and content to reflect current procedures. Added exhibit test incorrection process. Removed requirement for notation in pooled samples. Amended appendices titles.

10 Appendices

1 Appendix 1: Exhibit Result Lines
2 Appendix 2: Workflow for basic item submitted in entirety
3 Appendix 3: Workflow for basic item partial submission (rest of item returned)
4 Appendix 4: Workflow for basic item with retained portion
5 Appendix 5: Workflow for multiple items in one CSSE
6 Appendix 6: Workflow for submitting retained portions
7 Appendix 7: Pooling of samples
8 Appendix 8: Standardised wording for request/tasks
9 Appendix 9: Incorrect exhibit tests

10.1 Appendix 1: Exhibit Result Lines

Table 1 – Exhibit result lines

Exhibit Result Line	Automatic or Manual	Functions that trigger automatic results
1BPPSR – Presumptive blood test pos. Submitted-results pending	Automatic	TMB pos box ticked **and** DNA extraction selected
HAIRNFA – Hair located – not examined at this time	Manual	N/A
HOIS – Hair located on the outside of an in-tube submission	Automatic	"Hair located on the outside of tube" box ticked
IPNE – Items Prioritised. Not examined at this time	Manual	N/A
ISCB – Incorrect submission of cigarette butt	Manual	N/A
LDIS – Labelling discrepancy	Automatic	"Labelling discrepancy" box ticked
MIES – Sample required manual intervention - excess substrate	Automatic	"Excess substrate" box ticked
MIISB – Multiple items incorrectly submitted under single barcode	Manual	N/A
MISSTL – Sample required manual intervention - swab stick too long	Automatic	"Swab stick too long" box ticked
MITRI – Sample reqd manual intervention- tlift rolled incorrectly	Automatic	"Tapelift rolled incorrectly" box ticked
MNS – Micro neg for sperm	Automatic	See appendices 1 & 2 in QIS 33798 Examination of Sexual Cases
NBOS – No barcode on sample	Automatic	"No barcode on sample" box ticked
PAPPRP – Presump. PSA test positive, submitted - results pending	Automatic	See appendices 1 & 2 in QIS 33798 Examination of Sexual Cases
PBNSC – Presumptive blood test neg. Submitted for cells	Automatic	TMB neg box ticked **and** DNA extraction selected
PBTN – Presumptive blood test negative	Automatic	TMB neg box ticked (no extraction method selected)
PPSRP – Presump. AP test positive, submitted - results pending	Automatic	See appendix 2 in QIS 33798 Examination of Sexual Cases
PREBT – Presumptive blood test positive	Automatic	TMB pos box ticked (no extraction method selected)
PSNSC – Presump saliva negative. Submitted for cells	Automatic	Phadebas neg box ticked **and** DNA extraction selected
PSPSRP – Presump saliva positive. Submitted-results pending	Automatic	Phadebas pos box ticked **and** DNA extraction selection.
PSTN – Presump saliva test negative	Automatic	Phadebas neg box ticked (no extraction method selected)
PSTP – Presump saliva test positive	Automatic	Phadebas pos box ticked (no extraction method selected)
SEMND – Semen not detected	Manual	N/A
SOHAA – Sample on hold, awaiting advice	Manual	N/A
SPPDNA – Micro positive for sperm. Submitted-results pending	Automatic & Manual	See appendices 1 & 2 in QIS 33798 Examination of Sexual Cases
SRMI – Sample required manual intervention prior to DNA extraction	Automatic	"Other manual intervention required" box ticked

Exhibit Result Line	Automatic or Manual	Functions that trigger automatic results
SRP – Submitted-results pending	Automatic for in-tubes Manual for items	In-tube process selected and "DNA Extraction" selected in the technique field
TRQ – Testing restarted on advice from QPS	Manual	N/A
EXREV – Extra information on reverse of crime scene sample envelope	Automatic	"Additional Information on reverse of CSSE" box ticked
NWQPS – No further work required as per advice from QPS	Automatic / Manual	"No Testing Required" box is ticked by QPS Result can be added manually if advised appropriately
INT – Item has been examined/sub-sampled	Manual	N/A
PSFTN – Presump seminal fluid test negative	Manual	See appendix 2 in QIS 33798 Examination of Sexual Cases

10.2 Appendix 2: Workflow for basic item submitted in entirety

1. Scan barcode into the key identifier search icon, press enter or click search.
2. Using the exhibit movement table, track item to an examination bench.
3. Click thumbnail of CSSE. Check image. Close the image window.
4. Add additional images: Upload images into the Item Exam.
5. Check testing requirements for biological screening.
6. Exhibit Analytical/Testing table → create exhibit test icon
   - In the process field select Item Exam
   - Tick the relevant boxes under packaging and sample assessment notes
   - Use the notes field to enter examination notes, use the tick boxes if required
   - Enter a storage box barcode
   - Enter a tube lot number barcode
   - Save
7. Exhibit Analytical/Testing table → create exhibit test icon
   - In the process field select result
   - Select the appropriate result from the dropdown menu under Police Report
   - Save
8. Put CSSE in destruction box.

10.3 Appendix 3: Workflow for basic item partial submission (rest of item returned)

1. Scan barcode into the key identifier search icon, press enter or click search.
2. Using the exhibit movement table, track item to an examination bench.
3. Click thumbnail of CSSE. Check image. Close the image window.
4. Add additional images: Upload images to the Item Exam.
5. Exhibit Analytical/Testing table → create exhibit test icon
   - In the process field select Item Exam
   - Tick the relevant boxes under packaging and sample assessment notes
   - In the notes field type examination notes e.g. description of item and the sampling strategy
   - Save
6. Create subsample for portion that is being submitted.
   - Exhibit Analytical/Testing table → create exhibit test icon
   - In the process field select Subsample
   - In the SubID click the plus icon in the forensic exhibit no field to auto assign a new barcode
   - In the SubType dropdown list select MISC
   - In the notes field add a description of the subsample
   - Save
7. Convert sample to child exhibit.
   - Click on Exhibits tab
   - Click the add button
   - Enter barcode of subsample that was just created in the Forensic Exhibit No field
   - In the forensic category field select the relevant subsample type
   - Add description of subsample
   - In the Located/Owner field copy the relevant description from the parent item. Include any ownership details from the parent item into the "Located/Owner" field
   - Enter the parent barcode into the Parent Barcode field
   - Tick the following boxes: "Admission/Intel" and "Sample has been collected in strict compliance with CSE101 Biological Evidence"
   - Add a FR User ID in the Delivery Officer Rego field; press tab for surname to auto fill. Select Queensland Health Scientific
   - Save
8. Exhibit Analytical/Testing table → create exhibit test icon
   - In the process field select Item Exam (brief description of what the item is)
   - Add a storage location (ERT-AS storage box) and tube lot number
   - Save
9. Exhibit Analytical/Testing table → create exhibit test icon
   - In the process field select Result
   - Select the appropriate result from the dropdown menu labelled Police Report
   - Save
10. Create new exhibit movement for the parent barcode and track to a returns location.

10.4 Appendix 4: Workflow for basic item with retained portion

1. Scan barcode into the key identifier search icon, press enter or click search.
2. Using the exhibit movement table, track item to an examination bench.
3. Click thumbnail of CSSE. Check image. Close the image window.
4. Add additional images: Upload images to the Item Exam.
5. Exhibit Analytical/Testing table → create exhibit test icon
   - In the process field select Item Exam
   - Tick the relevant boxes under packaging and sample assessment notes
   - Tick relevant boxes in the testing detail tables
   - Add a storage location (ERT-AS box)
   - Add tube lot number
   - Save
6. Exhibit Analytical/Testing table → create exhibit test icon
   - In the process field select Subsample
   - In the SubID field click the plus icon in the forensic exhibit no field to auto assign a new barcode
   - In the SubType field click RETAIN
   - Fill in details of what was retained in the notes field
   - Add an item retention storage box barcode
   - Add a tube lot number
   - Save
7. Exhibit Analytical/Testing table → create exhibit test icon
   - In the process field select Result
   - Select the appropriate result from the dropdown menu labelled police report
   - Save
8. Put CSSE into the items destruction box

10.5 Appendix 5: Workflow for multiple items in one CSSE

1. Scan barcode into the key identifier search icon, press enter or click search.
2. Using the exhibit movement table, track item to an examination bench.
3. Click thumbnail of CSSE. Check image. Close the image window.
4. Add additional images: Upload images to the Item Exam.
5. Exhibit Analytical/Testing table → create exhibit test icon
   - In the process field select Item Exam
   - Tick the relevant boxes under packaging and sample assessment notes
   - Type relevant information on what is contained within the CSSE into the notes field
   - Save
6. Create subsamples (or an Examination Record) for individual items. Exhibit Analytical/Testing table → create exhibit test icon
   - In the process field select Subsample
   - In the SubID field click the plus icon in the forensic exhibit no field to auto assign a new barcode
   - In the SubType dropdown list select MISC
   - In the notes field add a description of the subsample
   - Save
   - Repeat for subsequent items.
7. Convert subsamples to child exhibits
   - Click on exhibits tab
   - Click the add button
   - Enter barcode of subsample that was just created in the forensic exhibit no field
   - In the forensic category field select the relevant subsample type
   - Add description of the subsample
   - In the Located/Owner field copy the relevant description from the parent item. Include any ownership details from the parent item into the "Located/Owner" field
   - In the parent barcode field add the parent barcode
   - Tick the following boxes: "Admission/Intel" and "Sample has been collected in strict compliance with CSE101 Biological Evidence"
   - Add a FR User ID in the Delivery Officer Rego field; press tab and your surname will automatically appear. Select Queensland Health Scientific
   - Save
   - Click the back button and repeat for subsequent subsamples
8. Complete an item exam the first child exhibit. Exhibit Analytical/Testing table → create exhibit test icon
   - In the process field select Item Exam
   - Tick relevant boxes under cigarette butt notes and fill in details in notes field.
   - Add a storage location (ERT-AS box)
   - Add tube lot number
   - Save

9. Exhibit Analytical/Testing table → create exhibit test icon
    - In the process field select Subsample
    - In the SubID field click the plus icon in the forensic exhibit no field to auto assign a new barcode
    - In the SubType field click RETAIN
    - Fill in details of what was retained in the notes field
    - Add an item retention storage box barcode
    - Add a tube lot number
    - Save
10. Exhibit Analytical/Testing table → create exhibit test icon
    - In the process field select Result
    - Select the appropriate result from the dropdown menu labelled police report
    - Save
11. Repeat steps 7 – 9 for subsequent items
12. Put CSSE into the items destruction box
13. Add new exhibit movement for the parent item and select DESTROYED in the location field
14. In parent Item Exam - Exhibit Analytical/Testing table → create exhibit test icon
    - In the process field select Result
    - Select: MIISB - Multiple items incorrectly submitted under single barcode
    - Save

10.6 Appendix 6: Workflow for submitting retained portions

1. Scan barcode into the key identifier search icon, press enter or click search.
2. Click subsample time/date hyperlink and use the subsample movement table to track item to an examination bench.
3. Exhibit Analytical/Testing table → create exhibit test icon
    - In the process field select Item Exam
    - In the notes field type examination notes e.g. description of retained portion and the sampling strategy
    - Save
4. Create a subsample (if necessary) for any remaining portions of the retained subsample to be submitted. Exhibit Analytical/Testing table → create exhibit test icon
    - In the process field select Subsample
    - In the SubID field click the plus icon in the forensic exhibit no field to auto assign a new barcode
    - In the SubType dropdown list select MISC
    - In the notes field add a description of the subsample
    - Save
    - Repeat for subsequent portions (if necessary).
5. Convert original subsample barcode to child exhibit
    - Click on exhibits tab
    - Click the add button
    - Enter barcode of the subsample into the forensic exhibit no field
    - In the forensic category field select the relevant subsample type (cigarette butt)
    - Add description of the subsample
    - In the Located/Owner field copy the relevant description from the parent item. Include any ownership details from the parent item into the "Located/Owner" field
    - In the parent barcode field add the parent barcode
    - Tick the following boxes: "Admission/Intel" and "Sample has been collected in strict compliance with CSE101 Biological Evidence"
    - Add a FR User ID in the Delivery Officer Rego field; press tab and your surname will automatically appear. Select Queensland Health Scientific
    - Save
    - Click the back button and repeat for subsequent subsamples
6. Complete an item exam on all child exhibits. Exhibit Analytical/Testing table → create exhibit test icon
    - In the process field select Item Exam
    - In the notes field type examination notes e.g. description of retained portion
    - Add a storage location (ERT-AS box)
    - Add tube lot number (unless portion is remaining in original retention tube, this should be noted)
    - Save
7. Exhibit Analytical/Testing table → create exhibit test icon
    - In the process field select Result
    - Select the appropriate result from the dropdown menu labelled police report
    - Save

10.7 Appendix 7: Pooling of samples

1. Complete an item exam on the parent barcode, create a RETAIN subsample for any retained portions (e.g. cigarette filter) and create an appropriate number of MISC subsamples.

2. Convert MISC subsamples to child exhibits and complete an item exam for each (include the storage location and tube lot number).

3. Create an Analytical note against each child exhibit stating, "Hold after EXT: sample to be pooled".

Examinations +

Exam Date	Location	Examination	Forensic Officer	Result
26/04/2022 12:30	PSD	1831 PH RM	[redacted]	POS

Exhibit Analytical / Testing

Date / Time	Technique	Testing Summary -	P3	Employee	Reviewer
26/04/2022 12:08	Subsample	[redacted] MISC]		[redacted]	[redacted]
26/04/2022 12:28	Item Exam	Half of entire filter paper (filter end of cigarette)			
26/04/2022 12:34	Result	Sample pooled and processed under [redacted]			
26/04/2022 12:40	Analytical Note	Hold after EXT, sample to be pooled.			

Figure 27 – Exhibit Analytical/Testing and Examination tables for pooled samples

4. Create a new Examination Record under one of the child exhibits, enter the new child exhibit barcodes that are to be pooled together into the Exhibit/s Examined field and add "For Pooling" in the Examination Notes. All other mandatory fields are to be completed as per a regular examination record.

5. Save the Examination Record and ensure the Exhibits Examined field appears as per Figure 28. The examination record will now appear in the Examinations table for each child exhibit.

Exhibits Examined	Total Exhibits 2
[redacted]	filter paper from filter end (Cigarette Butt) GR201 unsmoked Test street POE [redacted]
	filter paper from tobacco end (Cigarette Butt) GR201 unsmoked Test street POE [redacted]

Figure 28 – Exhibits Examined

6. Click the arrow 

icon next to the edit button and select add related exhibit to the examination record, click the plus icon to auto assign a new barcode (this will be the pooled barcode).

7. Select the appropriate category according to what the parent item is. The Description and Located/Owner fields are auto populated. The remaining fields are to be completed as per usual processes.

   Note: No parent barcode is required.

Exhibit Record

Forensic Exhibit No	Forensic Category	Description	Parts
[redacted]	Cigarette Butt	Pooled Sample	1

Location / Owner
Pooled from [redacted]

Figure 29 – Registration of pooled sample

8. The sample will now appear on the POOLING review list for analytical to check and validate.

   Note: ER staff are **not** to validate the Pooling line on the pooled barcode as it triggers downstream processing actions in Analytical (see Figure 30).

9. Add an analytical note to the pooled barcode "Please add to Quant worklist".

10. It is not necessary to add any result lines to a pooled sample as automatic result lines are sent upon validation.

Exhibit Analytical / Testing

Date / Time	Technique	Testing Summary -	P3	Employee	Reviewer
26/04/2022 12:34	Pooling	Pooled from [redacted]		[redacted]	
26/04/2022 12:41	Analytical Note	Please add to Quant worklist.			[redacted]

Link Chart

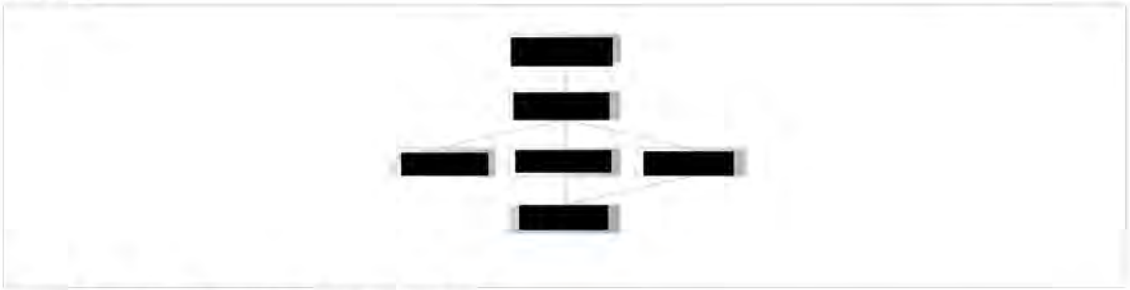


Figure 30 – Pooled sample on link chart

11. Use the Exhibit Movement table to track the parent barcode to 'DESTROYED'.

10.8 Appendix 8: Standardised wording for request/tasks

As each case / exhibit circumstance may be different, the wording below may be adjusted for content where appropriate.

10.8.1 Male/Suspect clothing for semen:

Date/Initials – Hello,
Regarding exhibit XXXXXXXXX - AP positive fabric, the FR indicates that this is a sample of fabric from underwear belonging to the suspect and semen testing is required. For cases of alleged male on female sexual assault, Semen testing on male suspect underwear is not routinely performed given that the presence of semen is not an unexpected finding. Please confirm if semen testing is still required. The item has been placed on hold pending your response.
regards
Your NAME

10.8.2 Adult Female undies for saliva testing:

Date/Initials – Hello,
Regarding exhibit XXXXXXXXX - underwear from complainant, this whole item/fabric has been submitted for saliva and seminal fluid testing. Saliva testing of the crotch area of adult female underwear is not routinely performed due to the high concentration of amylase present in vaginal secretions and faecal matter. False positive reactions, therefore, are likely. Please confirm if saliva testing is still required. The item has been placed on hold pending your response.
regards
Your NAME

10.8.3 SAIK without medical notes or QP127

Date/Initials – Hello,
We have received a SAIK barcode XXXXXXXXX without any accompanying Medical notes or a QP127. These notes assist in determining how these exhibits are examined. Please confirm if notes were taken during the SAIK examination and if so please forward to Forensic DNA Analysis. The SAIK has been placed on hold pending your response.
regards
Your NAME

10.8.4 Spelling of names on a SAIK doesn't match – paperwork/SAIK packaging/FR

Date/Initials – Hello,
We have received a SAIK barcode XXXXXXXXX which has discrepancies in the spelling of the complainants' name. The FR states XXXXXXXXX, the FMO notes state XXXXXXXXX and the SAIK packaging states XXXXXXXXX. Please confirm the correct name of the complainant.
regards
Your NAME

10.8.5 Lubricant testing – is it required?

Date/Initials - Hello,
We have received a SAIK barcode XXXXXXXXX into Forensic DNA Analysis with medical paperwork that states lubricant (namely XXXXXXXXX) was used during the alleged sexual assault however; the box for FSS Chemical Analysis has not been ticked. Can you please advise whether lubricant testing is required and if so, can you please tick the FSS Chemical Analysis box in the Examination Section on the Exhibit Record page. Please be aware that if lubricant testing is required a sample of the lubricant used during the alleged sexual assault will need to be sought for comparison. This SAIK has been placed on hold pending your response.
regards
Your NAME

10.8.6 AP Blotting paper and AP fabric received at same time

(note – if AP fabric has already been tested and is negative, do not use this wording)
Date/Initials - Hello,
We have received both an area of AP positive fabric (exhibit XXXXXXXXX) & the associated blotting paper (exhibit XXXXXXXXX) of the positive AP reaction of the same area. In our experience, the blotting paper used to perform AP testing does not yield informative results, and when AP testing with blotting paper is performed in our laboratory it is not retained for future testing. It is recommended that only the positive area(s) of the item tested be submitted for further testing. We are seeking permission to place the blotting paper (exhibit XXXXXXXXX) on-hold pending the outcome of DNA testing on the associated area of fabric (exhibit XXXXXXXXX). If informative DNA results are obtained from the fabric, we request that the blotting paper be returned untested.
regards
Your NAME

10.8.7 AP Blotting paper received and AP fabric already positive result

Date/Initials - Hello,
We have received both an area of AP positive fabric (exhibit XXXXXXXXX) & the associated blotting paper (exhibit XXXXXXXXX) of the positive AP reaction of the same area. In our experience, the blotting paper used to perform AP testing does not yield informative results, and when AP testing with blotting paper is performed in our laboratory it is not retained for future testing. It is recommended that only the positive area(s) of the item tested be submitted for further testing. As results have already been obtained for the associated area of fabric (exhibit XXXXXXXXX), we are seeking permission to return the blotting paper (exhibit XXXXXXXXX) untested. If this is acceptable, please mark the item with "No Testing Required"; alternatively, if testing is still required, please advise.
regards
Your NAME

10.8.8 Discrepancy for exhibit record description (Item placed on-hold):

Date/Initials – Hello,
Regarding exhibit barcode XXXXXXXXX, the Exhibit Record Description in the Forensic Register states "A B C", however the Crime Scene Envelope states "X Y Z". Please confirm the correct description for this exhibit and adjust any Forensic Register records as necessary, or alternatively the item can be returned for your correction. This item has been placed on hold pending advice.
regards
Your NAME

10.8.9 FR number discrepancy (Item placed on-hold):

Date/Initials – Hello,
Regarding exhibit barcode XXXXXXXXX, the exhibit is registered in the Forensic Register under FR number "1 2 3", however the Crime Scene Envelope states "3 2 1". Please confirm the correct FR number for this exhibit and adjust any Forensic Register records as necessary, or alternatively the item can be returned for your correction. This item has been placed on hold pending advice.
regards
Your NAME

10.8.10 Discrepancy for exhibit record description (Item NOT placed on-hold):

Date/Initials – Hello,
Regarding exhibit barcode XXXXXXXXX, the Exhibit Record Description in the Forensic Register states "A B C", however the Crime Scene Envelope states "X Y Z". Please confirm the correct description for this exhibit and adjust any Forensic Register records as necessary.

regards
Your NAME

10.8.11 Discrepancy in forensic category (Item placed on-hold):

Date/Initials – Hello,
Regarding exhibit barcode XXXXXXXXX, the Exhibit Record Forensic Category in the Forensic Register states "A B C", however the exhibit received with the Crime Scene Envelope is an "X Y Z". Please confirm the correct exhibit type and adjust any Forensic Register records as necessary, or alternatively the item can be returned for your correction. The item has been placed on hold pending advice.
regards
Your NAME

10.8.12 Sample requires additional analysis confirmation (Item placed on-hold):

Date/Initials – Hello,
Regarding exhibit barcode XXXXXXXXX, this item has been ticked as "Sample requires additional analysis (lubricant, fibre, glass, soil etc.)" with no additional information provided as to what form of additional analysis is required. Please advise the nature of the additional analysis required, or alternatively, if none is required, please uncheck. The item has been placed on hold pending advice.
regards
Your NAME

10.8.13 Is semen or saliva testing required (Item placed on-hold):

Date/Initials – Hello,
Regarding exhibit barcode XXXXXXXXX. Due to the nature of this case could you please confirm whether semen or saliva testing is required. This item has been placed on hold pending advice.
regards
Your NAME

10.8.14 Name missing from the Exhibit Description or Located/Owner fields (SAIK)

Date/Initials – Hello,
The Exhibit Record page for SAIK exhibit barcode XXXXXXXXX has no name listed in either the Exhibit Description or Location/Owner fields. This information is used (in conjunction with the exhibit barcode) as a second identifier when checking exhibit details. Can this information please be added to the registration of this exhibit so that testing may proceed.
regards
Your NAME

10.8.15 Clothing located within SAIK

Date/Initials – Hello,
SAIK exhibit barcode XXXXXXXXX has been received. Upon opening, SAIK contains 1 x pair of socks and 1 x pair of underwear. The clothing will be repackaged in the SAIK and returned for examination by QPS Scientific. Alternatively, they can be examined by Forensic DNA Analysis, however whole item authorisation must be sought from an Inspector with details of testing requirements.
regards
Your NAME

10.9 Appendix 9: Incorrect exhibit tests

If there is an error in the exhibit analytical/testing table, the line which contains the error must be marked as incorrect by the user who made the error, examples of this include

- An incorrect exhibit result line has been selected
- An incorrect examination has been performed
- The examination is duplicated

A line within the exhibit analytical/testing table can only be marked as incorrect by the examiner if it has not yet been validated. If the line has been validated, or it is a line that auto-validates, it must be marked as incorrect by a Senior Scientist. **Note:** If the line has not yet been validated then the examiner should delete all information within the record before marking it as incorrect.

1. Click on the date/time hyperlink of the incorrect/duplicate process in the exhibit analytical/testing table.

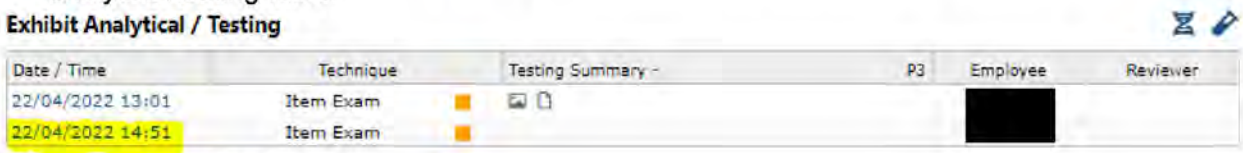


Figure 31 – Date/time hyperlink

2. Click the arrow 

icon next to the edit button and select "Incorrect Test.

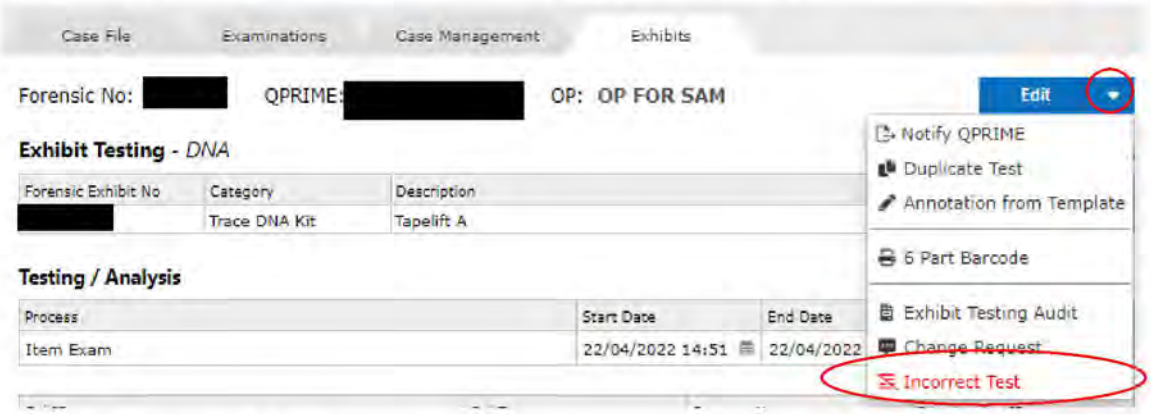


Figure 32 – Incorrect Test

3. Click the [CLICK TO INCORRECT] bar.

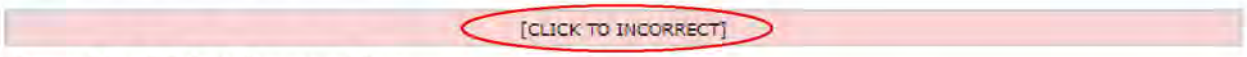


Figure 33 – Click to incorrect bar

4. This process will now have a line through it in the exhibit analytical/testing table. As the result was not validated before being marked as incorrect, the orange traffic light will remain.



Figure 34 – Incorrect exhibit test

CA-68

Queensland Health

Forensic and Scientific Services

Examination of Sexual Cases

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1 Purpose

The purpose of this procedure is to describe the processes required for the examination of sexual assault cases by Evidence Recovery scientists and technicians in Forensic DNA Analysis, in addition to those described in QIS 33800 Examination of Items.

2 Scope

This procedure applies to all Forensic DNA Analysis staff that examine or interpret examinations of evidentiary items. This standard operating procedure is used in conjunction with individual methods for screening tests. Interpretations and limitations of reporting are to be found in each method.

3 Definitions

- Refer to QIS 23849 (Common Forensic DNA Analysis Terms and Acronyms) for a comprehensive list of abbreviations.
- All references to microscopy, refer to QIS 17189 (Examination For & Of Spermatozoa).
- All references to Acid Phosphatase (AP), refer to QIS 17186 (The Acid Phosphatase Screening Test for Seminal Stains).
- All references to Phadebas, refer to QIS 33998 (Phadebas Test For Saliva).
- All references to Tetramethylbenzidine, refer to QIS 17190 (Tetramethylbenzidine Screening Test for Blood).
- All references to p30, refer to QIS 17185 (Detection of Azoospermic Semen in Casework Samples).

4 Actions

Refer to the general principles contained in QIS 33800 Examination of Items.

4.1 Sexual Assault Investigation Kits (SAIKs)

Before commencing the examination of a SAIK an examination strategy must be devised and reviewed in accordance with Section 4.12.1 of this document by different scientists that are competent to perform the examinations contained in the strategy. This strategy must include:

- For each item to be examined, what biological fluid is to be screened for,
- Items which require no further action,
- Sample submission strategies (i.e. extraction type, pooling, retain supernatant for Phadebas testing etc.).

The following are general principles which are used to develop examination strategies for SAIKs, however these principles must be considered within the context of the case history:

- Where the complainant is a minor or has an intellectual impairment, which may mean that the provided case history is unreliable, all possible offence scenarios are considered,
- Where the complainant is an adult who has lost consciousness, has impaired memory or has consumed alcohol or drugs prior to or during the offence which may impact on memory, all possible offence scenarios are considered,
- Consider previous intercourse with same or different partner, prior to the offence. For digital only female complainant cases with prior intercourse, submit external swabs for diff lysis with no presumptive testing.

- For male offender SAIK swabs, consider submitting penile swabs for diff lysis where the victim has had previous intercourse with another person,
- Consider the number of offenders – for male SAIKs consider submitting penile swabs for diff lysis (with no presumptive testing) to separate epithelial cells and spermatozoa,
- Samples taken from areas of biting, licking or kissing (or other oral contact) are submitted for presumptive saliva testing (retain supernatant). This does not include swabs taken from the mouth (internal or external), anal and vaginal areas which may give false positive results,
- Internal and external vaginal swabs can be submitted for retain supernatant only if the female is under 16 years old,
- For internal swabs on adult females (16 years and older), an Analytical Note for the Epithelial Fraction to be processed as "Extract and Hold on EFRAC" is required. This rule applies for both SAIK swabs and PM SAIK swabs. This does not apply to priority 1 samples.
- If an oral swab has been received which is labelled as a reference, the SAIK is to be placed on hold and a request/task sent for further advice from QPS. If QPS advise that the sample is not required as a reference it can be examined accordingly with the other SAIK contents.

If FMO prepared slides are received within a SAIK, the following workflow applies:

- Where the swab and smear are clearly labelled the same (can be identified as matching), create a microscopic entry under the swab barcode and record the slide labelling details in the notes field. Stain and examine the slide, if sperm is observed the diff slide from the examined swab does not require reading after extraction.
- In the instances where the pre-prepared smear is microscopy negative, proceed with routine processing.
- If the swab and slide cannot be connected (e.g. unlabelled or labelled differently) register the slides as separate child exhibits and perform microscopy. Proceed with routine processing of the swabs.

Additional items such as pads, tampons or fluid samples received within a SAIK are to be examined at the same time as the rest of the SAIK samples, refer to section 4.5 for testing requirements for sanitary items and section 4.20 for examining fluid samples.

If there are any issues relating to the collection or documentation of a SAIK, send a request/task to the forensic officer or to SSLU, refer to QIS 33771 to create and complete a request/task and QIS 33800 for standard wording. In some cases the FMO / FNE (direct or through SSLU) may need to be contacted. Examples of issues include:

- Missing paperwork
- Insufficient case history to determine an examination strategy
- Labelling issues/inconsistencies

If serum coated, charcoal swabs, expired swabs, or other unsuitable swabs/media are received notes must be made in the item exam of the affected swabs detailing the type of swab submitted. An analytical note must be added for swabs that are received in transport medium.

Refer to appendix 8.3 for the workflow of presumptive/screening testing of SAIKs.

4.2 Acid Phosphatase (AP) Positive Fabrics

Refer to appendix 8.3 for the workflow of presumptive/screening testing of AP positive fabrics.

AP positive fabrics are submitted by QPS. The AP positive area/s should be clearly marked on the fabric, refer to the QPS images for guidance if necessary. If the fabric is not marked then the entire item should be sampled, including both sides of fabric.

AP positive fabrics should be submitted with an additional area surrounding the circled AP positive area to enable the examining scientist to safely hold the fabric during sampling. When a large AP positive fabric has been received it may be necessary to divide marked area/s into sections for separate sampling. Examining scientists are to liaise with the senior scientist if a fabric requires more than 3 samples to be taken.

Images of AP fabrics must clearly indicate the side that is being photographed (e.g. side A or B). If a fabric has no marked areas and both sides of the fabric cannot be visually differentiated, the examiner should label or mark the fabric so sides can be easily identified if a further examination is required. If a fabric contains a seam which can be identified as the I/S or O/S, this should be noted in the item exam.

The entire marked area must be sampled no matter the sampling technique (scraping, excision, tape lifting or swabbing). **Extreme care must be taken during sampling to avoid sharp related injuries**.

Refer to appendices 8.5 and 8.6 for standard labelling of AP positive fabrics.

4.3 Semen in-tubes

Refer to appendix 8.3 for the workflow of presumptive/screening testing of semen in-tubes. All in-tubes that require semen testing are to be examined by scientists only. If semen in-tubes are stored in an in-tube box, they must be transferred to an items box and added to the examination worklist. If an in-tube check has been completed the tube must be stored to an ERT-AS box and transferred to an examination bench. If an in-tube check has been performed but has not been validated it must be validated by the scientist performing the examination. Three scenarios are as follows:

- In-tube contained within CSSE, no in-tube check performed
- In-tube removed from CSSE, in-tube check performed
- In-tube contained within CSSE, in-tube check performed

1. Track ERT-AS box, the in-tube or CSSE to an examination bench
2. Check the image/s of the CSSE to ensure the details match the FR
3. Remove the tube from the CSSE if necessary, sign and date the opening
4. Create an item exam as per appendix 8.3 and describe the tube and contents, note any staining visible if the item is a swab and if a tape lift has been received note whether it appears used or not.
5. No tube lot number is required on the item exam as the sample will be submitted in the original in-tube. Scan the ERT-AS box into the storage box ID field.
6. If the sample received is a swab, all the swab material is to be cut from the stick and the stick disposed of.
7. Follow steps 4 – 9 in section 4.12.6.
8. Refer to section 4.18 to add a result line.

4.4 Condoms

Refer to appendix 8.3 for the workflow of presumptive/screening testing of condoms.

A condom should be described in terms of "O/S surface as received" and "I/S surface as received". Describe any fluid that may be present on or within the condom. Measure the length and diameter and describe any damage, colour, patterning and translucency.

Collect one wet and one dry swab from the O/S and I/S surfaces of the condom. If fluid is visible within the condom then only a dry swab is needed for the I/S surface. Combine the I/S wet and dry swabs into one tube and the O/S wet and dry swabs into another tube.
Note: When sampling the swabs, to ensure that there is not excess substrate submitted, sample the entire wet swab material, but only submit the outer layer of the dry swab.

4.5 Sanitary Pads and Tampons

Sanitary pads are AP tested on the side worn in contact with the skin.

The body of a tampon is cut through the middle and splayed out. The outer sides that were in contact with the skin are to be AP tested, including the string.

4.6 Post-mortem Samples

Refer to appendix 8.3 for the workflow of presumptive/screening testing of post-mortem samples.

PM samples may include sexual assault swabs and/or slides (high vaginal, low vaginal, vulval etc.), pubic hair, head hair, fingernail clippings or scrapings. The testing requirements are to be confirmed by QPS prior to sampling.

Refer to QIS 34300 Examination of post mortem and associated samples from deceased persons, for further detail on post mortem examinations.

4.7 Clothing and Bed sheets

Refer to appendix 8.2 for different scenarios and required result lines for whole item AP testing.

For large items, an examination strategy should be formulated based on the case history and if necessary, in consultation with the QPS. This must be recorded in the item exam or as a notation in the FR.

If the case history suggests that the item has been washed, then it may be necessary to perform microscopy only considering the water-soluble nature of AP and p30.

When describing the I/S, O/S, right side or left side of a garment; examiners should be aware that these terms are used in relation to 'as would be worn'.

4.8 Wet and Dry swabs – QPS submitted

When wet and dry swabs are received from the same site (e.g. high vaginal swab from a SAIK, an item) submit each of the swabs separately.

4.9 Multiple Presumptive/Screening Tests

Consideration should be given to the order in which screening tests are conducted in order to conserve the possible biological material on an item. Where both AP and Phadebas screening tests are required, perform Phadebas testing on the exhibit first (using

commercial paper), once the Phadebas test is complete the Phadebas paper can be sprayed with AP reagent.

4.10 Penile Swabs

The presence of spermatozoa on penile swabs is not unexpected. These swabs are generally submitted for cells only, however where the case history indicates multiple offenders, or the female has had previous sexual contact, they should be submitted for diff lysis with no semen screening performed.

Samples that are submitted straight for diff lysis only that do not require semen screening must have an analytical note "Quant and Amp on SFRAC and EFRAC" (refer to section 4.13).

The diff slide is not read for these samples, microscopic process notes are to be removed and replaced with 'slide not read at this time' should be added to the microscopic process.

4.11 Lubricant Testing

If the lubricant box has been ticked on the SAIK paperwork, QPS must indicate whether lubricant testing is required prior to examination of the SAIK. The SAIK must be placed on hold and a request/task must be sent to the forensic officer or SSLU by the validator or examining scientist, refer to QIS 33771 to create and complete a request/task and QIS 33800 for standard wording. **Note:** Lubricant testing cannot be performed if Phadebas supernatant testing is also required. Refer to section 4.19 for the lubricant process.

4.12 SAIK examination

4.12.1 SAIK examination strategy

1. New SAIKs will be listed on the received worklist, click on the DNA  icon and select worklist to view the received worklist. New SAIKs will be tracked to freezer shelf 2 (FDNA-EXFZ-0002) and the SAIK paperwork will be located in the ER in-tray.

2. On any page, click the key identifier search  icon and scan the barcode attached to the SAIK paperwork, press enter or click search. In the files table click the  icon to open the FMO notes pdf. The download box will appear in the bottom left corner. Compare the physical and electronic notes to ensure all pages are scanned, scan and upload any missed pages to a case file notation (refer to appendix 8.7). If a case file notation has been created by FPP but no scanned notes are present, FPP will need to be contacted (3096 2962) to upload the notes.

3. Review the FMO notes and ensure any identifiers on the paperwork match the FR exhibit record and forensic case file record pages. Ensure the patient the SAIK was collected from is visible on the exhibit record page in the description or location/owner fields.

4. Scroll to the exhibit analytical/testing table on the exhibit record page and ensure the priority is listed as either P1 (if requested) or P2, if the SAIK is listed as P3 a request/task will need to be sent to SSLU requesting that the priority be changed.

5. Click the create exhibit test icon in the exhibit analytical/testing table and select a notation from the process field.

6. In the notes field type the examination strategy for the SAIK.

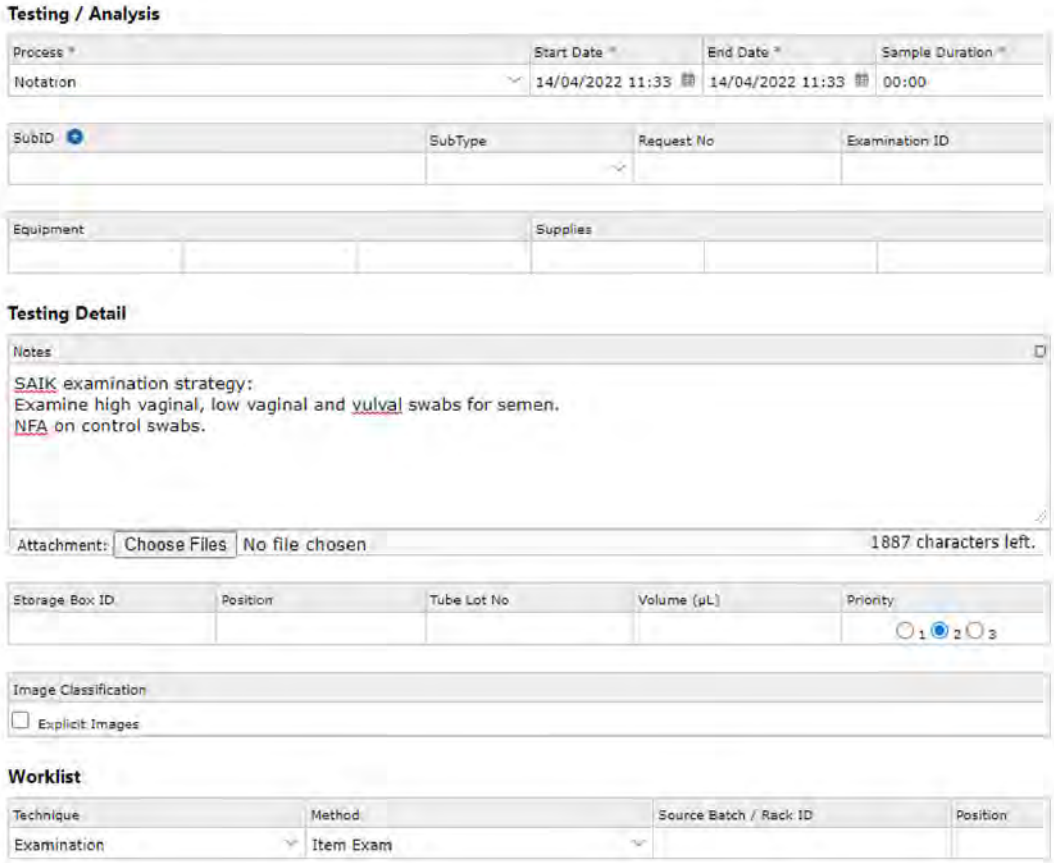


Figure 1 – SAIK examination strategy

7. In the worklist table select Examination from the technique dropdown menu and Item Exam from the method dropdown menu.

8. Click on the save button.

4.12.2 Validation of SAIK examination strategy

1. The examination worklist will indicate SAIKs that require examination.

2. Click on the exhibit number of the SAIK to be examined, navigate to the exhibit record page and read the FMO notes, which can be found in the "Case Management Reports" table.

3. Scroll down to the exhibit analytical/testing table, find the relevant notation and click the date/time hyperlink.

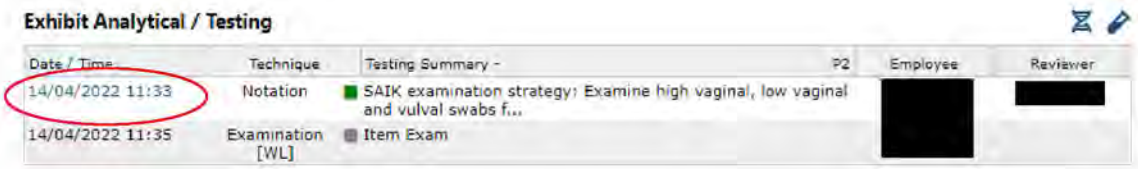


Figure 2 – Hyperlink to notation

4. Read the SAIK examination strategy in the notes field. If you do not agree with the SAIK examination strategy discuss with the scientist who created the strategy, they can edit the original notation if necessary.

5. Once you are satisfied that everything is correct and you agree with the SAIK examination strategy click the edit button.

6. In the notes field add an additional note to agree to the examination strategy.

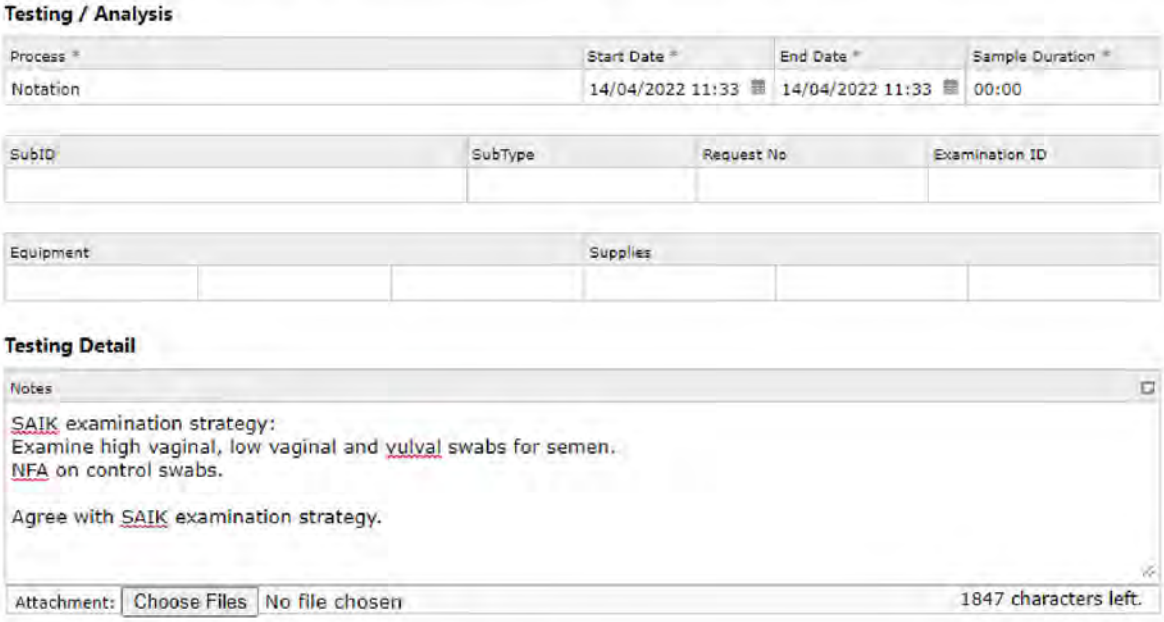


Figure 3 – Checking SAIK examination strategy

7. Click on the save button.

4.12.3 Description of SAIK packaging

1. Retrieve SAIK from the freezer location and track to an examination bench in the evidence recovery laboratory via exhibit movement.

2. Photograph the packaging and upload images to I:\FR Images.

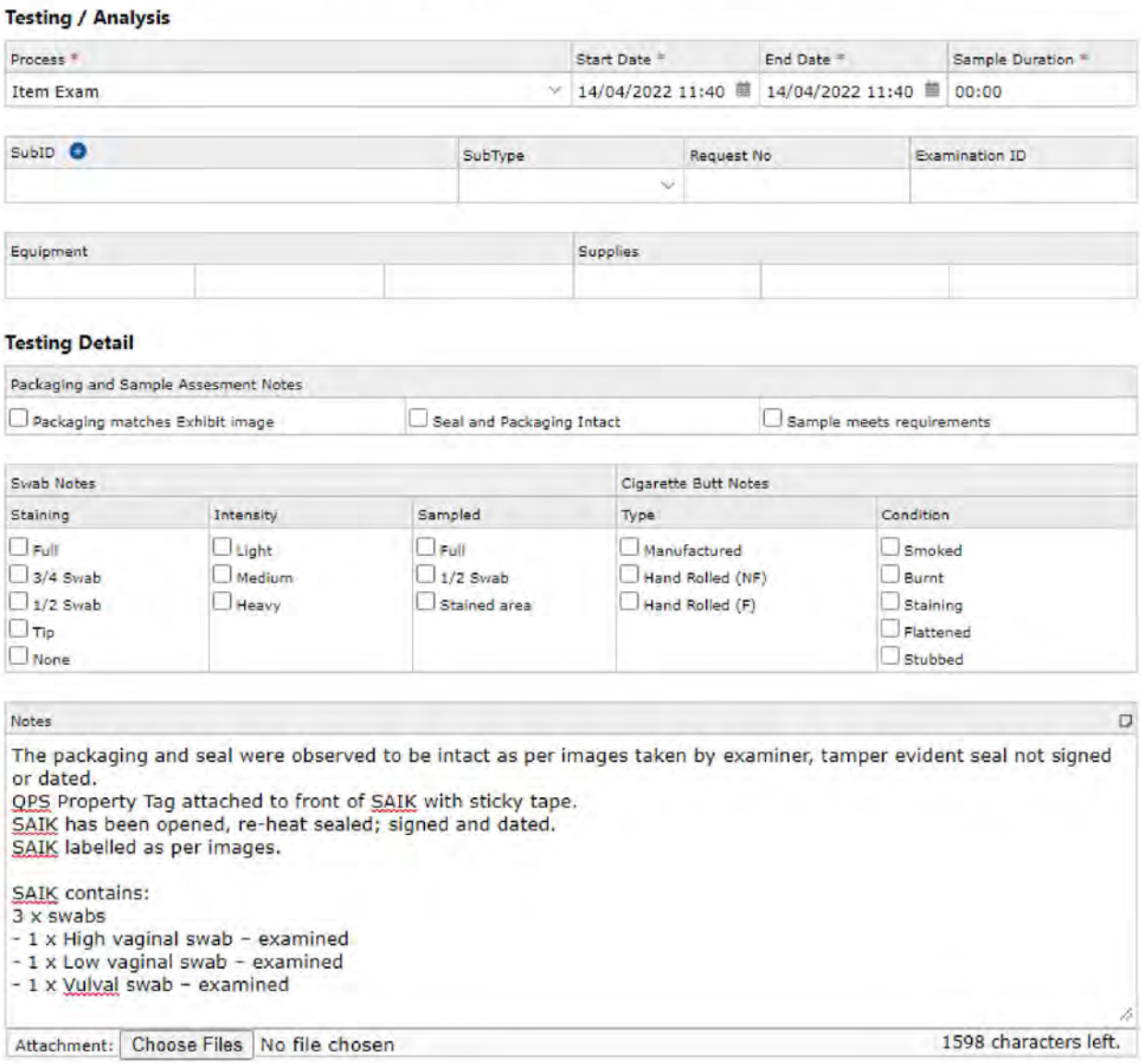
3. Scroll down to exhibit analytical/testing table, click the create exhibit test icon.

4. In the Testing/Analysis table process field select Item Exam from the dropdown menu.

5. In the packaging and sample assessment notes field tick the "Seal and Packaging Intact" box if this is the case. If the packaging and seals are not intact use the notes

field to describe the nature of the packaging and seals. **Note:** The "Sample meets requirements" box is specific to in-tubes and is not to be used for Item Exam's.

6. It is standard practice for FPP to open SAIK packaging to retrieve paperwork prior to delivery to Forensic DNA Analysis. Note whether the packaging has or has not been opened including if it has been re-sealed, signed and dated. Describe any labelling on the SAIK packaging, it is acceptable to state "labelled as per images". List the contents of the SAIK and for each item state whether it is to be examined or not. If all contents are labelled with identical printed labels, this can be detailed in the notes field and referred to in each of the subsequent examination notes.



Testing / Analysis

Process *	Start Date *	End Date *	Sample Duration *
Item Exam	14/04/2022 11:40	14/04/2022 11:40	00:00

SubID	SubType	Request No	Examination ID

Equipment	Supplies

Testing Detail

Packaging and Sample Assesment Notes		
☐ Packaging matches Exhibit image	☐ Seal and Packaging Intact	☐ Sample meets requirements

Swab Notes			Cigarette Butt Notes	
Staining	Intensity	Sampled	Type	Condition
☐ Full	☐ Light	☐ Full	☐ Manufactured	☐ Smoked
☐ 3/4 Swab	☐ Medium	☐ 1/2 Swab	☐ Hand Rolled (NF)	☐ Burnt
☐ 1/2 Swab	☐ Heavy	☐ Stained area	☐ Hand Rolled (F)	☐ Staining
☐ Tip				☐ Flattened
☐ None				☐ Stubbed

Notes

The packaging and seal were observed to be intact as per images taken by examiner, tamper evident seal not signed or dated.
QPS Property Tag attached to front of SAIK with sticky tape.
SAIK has been opened, re-heat sealed; signed and dated.
SAIK labelled as per images.

SAIK contains:
3 x swabs
- 1 x High vaginal swab – examined
- 1 x Low vaginal swab – examined
- 1 x Vulval swab – examined

Attachment: Choose Files No file chosen 1598 characters left.

Figure 4 – Description of SAIK packaging

7. Click on the save button.

4.12.4 Description of SAIK contents and image upload

1. Click the Examinations tab.

2. Click the add button.
3. Change the start time to a time before images were taken. In the duration field add an estimate time for the examination.

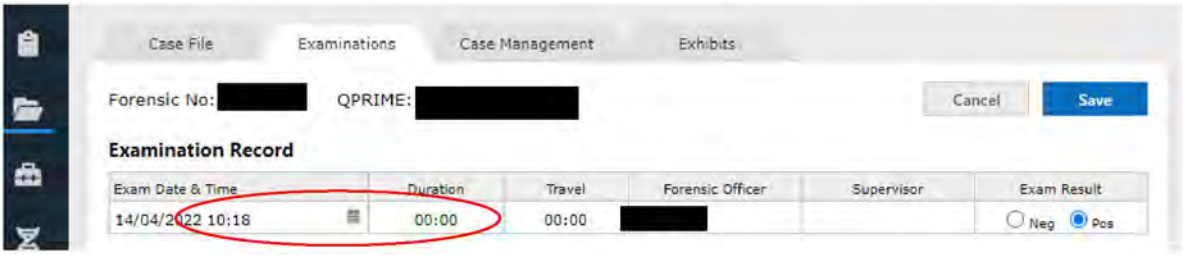


Figure 5 – Examination Record Time and Duration fields

4. The following check boxes must be ticked as this is required for compliance with software requirements: Examination location – General, Recording Method – Photo General (can tick Photo Explicit if images are of a sensitive nature) and No Case File.

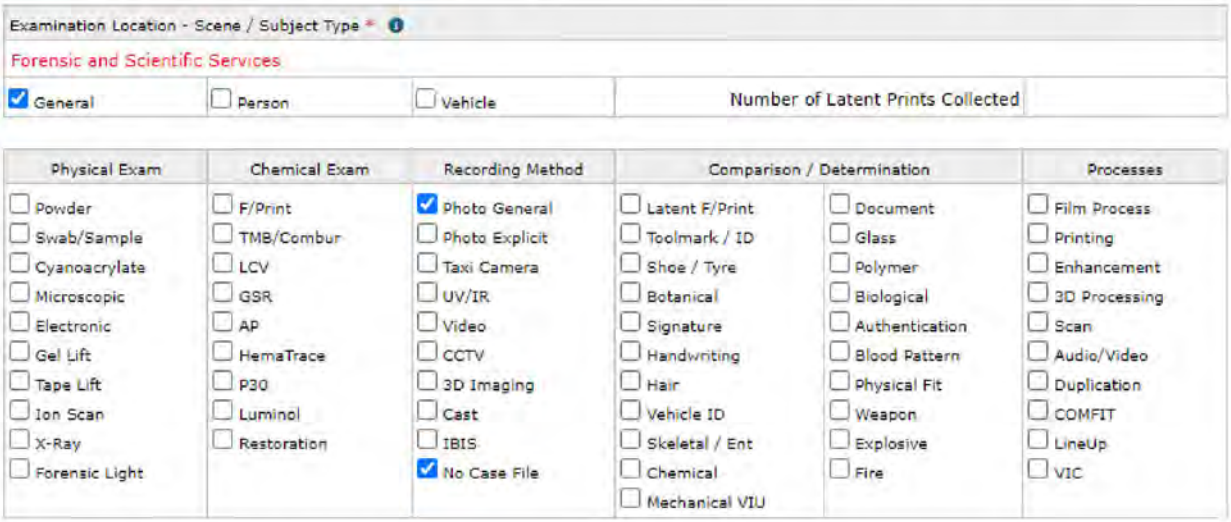


Figure 6 – Examination record check boxes

5. In the Examination notes field type a summary of the SAIK contents including items not examined such as unused swabs etc. **Note:** Abbreviations such as HVS or LVS cannot be used. Do not state "examined" or "not examined".
6. In the exhibits examined field, scan the SAIK barcode.



Figure 7 – Description of SAIK contents

7. Click on the save button.
8. Click the arrow 

icon next to the edit button and select upload files/images.
9. Alternatively scroll to the images table and click the upload images plus icon.
10. The examination file upload box will open, click the add files button 

.

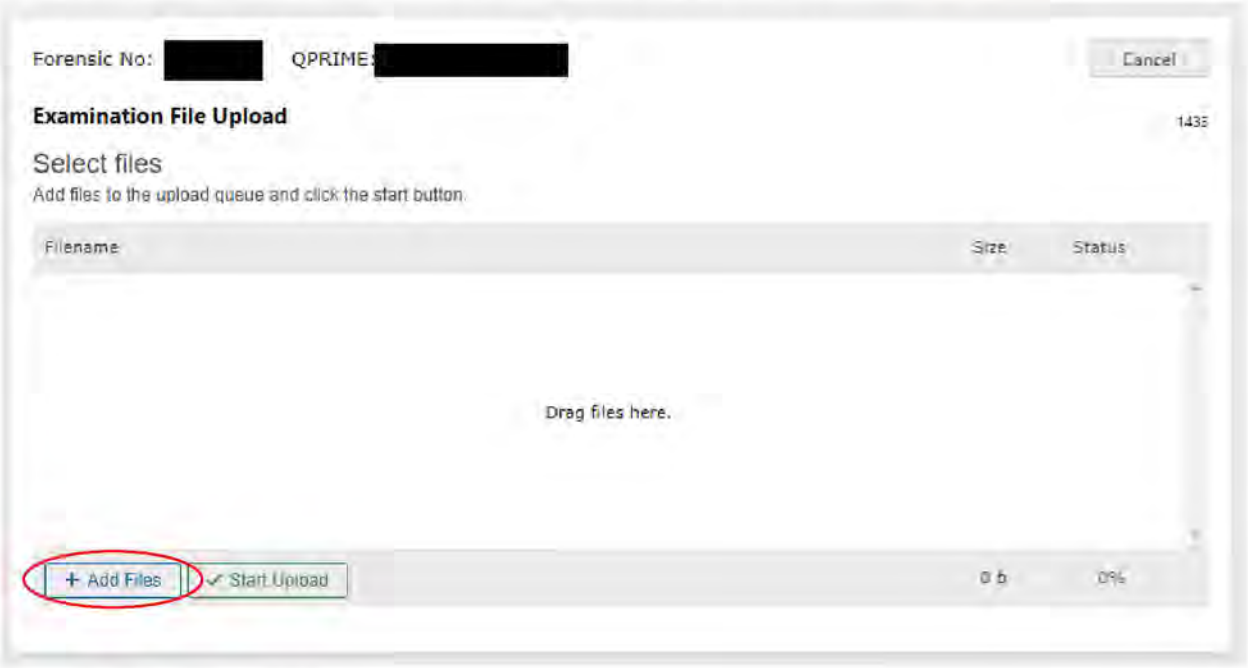


Figure 8 – File Upload table

11. Navigate to I:\FR Images and find the relevant packaging images. Multiple images can be selected by holding down the Ctrl button. Click open.
12. Click the start upload button.
13. Once the images have uploaded click the save button.

4.12.5 Registration of SAIK contents – creating child exhibits

1. Click the arrow 

icon next to the edit button and select add related exhibit.
2. Click the plus  icon in the forensic exhibit no field to auto assign a new barcode.
3. Choose the forensic category (e.g. swab).
4. Type in the description (e.g. high vaginal) **Note:** Abbreviations must not be used.
5. The Located/Owner field will auto fill from the parent item, any information that is not required can be removed. Any additional details in the description field of the parent item must be manually transferred. The located/owner field should indicate ownership, for example "SAIK – name of complainant".

6. The parent barcode field will auto fill.
7. Tick the Admission/Intel and Sample has been collected in strict compliance with CSE101 Biological Evidence boxes.

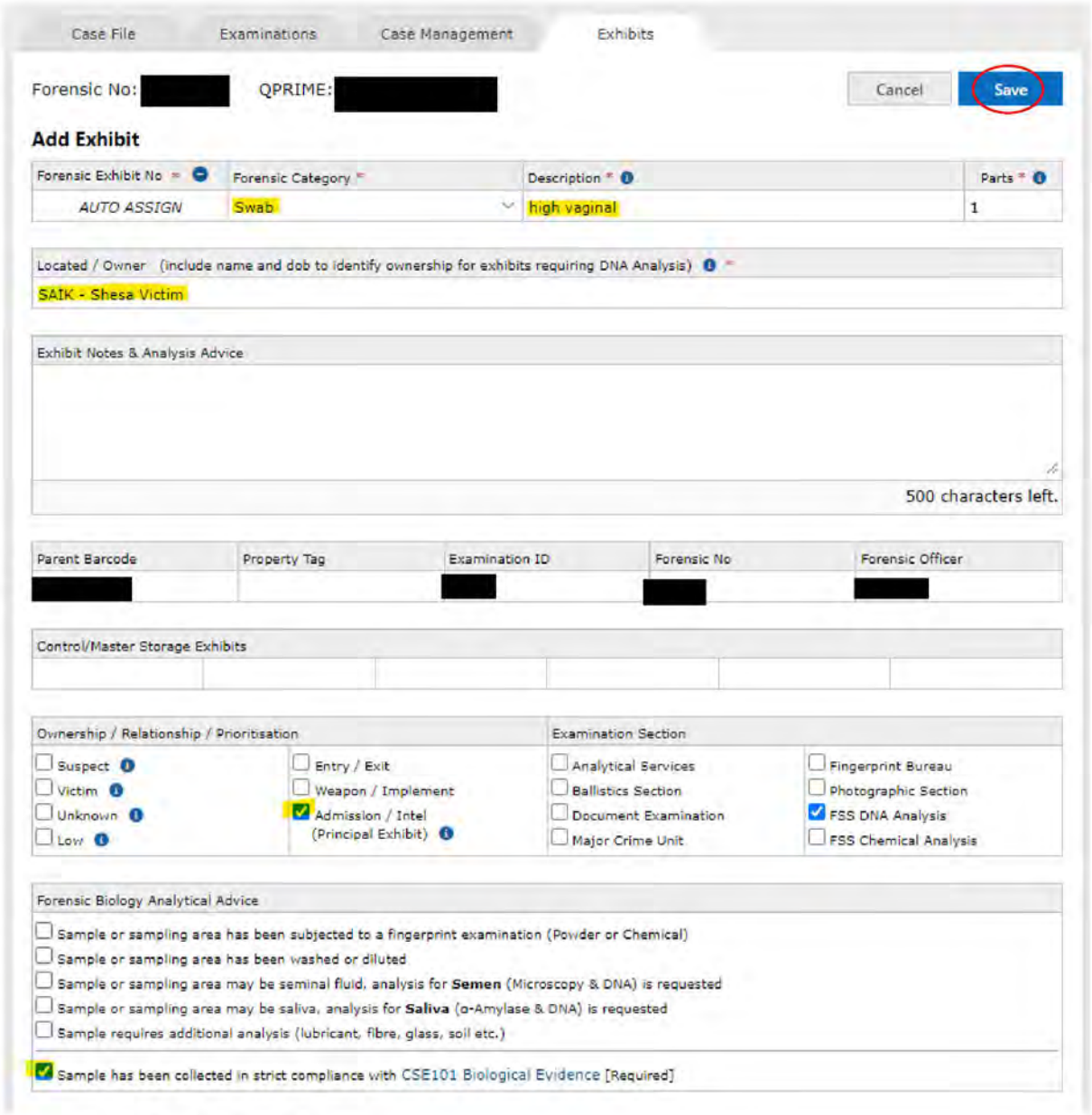
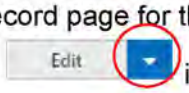


Figure 9 – Adding Child Exhibits

8. Click on the save button.
9. To add more child exhibits, click on the back button.
10. Click the plus icon in the forensic exhibit no field to auto assign a new barcode and edit the category and description of the 2nd child exhibit.
11. Click on the save button.

12. Repeat steps 9 – 11 for every component of the SAIK.

These steps are not required for SAIK components that do not require examination, for example control swabs.

Note: To add an additional child exhibit after completion of the above steps, return to the Exhibit Record page for the exhibit, open the examination from the Examinations table, click the arrow 

icon next to the edit button and follow the steps above.

4.12.6 Examination of SAIK swabs

1. For each item in the SAIK perform the item exam procedure. Refer to SOP 33800 Examination of Items for detailed procedures. Ensure to add:

    a. The **Tube Lot number** and **Storage Box ID** (position will autofill)

    b. Any labelling present

    c. Sampling details

Testing / Analysis

Process *	Start Date *	End Date *	Sample Duration *
Item Exam	14/04/2022 11:00	14/04/2022 11:00	00:00

SubID	SubType	Request No	Examination ID

Equipment			Supplies		

Testing Detail

Packaging and Sample Assesment Notes

☐ Packaging matches Exhibit image ☐ Seal and Packaging Intact ☐ Sample meets requirements

Swab Notes			Cigarette Butt Notes	
Staining	Intensity	Sampled	Type	Condition
☑ Full	☑ Light	☑ Full	☐ Manufactured	☐ Smoked
☐ 3/4 Swab	☐ Medium	☐ 1/2 Swab	☐ Hand Rolled (NF)	☐ Burnt
☐ 1/2 Swab	☐ Heavy	☐ Stained area	☐ Hand Rolled (F)	☐ Staining
☐ Tip				☐ Flattened
☐ None				☐ Stubbed

Notes

Swab labelled with handwritten [redacted]VICTIM cervical wet". F box ticked.

The entire swab head was stained yellow in colour.
The swab head was lightly stained.
The entire swab head was sampled for further analysis.

Suspension created with the addition of 400 uL nano H2O.
200 uL of supernatant retained.

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Storage Box ID	Position	Tube Lot No	Volume (µL)	Priority
[redacted]	[redacted]	[redacted]		○ 1 ◉ 2 ○ 3

Figure 10 – SAIK swab item exam

2. Perform any necessary TMB presumptive testing as needed.
3. Place sample in a 1.5ml tube (for diff lysis) or 2mL tube (for cells) and label.

Note: Steps 4 – 9 are for samples that require semen screening only.

4. Add 400uL of nanopure water to the tube to form a suspension
5. Vortex mix thoroughly
6. Incubate on a hot block at 30°C for 15 minutes.
7. Vortex mix the sample and spin using the centrifuge for 3 minutes.
8. Register a 'RETAIN' subsample and print a tube label.
9. Pipette 200uL of supernatant and transfer to a new 1.5ml tube and store frozen in the p30 supernatant box 1.

4.13 Analytical notes

An analytical note e.g. "extract & hold EFRAC" must be added to each sample if required. For "quant & hold" samples submitted for diff lysis (e.g. cold case samples) it must be specified in the analytical note that this applies to both the SFRAC and the EFRAC.

1. Scroll down to the exhibit analytical/testing table and click the create exhibit test icon.
2. In the Testing/Analysis table process field select Analytical note from the dropdown menu.
3. Use the notes field to type the comment for the analytical team.

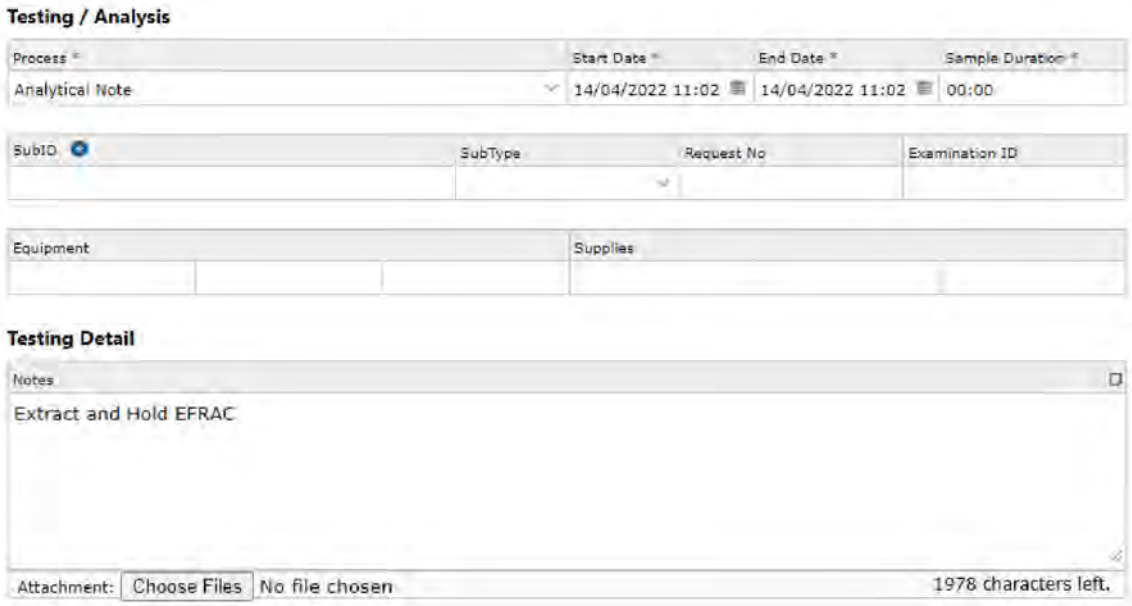

Figure 11 – Analytical note

4. Click on the save button.

Note: Analytical notes will auto-validate and do not require validation from a second scientist.

4.14 Drop Sheets

Drop sheets need to be registered regardless of whether they appear used or not. If the drop sheet is marked "not used" (or similar), registration or examination is not required.

1. Ensure the category is 'Paper' and the description is 'Dropsheet' when registering.
2. Add an item exam, include any packaging and labelling details as appropriate, state what is visible on the drop sheet – if it appears used or unused. State if any possible hairs are present "No possible hairs present – NFA".
3. If any possible hairs are visible, they must be collected and placed into a CSPB, a 'MISC' subsample must be created (refer to 33800 for creation of subsamples) and the CSPB labelled with the subsample barcode. The number of possible hairs collected must be noted in the item exam and subsample notes field.
4. Note in the item exam that the CSPB containing possible hair/s has been retained within the dropsheet CSPB.
5. The result line 'HAIRNFA: Hair located – not examined as this time' must be added to the dropsheet barcode.

4.15 Finalisation of SAIK examination

Once the SAIK examination is complete, repackage, seal, sign date and track the SAIK to the freezer returns location ([redacted]) or to freezer box 4 ([redacted]) for lubricant testing.

Store all samples to an ERT-AS box if not already stored during examination, track the ERT-AS box to [redacted] and place into the hatch for collection.

4.16 Microscopy of diff slides

Refer to QIS 17189 (Examination for and of Spermatozoa) for staining and examination of microscopic slides.

Refer to Appendix 8.4 for the diff slide process.

4.17 p30 testing

If microscopy is negative for spermatozoa, add a new exhibit test and select 'Presumptive' and select the p30 supernatant subsample barcode from the dropdown list in the SubID, type "p30 required" into the notes field and click save.

Note: P30 testing is not required on AP positive fabrics that have been sectioned and one or more sections are positive for spermatozoa. Add a notation "p30 not performed as alternate section <barcode> is micro pos for sperm".

1. Click the DNA  icon and select "Worklist", click the "Worklist" tab and select "Awaiting Review", "Presumptive".

2. Click and open only the presumptive tests created by the person performing p30 testing as other presumptive tests from examinations may appear on this list.
3. Refer to QIS 17185 to perform the p30 test

Note: If a p30 kit is faulty (e.g. control line doesn't appear) create the presumptive record but don't select a result. Enter the batch number of the p30 kit in the reagent field and add a comment in the notes section.

4. Edit the presumptive and add the p30 reagent code into the reagents field, select the appropriate radio button and remove the comment in the notes field.
5. Follow section 4.18 and refer to appendix 8.1 to add and select an appropriate result line.

Create an exhibit movement for each used p30 supernatant tube and discard.

1. Navigate to the Forms/Toolbox icon and select "Batch Move Exhibits"
2. Scan each supernatant tube barcode into the "Exhibit Movement" table.
3. In the location field select "DESTROYED".

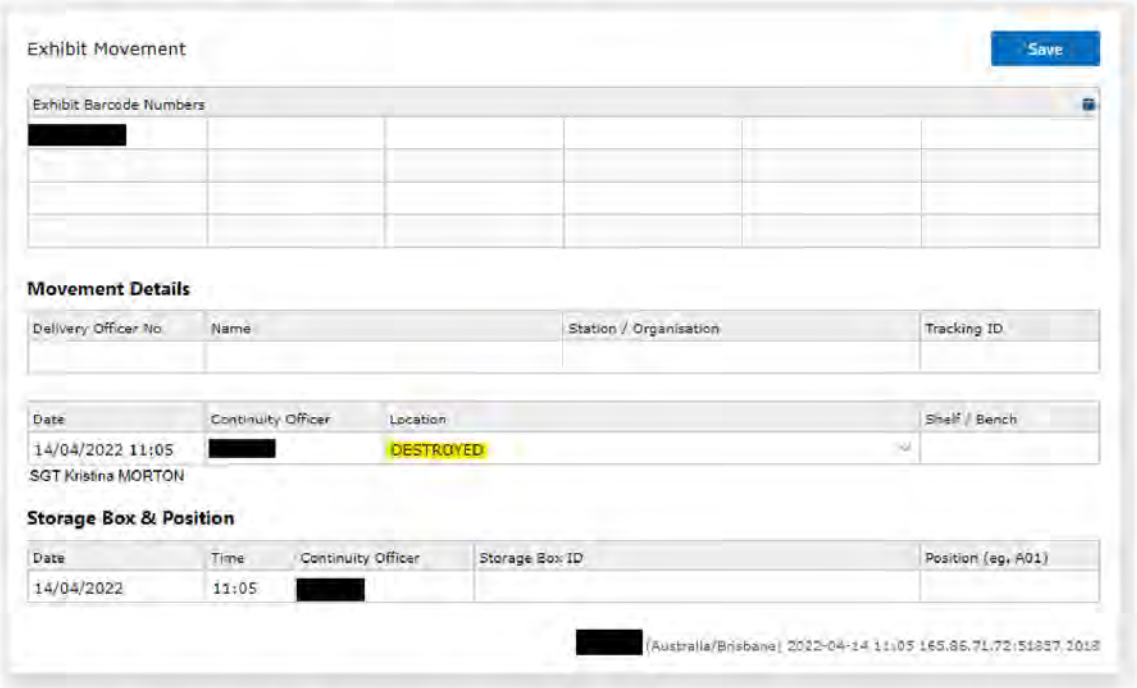

Figure 12 – Batch Exhibit Movement

4. Click on the save button.

A box audit must be performed on the p30 supernatant box 1 each week to ensure samples have not been missed.

Positive microscopy p30 supernatants are to be transferred to appropriate month box to be stored for 3 months.

On the first day of the month the person rostered on slide reading is to audit the oldest p30 retain supernatant box and send tubes to "DESTROYED" as per steps above. If tubes are present within the box that have had a NWQPS result line added prior to extraction the p30 supernatant tube must be transferred to the long term freezer storage box located in freezer box 3 ([redacted]).

4.18 Result lines

Add a new exhibit test to the exhibit analytical/testing table and select "Result", use the drop-down menu to select the appropriate result line and click save (refer to Appendix 8.1 and 8.2).

4.19 Lubricant testing

1. If QPS have confirmed the SAIK requires lubricant testing, each child exhibit must have an Analytical note added during examination that states:

   "***All substrates[swab/tapelift/scraping/excised], spin baskets, supernatants and any remaining tubes (that do not contain DNA extract) need to be retained and returned to ER to be submitted to Trace Evidence for lubricant comparison examination***".

2. All samples for lubricant testing must be added to the extraction worklist **"Diff Lysis Retain Supernatant".** The SAIK must be tracked to freezer box 4 ([redacted]) after the examination.

3. Each Wednesday, the Scientist rostered on supernatant testing must check the Trace Evidence worklist and freezer box 4 for samples that require lubricant testing, they are responsible for packaging the samples for transfer.

4. Analytical will store the Trace Evidence samples and their associated components for lubricant testing in allocated boxes namely: [redacted]. All tubes from the child exhibit (swab site) are stored per row within the box, only tubes with subsample barcodes (SUPNAT and SPIN) will be stored in FR. All other tubes will be labelled with the child exhibit barcode. E.g. All components from a high vaginal swab will be stored in positions A01 – A08 and components from a low vaginal swab will be in positions B01-B08.

5. Retrieve the storage box from Analytical and the SAIK from freezer box 4 ([redacted]) and transfer both to an examination bench.

6. Perform a subsample movement for the 'SUPNAT' and 'SPIN' barcodes relating to each swab site from the SAIK and track to [redacted] or 'Stored in primary packaging'.

7. Package all components of each swab site in a CSPB together, label each CSPB with the child exhibit barcode. E.g. all tubes relating to the high vaginal swab are packaged together and the CSPB labelled with the high vaginal barcode.

8. Take a photo of the sealed and labelled CSPBs for each swab site and upload the photo to a notation on the SAIK barcode. All individual CSPBs can be photographed together as long as the label of each is clear.

9. Place individual CSPBs into a larger CSPB, seal with evidence tape, sign and date the seal and label with the SAIK barcode.

10. Create a notation under the SAIK barcode and describe the packaging and the contents.

a. Example for a high vaginal swab: 1 x tube labelled SUPNAT XXXXXXXX, 1 x tube labelled SPIN XXXXXXXX, 4 x tubes labelled with barcode XXXXXXXX from the high vaginal swab packaged together for lubricant testing.

11. Open the SAIK packaging and place the large CSPB inside the SAIK packaging, re seal the SAIK following standard procedures.

12. If there are extraction control tubes stored amongst the SAIK tubes within the storage box, these will need to be sent to Forensic Chemistry. Only the 'SUPNAT' subsample will be stored within the box, this sample will need to be converted to an exhibit for tracking purposes. Follow step 8 of appendix 8.3 to convert a subsample to an exhibit.

13. Place the extraction control supernatant into a 5mL tube and label, place the 5mL tube into a HSPB, heat seal, sign, date and label. Enter a notation on the negative extraction control to state 'supernatant XXXXXXXX sent with SAIK XXXXXXXX for lubricant testing'. Add a notation to the supernatant barcode and detail the packaging and contents, upload an image of the packaging.

14. Attach the HSPB containing the negative extraction supernatant to the SAIK packaging with staples.

15. Enter the SAIK barcode and negative extraction supernatant barcode to the exhibit transfer manifest form QIS 36268. Print and complete the packaged by field, another Scientist must review the contents and complete the exhibit list reviewed by field on the form. Scan and upload into FR the transfer manifest form as a case file notation on the SAIK (refer to 8.7). Attach the exhibit manifest form to the SAIK packaging with staples.

16. Track the SAIK and the negative extraction supernatant HSPB to freezer returns (FDNA-RTFZ-0001). Send an email to [redacted] to alert FPP that samples are located in freezer returns that are ready to be collected to be forwarded to Forensic Chemistry for lubricant testing. Upload the email correspondence as a case file notation to the SAIK in FR.

17. If the SAIK requires urgent transport to FPP the SAIK and negative extraction supernatant must be tracked to the DNA storage bench within Forensic Property Point [redacted]. Call FPP [redacted] to notify them of the incoming SAIK for forwarding to Forensic Chemistry and lubricant testing, deliver the SAIK to FPP.

18. Once the SAIK has been tracked to the appropriate location the samples must be reallocated from the Trace Evidence worklist. Click into each barcode on the worklist, add a new exhibit test and select reallocate, ensure the supernatant barcode is entered into the SubID field.

4.20 Fluid samples

If a fluid sample is received for testing for semen (e.g. oral rinse), the following procedure should be followed.

1. Transfer the fluid from the original container to a 1.5mL tube.

Note: Depending on the volume received multiple 1.5mL tubes or 50mL falcon tubes may be necessary.

2. Create a balance tube and centrifuge the sample for 3 minutes. If a falcon tube is used it must be transferred and centrifuged in the Analytical laboratory.

3. Carefully remove the supernatant from the tube without disrupting the pellet and return to the original container.
4. If a falcon tube is used, transfer the pellet using a single use pipette to a 1.5mL tube. Alternatively the pellet can be collected using a swab.
5. Follow steps 4 – 9 in section 4.12.6.

5 Associated Documentation

QIS: 17185 – Detection of Azoospermic Semen in Casework Samples
QIS: 17186 – The Acid Phosphatase Screening Test for Seminal Stains
QIS: 17189 – Examination For & Of Spermatozoa
QIS: 17190 – Tetramethylbenzidine Screening Test for Blood
QIS: 22857 – Anti-Contamination Procedure
QIS: 23849 – Common Forensic DNA Analysis Terms and Acronyms
QIS: 33771 – Examination of in-tube samples
QIS: 33773 – Procedure for Profile Data Analysis using the Forensic Register
QIS: 33800 – Examination of Items
QIS: 33998 – Phadebas Test for Saliva
QIS: 34006 – Procedure for the Release of Results Using the Forensic Register
QIS: 34300 – Examination of post mortem and associated samples from deceased persons
QIS: 36268 – Exhibit Transfer Manifest

6 References

AS2243.1:2005 Safety in Laboratories Part 1 - General

Workplace Health and Safety Act 2011

Workplace Health and Safety Regulation 2011

Workplace Health and Safety Advisory Standards – various

Health, safety and wellbeing | HSQ staff site

7 Amendment History

Version	Date	Updated By	Amendments
1	10/06/2016	A. Houlding	First issue.
2	14/06/2017	A. Ryan	Added examination summary, upload of images for SAIKs and creating related exhibits for each component of the SAIK. Added analytical notes. Added appendices 6-10
3	14/07/2017	A. McNevin	Updated information on required fields for an Examination, information on diff slide process
4	13/12/2017	A. McNevin	Minor edits to reflect current practices in FR; updated screen shots and associated documents
5	02/11/2018	C. Savage	Amendments to Appendices, Updated examination guidelines for SAIKs, other minor wording adjustments to reflect current processes as discussed in team meetings.
6	31/08/2020	S. Byrne & A. McNevin	Added additional information on numbering of areas, other minor wording adjustments, removed "Forensic Register" from title of document, further information on lubricant testing.
7	23/02/2021	A. Ryan	Changes in process following implementation of project#181. Appendices updated.
8	22/04/2022	K Morton	Updated template, added a process for examining fluid samples, semen in-tubes and case file notation creation. Updated lubricant and p30 processes, associated documents, references, appendices and screenshots. Updated content to reflect current procedures.

8 Appendices

1 Appendix 1: SAIKs, PM Intimate Exhibits, Semen In-Tubes and AP Fabrics
2 Appendix 2: Fabrics/Clothing requiring AP testing
3 Appendix 3: Workflow for items – semen testing
4 Appendix 4: Diff slide process
5 Appendix 5: Standardised wording for describing sides of an exhibit
6 Appendix 6: Standardised wording for describing subsamples
7 Appendix 7: Creating a case file notation

8.1 Appendix 1: SAIKs, PM Intimate Exhibits, Semen In-Tubes and AP Fabrics

Table 1 – Semen testing result lines and processing workflow

Scenario	Result Line/s	Manual / Automatic Result	Quant/Cease testing
Micro pos	Micro positive for sperm – submitted results pending	Manual	Quant
Micro neg, p30 pos	Presumptive PSA test positive – submitted results pending	Manual	Quant
	Micro neg for sperm	Automatic	
Micro neg, p30 neg	Micro neg for sperm	Automatic	Cease testing
	Semen not detected	Manual	
Micro not performed (slide broken), p30 pos	Presumptive PSA test positive – submitted results pending	Manual	Quant
Micro not performed (slide broken), p30 neg	Semen not detected	Manual	Quant
Micro neg, p30 not performed (faulty p30 kit)	Micro neg for sperm	Automatic	Quant
Micro neg, p30 not performed (fabric sectioned by ER and one section is micro positive)	Micro neg for sperm	Automatic	Quant

8.2 Appendix 2: Fabrics/Clothing requiring AP testing

Table 2 – AP testing result lines and processing workflow

Scenario	Result Line/s	Manual / Automatic Result	Quant/Cease testing
AP neg	Presumptive seminal fluid test negative	Manual	Cease testing
AP Pos - Micro pos	Presumptive AP test positive – submitted results pending ^	Manual	Quant
	Micro positive for sperm – submitted results pending	Manual	
AP Pos - Micro neg, p30 pos	Presumptive AP test positive – submitted results pending ^	Manual	Quant
	Presumptive PSA test positive – submitted results pending	Manual	
	Micro neg for sperm	Automatic	
AP Pos - Micro neg, p30 neg	Presumptive AP test positive – submitted results pending ^	Manual	Cease testing
	Micro neg for sperm	Automatic	
	Semen not detected	Manual	

8.3 Appendix 3: Workflow for items – semen testing

1. Click the key identifier search icon and scan the barcode, press enter or click search.
2. Using the exhibit movement table, track item to an examination bench.
3. Click thumbnail of CSSE, check image, close the image window.
4. Add image/s to the item exam or the examination record. **Note:** Paint or the FR annotation application can be used to annotate images.
5. Check testing requirements for biological screening.
6. Exhibit analytical/testing table → create exhibit test
   - In the process field select item exam.
   - Tick relevant boxes under packaging and sample assessment notes.
   - Enter notes into the notes field including details of the item, details of any staining and markings and how the item is to be sampled.
   - Save.
7. Create subsample of scraping/tape-lift/swab/excision. Exhibit analytical/testing table → create exhibit test
   - In the process field select subsample.
   - In the SubID field select the plus icon to auto assign a new barcode.
   - In the subtype dropdown list select MISC.
   - In the notes field add a description of the subsample.
   - Save.
   - Repeat for any other subsamples.
8. Convert subsamples to child exhibits:
   - Click on the exhibits tab.
   - Click the add button.
   - Enter barcode of subsample you have just created in the exhibit barcode field.
   - In the category field select the relevant subsample type.
   - Add description of subsample.
   - In the Located/Owner field copy the relevant description from the parent item. If there is additional information within the "Located / Owner" field of the parent item

which will indicate ownership, e.g. a name, "victim" or "suspect" etc. this is also to be included.

- Add the parent barcode in the parent barcode field.
- Tick the following boxes: admission/Intel, FSS DNA Analysis, and sample has been collected in strict compliance with CSE101 Biological Evidence.
- Add your FR User ID in the Delivery Officer Rego field; press tab and your surname will automatically appear. Select Queensland Health Scientific.
- Save.
- Repeat steps for all subsamples.

Note: Samples can be created as part of the Examination Record process as outlined in 4.12.5 above.

9. Exhibit analytical/testing table → create exhibit test
   - In the process field select item exam.
   - Enter notes into the note field detailing how much water was added to the tube and how much is retained.
   - Add storage box location and tube lot number.
   - Save.
10. Create subsample for the retained p30 supernatant:
    - In the process field select subsample.
    - In the SubID field select the plus icon to auto assign a new barcode.
    - In the subtype dropdown list select RETAIN.
    - In the notes field add a description of the subsample.
    - Add tube lot number.
    - Save.
    - Store tube to p30 supernatant box 1.
11. Add result line if required. Exhibit analytical/testing table → create exhibit test
    - In the process field select result and select 'submitted results pending' result from the dropdown menu labelled police report.
    - Save.
12. Repeat steps 9 - 11 for all child exhibits.
13. Track exhibit to returns.

8.4 Appendix 4: Diff slide process

HP2:

1. Locate batches ready for microscopy slide processing:
   - Click on the DNA  icon, select "Worklist" and click the "Administration" tab.
   - From the dropdown menu select "Workflow Diary"
   - Click "View History"
   - Change the date to the previous working day
   - Look for batches "DNA Extraction Differential Lysis DNA IQ" or "DNA Extraction Diff Lysis Retain Supernatant". The slides from these batches require microscopy.
2. Alternatively, click the equipment and supplies  icon and select "Storage Box Search". Enter 'slide transfer' into the storage box description and press enter. This will show any slide boxes containing slides ready for staining.
3. Retrieve the blue slide storage box from the extraction sorting hatch. An empty slide box needs to be placed into the hatch for the next batch.
4. Track the blue slide storage box to an examination bench.
5. Transfer each slide to Evidence Recovery lab [redacted] and place into a slide carrier.
6. Stain the slides using Haematoxylin and Eosin, coverslip and allow to dry on the heat block.
7. For each individual slide:
   - Exhibit analytical/testing table → create exhibit test  and choose Microscopic.
   - Add diff slide barcode to SubID field.
   - In the SubType field select "SLIDE" from dropdown list.
   - In the Reagents field add the Haematoxylin and Eosin lot numbers, which can be copied and pasted from "equipment and supplies  icon → Supply Search → Category field type "Haematoxylin" and "Eosin".
   - Save.
8. Track the empty blue slide storage box to Evidence Recovery Evidence Sorting room [redacted] Place the slide carrier into the hatch and attach the relevant laminated sign.

Note: The negative control slide does not require staining or a microscopic process, this slide is to be stored by the HP3.

HP3:

1. Scan slide barcode and check whether the diff slide requires reading. FMO prepared slides that were positive or samples that don't require semen testing will not require diff slide microscopy. Add a note to the microscopic page stating, "slide not read at this time".
2. Perform microscopy. Edit the existing Microscopic process with the results of the microscopic examination.
3. In the "Equipment No" field enter the equipment number for the specific microscope used. Enter the asset barcode of the microscope into the asset number field of the equipment search page from the equipment and supplies  icon to locate the equipment number.
4. Use radio buttons to record if "spermatozoa were detected" or "no spermatozoa were detected". **Note:** If the slide cannot be read (e.g. broken), select 'no result' and enter notes.
5. Use the notes field to add specific details of the microscopy and any England finder coordinates.
6. Click on the save button.
7. Store the slide in a diff slide storage box.

8.5 Appendix 5: Standardised wording for describing sides of an exhibit

The following examples detail the standard wording/labelling for describing various sides of an exhibit such as a piece of fabric.

8.5.1 Marking on one side

A piece of fabric received with a marking on one side, item description states item is of AP positive area.

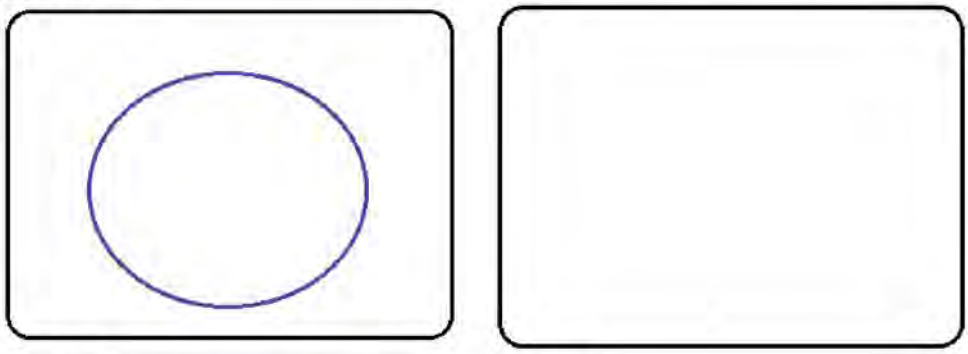

Figure 13 – AP fabric, marking visible on one side

Examination notes should state that the marked side has been designated as side A and the unmarked side has been designated as side B by the examiner.

8.5.2 Corresponding marking on both sides

Piece of fabric received with a marking on one side, item description states item is of AP positive area. Due to material type and / or marker used for marking, the marked area is visible on the other side.

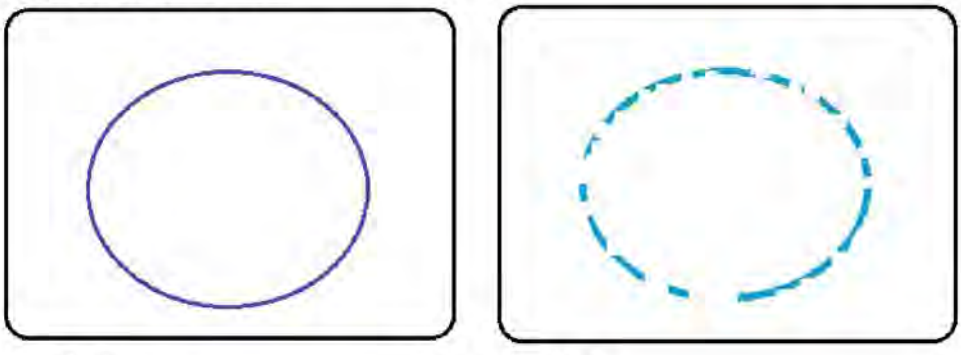

Figure 14 – Marked area partially visible on reverse

Examination notes should follow section 8.5.1 and state that the marking from side A appears to have soaked through to side B.

8.5.3 Multiple marked areas on both sides

If both sides of a fabric have markings, the numbering of each marked area will be consecutive and individual for each side.

Example: Side A and side B have multiple marked areas, each area on both sides is to be designated an area number by the examiner. Label side A areas 1 – 3; and side B areas 1 – 3.

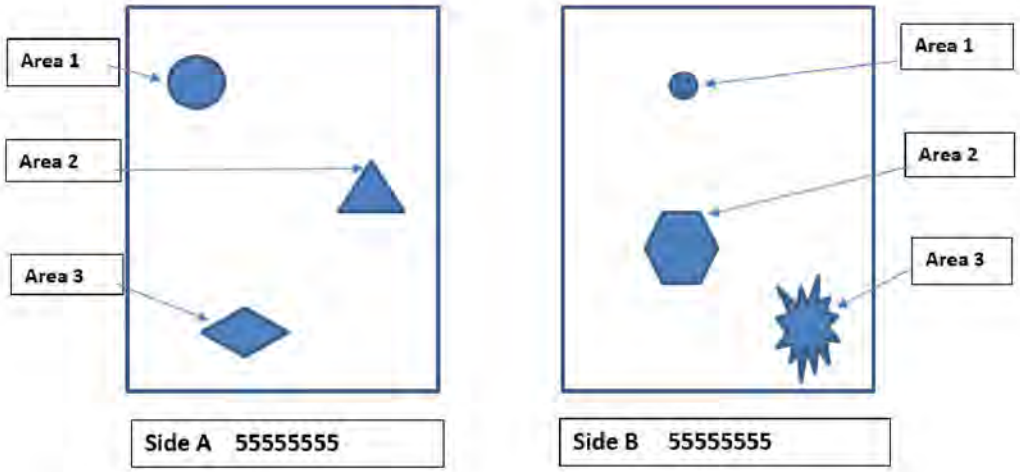

Figure 15 – Numbering of marked areas on both sides of a fabric

8.6 Appendix 6: Standardised wording for describing subsamples

The following examples detail the correct wording to use in the following instances:

- Where multiple stains / marked areas exist on the same item,
- Where one or more stains / marked areas needs to be divided into two or more smaller sections for sampling.

Note: When designating a section, side etc. as per the guidelines below, annotated images is advised.

8.6.1 Creating sections

A piece of fabric that is not marked or the marked area is too big to sample into one tube. Each of the subsamples will be referred to as "sections" i.e. Section 1, Section 2 etc.

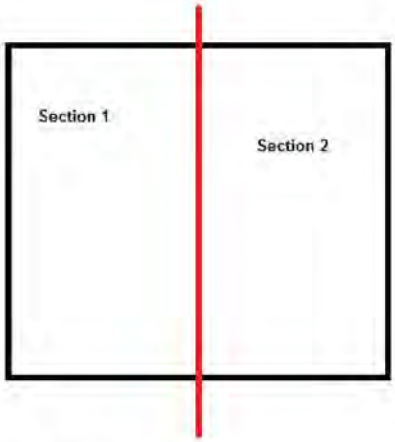

Figure 16 – Sections

8.6.2 Multiple marked areas on one side

A piece of fabric that has two marked areas, each area is small enough to be sampled into a single tube each. Each subsample is to be referred to as an "Area" i.e. Area 1, Area 2 etc.

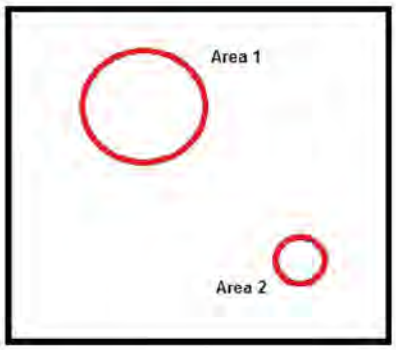

Figure 17 – Areas

8.6.3 Multiple marked areas with sectioning

A piece of fabric that has two marked areas, one area sampled as a single subsample, another divided into two sections (too large to sample into one tube).

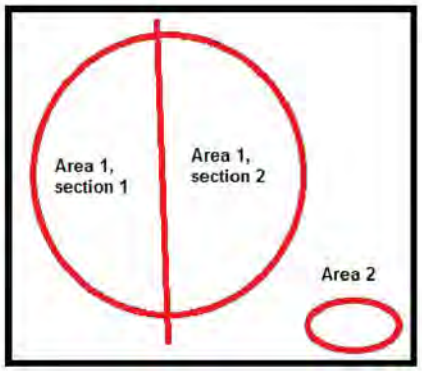

Figure 18 – Two Areas, Area 1 two subsamples

8.6.4 Whole item

Follows convention as for piece of fabric above, each area to be referred to as Area 1, Area 2 etc. regardless of whether same or different presumptive result.



Figure 19 – Whole item, different presumptive positive areas

8.7 Appendix 7: Creating a case file notation

1. Click on the case management tab for the relevant exhibit and click the add button.
2. Select the Case File Notation check box in the "Report Type" field.
3. Enter the exhibit barcode into the forensic exhibit no field.
4. Enter in relevant notes to the comments field (i.e. QP127 scanned).
5. Click on the save button.

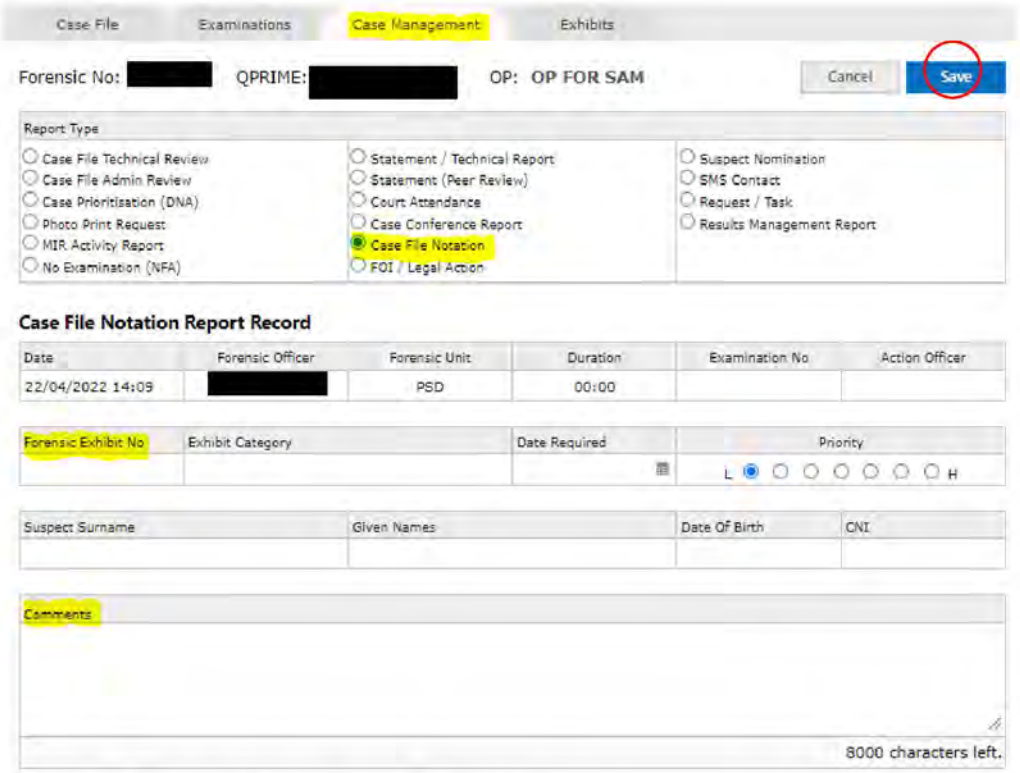

Figure 20 – Creating a new case file notation

6. In the files table, click the add files plus icon.
7. Click "Add Files" or drag the document/s from a folder into the table, click start upload.
8. Click on the save button.

CA-69

Queensland Health
Forensic and Scientific Services

Examination for and of Spermatozoa

1 Purpose

The presence of spermatozoa is a confirmatory test for the presence of semen. This document describes the method by which a scientist performs microscopic examination for the presence of spermatozoa which includes the preparation of microscopic slides from exhibits, staining of slides and interpretation of the microscopic smears/slides for spermatozoa and other cellular material.

2 Scope

This Standard Operating Procedure (SOP) applies to all scientists performing the examination of items for the presence of semen.

3 Definitions

In this document, where reference is made to spermatozoa, it refers to human spermatozoa unless otherwise specified.

4 Principle

The investigation of sexual assault cases may require the testing of exhibits collected as part of a forensic medical examination or scene examination for the presence of semen. Within the laboratory the detection of spermatozoa confirms the presence of semen. A reliable and accurate staining method is essential to aid the examining scientist the ability to differentiate between cellular types; most significantly spermatozoa from epithelial, yeast and white blood cells.

Currently the Haematoxylin and Eosin (H&E) stain is adopted for this process. The H&E staining method has been used for this purpose within the laboratory for many years. The haematoxylin (basic stain) stains the deoxyribonucleic-acid (DNA)/histone rich base of the spermatozoa head deep purplish-blue. The eosin (acidic stain) stains the acrosomal cap pink and the tail pink if the spermatozoa are intact (N.B. because Forensic DNA Analysis uses a water based eosin stain, the acrosomal cap often appears very light pink or clear). The use of counterstaining differentiates spermatozoa from most cellular debris.

Confusion with yeasts, especially monilia, can occur and extreme care must be taken when monilial infections such as thrush are suspected. With experience, spermatozoa and yeasts can be distinguished by size and/or the presence of cell walls. In addition, yeasts do not display the typical biphasic staining that spermatozoa do (refer staining characteristics in paragraph above).

Haematoxylin is a natural dye. Its active colouring agent is haematin, which is formed by the oxidation of haematoxylin. This oxidation process or "ripening" occurs when

haematoxylin solutions are allowed to stand for several days. However, the process can be accelerated with the introduction of an oxidising agent such as sodium iodate. During oxidation the haematoxylin loses two atoms of hydrogen, and its formula changes from $C_{16}H_{14}O_6$ to $C_{16}H_{12}O_6$. Sufficient haematoxylin should be left unoxidized in the solution so that natural oxidation can continue thus prolonging the shelf life and useability of the stain. Completely oxidized haematoxylin becomes colourless. As the oxidation process occurs when haematoxylin is exposed to light and continues over the life of the solution, haematoxylin should be stored in dark bottles until ready for use. Haematoxylin is an excellent nuclear stain. Haematin, via the aluminium ion mordant, binds to the anionic sites in the nuclei (a mordant is a substance that causes certain staining reactions to take place by forming a link between the tissue and the stain). At this stage the nuclei stain red, which is then converted to the blue-black colour when the pH is raised (by a weak alkali wash such as Scott's tap water substitute in some H&E staining methods) known as "blueing".

To avoid stain precipitation on the slide, the haematoxylin solution must be filtered. It should be changed immediately if staining quality deteriorates.

Eosin is an acid dye which combines electrostatically with the acidophilic tissue components such as cytoplasm (an anionic dye that stains the cationic tissue components). Alcoholic and acidified solutions of eosin tend to stain much more vividly than do the aqueous solutions. With water soluble eosin, rinse in water very quickly or else eosin will wash out.

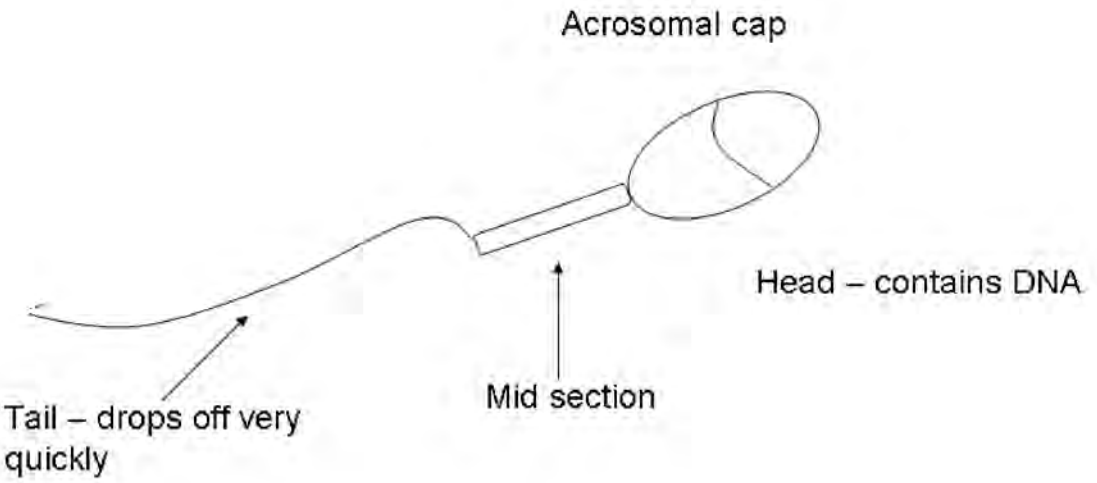

Figure 1 Spermatozoa

5 Actions – Staining procedure

5.1 Slide Staining

Slides are created by Analytical Scientists and stored to a slide box, this box is tracked to the Analytical laboratory. The slide box containing the stored and prepared slides are retrieved by Evidence Recovery staff from the extraction sorting hatch and tracked to the Evidence Recovery laboratory. Individual slides are then tracked to the Evidence Recovery laboratory and the empty slide box is returned to the extraction sorting hatch after processing.

Add a Microscopic process from the Exhibit testing table, complete the SubID, SubType and the Reagents lot numbers fields in the Forensic Register.

Testing / Analysis 440131 CALDWELL, V PSD FSS

Date	Process	SubID	SubType	Equipment No
31/01/2022 15:25	Microscopic	[redacted]	SLIDE	

Results of Microscopy Examination		
○ Spermatozoa were detected.	○ No spermatozoa were detected.	◉ No result.

Reagents				
[redacted]	[redacted]			
Haematoxylin Harris non toxic	Eosin Y 1% Aqueouus			

Notes
Whole Sperm: Sperm Heads: Epithelial Cells: Other: Magnification: x400
Attachment:

Figure 2 Creating a microscopic process

Microscopic slides are stained using Haematoxylin and Eosin (H&E). The method for performing manual staining is as per procedure detailed in Appendix 1.

5.2 Microscopic Examination

Examine slide using the x40, x50 or x100 objectives. Quantitate the number of whole spermatozoa, spermatozoa heads and epithelial cells observed in the "Microscopic" process under subsample barcode of the microscopy slide. Do this by appending the pre-formed text using the following criteria as a guide:

Table 1 Quantitation criteria

Quantity	Description
0	None seen
<1+	Very hard to find *
1+	Hard to find
2+	Easy to find
3+	Very easy to find
4+	Abundant

* If less than ten spermatozoa are observed on the whole slide, a quantitation of <1+ must be used and for at least one spermatozoa, note the location on the slide with the use of the England Finder Graticule (see Appendix 3).

Human spermatozoa are distinguished from non-human mammalian sources by their morphology and by their behaviour toward H&E, resulting in a purplish/blue head and light pink/clear cap (see Section 5.4). Record whether there are bacteria or yeast present next to "Other:" If no bacteria or yeast seen record "N/A".

The default Magnification: x400 is used when adding the Microscopic process. Edit if applicable, e.g. x500. Record the Equipment No. used and select the appropriate radio button in the Results of Microscopy Examination field.

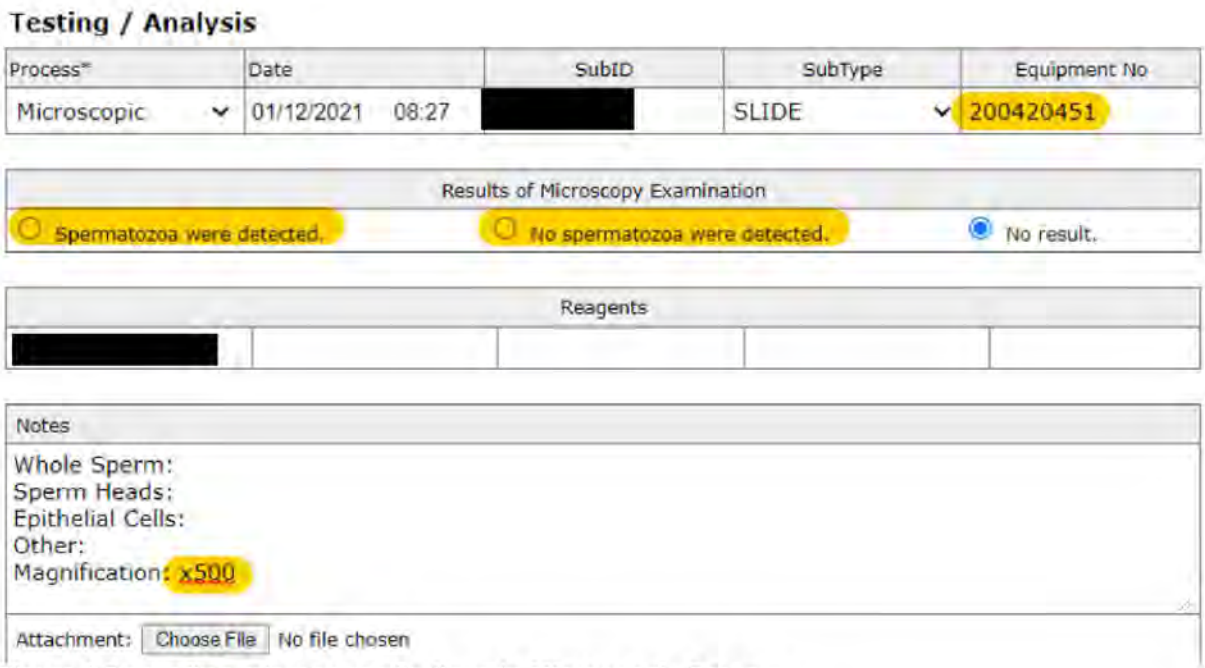

Figure 3 Recording microscopy findings in Microscopic Process

5.3 Animal Semen

Animal spermatozoa are morphologically different to human spermatozoa and react differently to staining. Where suspected spermatozoa are located which are morphologically different to human spermatozoa, the examining scientist should consider the possible presence of animal spermatozoa. N.B. Forensic DNA Analysis does not identify or characterise animal spermatozoa.

5.4 Spermatozoa Interpretation

If slides are stained properly spermatozoa should be easily distinguished from epithelial cells, cellular debris, fibres etc. Spermatozoa heads can look similar in shape and colour to yeasts, however they do have different staining characteristics. If in any doubt consult an experienced examiner.

The recovery of semen is dependent on a number of factors but not limited to

- The amount of spermatozoa in the ejaculate
- The amount of ejaculate
- The environment the ejaculate is deposited on
- Washing
- Douching
- Menstruation
- Efficiency of the sampling process
- Time between ejaculation and sampling
- Storage of the samples
- Natural drainage or degradation of spermatozoa in certain environments

With respect to the above influences, the time since ejaculation has occurred can only be estimated. A number of studies have been conducted regarding the persistence of spermatozoa in the vagina. References to these studies can be found in Appendix 2.

6 Records

Nil

7 Quality assurance/acceptance criteria

Controls are used to test the quality and validity of the staining reagents prior to use. A positive control slide should be tested and read by a Scientist prior to the staining of slides for microscopy, (once daily), each time a new batch of Haematoxylin and Eosin solution is received/opened and when positive control slides are prepared.

7.1 Creation of H&E control slides

Collect human semen in a sterile yellow-capped Specimen jar. The tube is to be labelled with the following information:

- Sperm donor number
- Date and time of collection

Each new collection of positive control material should be checked with a previously accepted batch of stain.

The semen is to be stored within a freezer until required to create H&E positive control slides using the following process:

1. Clean heating block using bleach and 70% ethanol solution.
2. Clean frosted microscope slides with ethanol and label with white label (H&E Pos Ctrl: Sperm donor number; Lot No.).
3. Spread slides out on heating block to heat before use.
4. Clean automatic pipette with bleach and 70% ethanol solution.
5. Using a new filtered pipette tip, add 20µL of the neat semen to 10.0ml nanopure water using a clean 10ml tube. Vortex.
6. Add 20 µL of the diluted semen solution to each slide, put a circle around the sample using a black marker pen.
7. Heat fix the slides on a heating block at 50ºC for approximately 30 minutes.
8. Store the slides in labelled plastic slide box "Unstained H&E Positive Control Slide Storage" and store the box in Rm 6124.

7.2 Testing and interpretation of control slides

The following process is used to test, interpret and record control slide results:

1. Remove a H&E control slide from slide box, label with date, initials, and stain with H&E using the method in Appendix 1.
2. Dry slide on heating block at 50ºC.
3. Coverslip slide using Pertex® mounting medium. A small amount of xylene can be used to assist with slide mounting.
4. A scientist must examine and pass or fail control slides microscopically before processing exhibit slides can occur.
5. Completed control slides get transferred to a plastic box labelled H&E Control Slide Storage box #
6. Once a slide box is full of completed positive control slides, write the date range of the slides contained within the box on the outside of the box and transfer the box to Rm 6106B, 'Exhibit Room' for long term storage.

Acceptance of the reagents is based on the interpretation of the Positive control slide. The following criteria must be met before passing the reagent for use:

1. Spermatozoa head stains a deep purplish-blue.
2. Acrosomal cap stains light pink/clear.
3. Tail stains pink.

In the event the control slide fails the following process is to be completed:

1. Repeat the staining procedure with a new control slide and assess as above.
2. If the control slide fails again then discard the in-use stain and then stain a new slide using a fresh batch from the stock solutions and assess slide as above.

8 Associated Documentation

QIS: 17185 Detection of Azoospermic Semen in Casework Samples
QIS: 17186 The Acid Phosphatase screening test for seminal stains
QIS: 23849 Common Forensic DNA Analysis Terms and Acronyms
QIS: 25747 Use and routine care of compound optical and stereo microscopes
QIS: 30800 Investigating Adverse Events in Forensic DNA Analysis
QIS: 33798 Examination of Sexual Cases
QIS: 33800 Examination of Items
QIS: 34103 Receipt, Storage and Preparation of Chemicals, Reagents and Kits in Forensic Register

9 References

1 *Biology Methods Manual*, Metropolitan Police Forensic Science Laboratory, Great Britain, 1978.

2 Allard, J.E (1997). "The collection of data from findings in cases of sexual assault and the significance of spermatozoa on vaginal, anal and oral swabs." *Science and Justice* V37(2): April; 99-108.

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4 Brown, G. (1978) "An Introduction To Histo Technology"

5 Chiasson, D.A., Vigorito, R., Lee, Y.S., Smialek, J.E. (1994). "Interpretation of postmortem vaginal acid phosphatase determinations." *American Journal of Forensic Medicine and Pathology* 15(3): 242-246.

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12 Ricci, L. R., Hoffman, S.A., (1982). "Prostatic acid phosphatase and sperm in the post-coital vagina." *Annals of Emergency Medicine* 11(10): 530-534.

13 Silverman, E. M., Silverman, A.G. (1978). "Persistence of spermatozoa in the lower genital tracts of women." *JAMA: The Journal of the American Medical Association* 240(17): 1875-1877.

14 Willott, G.M. and Allard, J.E. (1982). "Spermatozoa - their persistence after sexual intercourse." *Forensic Science International* 19(2): 135-154.
Example

15 Casey D.G, Domijan, K, MacNeill S, Rizet D, O'Connell D, Ryan J (2016) "The Persistence of Sperm and the Development of Time Since Intercourse (TSI) Guidelines in Sexual Assault Cases at Forensic Science Ireland, Dublin, Ireland" *Journal of Forensic Sciences* 1-8

16 Nittis M, Franco M, Cochrane C (2016) "New oral cut-off time limits in NSW" *Journal of Forensic and Legal Medicine* 44 92-97
Reference sources of information for this document according to "Scientific Style and Format: The CBE Manual for Authors, Editors and Publishers.

10 Amendment History

Revision	Date	Author/s	Amendments
0	Unknown	Unknown	Unknown
1	Unknown	Unknown	Unknown
2	Unknown	Unknown	Unknown
3	27 Nov 2002	V Ientile	Format updated, manual staining to appendix. Removed notes on examination of swabs, removed unpublished paper, as work wasn't completed.
4	19 Nov 2003	L Freney	Updated references
5	12 Jul 2006	J Howes/A Williamson	"Reference" put after "Actions".
6	05 Aug 2006	J Howes	Added in Sexual Assault Investigation Flowcharts, examination of SAIK Swabs, Photograph or Witness required for ++ (1+) sperm and PSA test.
7	23 Oct 2006	J Howes	Reporting results Eg. ++ **or** 2+
8	25 Jun 2007	J Howes	Unified grading scale comments. Added Crimelite flowchart.
Version	**Date**	**Updated By**	**Amendments**
9	13 Mar 2008	QIS2 Migration Project	Headers and Footers changed to new CaSS format. Amended Business references from QHSS to FSS, QHPSS to CaSS and QHPS to Pathology Queensland
10	16 July 2010	A Lloyd	Removal of Crimelite in scope and the Crimelite flowchart. Changed section 2.2 to include use of suspensions. Removal of section 2.8 – Vaginal Secretions. Changes to section 2.10 to remove AP testing on smears positive to spermatozoa. Photograph or locations required for smear with 1 or 2 sperm seen. Clarification of flowchart regarding previously screened items by QPS. Changes to SAIK flowchart. Removal of animal sperm diagrams and insertion of photographs of animal sperm.
11	03 Feb 2011	A Lloyd	Amended use of vernier for slides to use of the England Finder Graticule.
12	31 Oct 2013	A Lloyd J Seymour-Murray	Removed animal sperm photos. Amended workflow charts, changed headings from CASS to HSSA. Change H&E solutions and staining, add England Finder information. Updated some hyperlinks.
13	03 July 2015	J Seymour-Murray	New template, update hyperlinks, some formatting updates and minor wording changes.
14	17 February 2017	A McNevin	Added storage of cell suspensions at 4 °C, removed "The" from title, typographical corrections, included product name for mounting medium,
15	29 August 2018	A McNevin	Additional references added; further information added to Appendix 2 regarding persistence of spermatozoa in oral and anal

			samples; other minor changes reflecting FR processes
16	06 May 2020	N Roselt, A McNevin	Minor updates
17	01 December 2021	C Chang	New Template. Added QIS:25747 hyperlink. Formatting updates. Updated document to reflect current processes.

11 Appendices

1 Appendix 1: H & E Manual Staining Procedure
2 Appendix 2: Persistence of Spermatozoa
3 Appendix 3: England Finder Package Insert

11.1 Appendix 1: H & E Manual Staining Procedure

11.1.1 Chemical Hazards

Pertex Mounting medium
WARNING: Pertex is irritating to eyes, respiratory system and skin.
Wear PPE and eye protection.

11.1.2 Manual Staining Procedure

Staining is performed in the staining fumehood in Rm 6124, Evidence Recovery laboratory, Forensic DNA Analysis.
Procedure:

1. Place slide on staining rack over sink, stain with haematoxylin for five minutes (add one volume and let rest)
2. Wash with nanopure water.
3. Stain with eosin for one minute.
4. Wash with nanopure water (quick wash).
5. Allow to dry on hot plate.
6. Mount coverslip in Pertex

11.1.3 Staining Quality Controls

The following quality steps should be implemented:

- Haematoxylin should be filtered before use as the crystals in solution can result in stain deposit on the slides which affects the reading of the slide. (Once a month) Filtering should also occur when refilling the Schott bottle from the stock solution. Eosin does not require filtering.

Commercial haematoxylin and eosin have expiry dates which are added to the reagent's registration page

11.2 Appendix 2: Persistence of Spermatozoa

The following information is provided to assist with the provision of expert opinion evidence in court.

Literature provides a range of time periods for the persistence of non-motile spermatozoa in the vagina:

- Up to 24 Hours[1]
- Up to 3-4 days[2]
- Up to 9 days or 12 days in the cervix, sometimes after menstruation[3]
- Up to 3 to 4 days, but may be longer[4]

Literature provides a range of time periods for the persistence of motile spermatozoa in the vagina:

- The number of motile spermatozoa discernible in the vagina may be normal after one hour and markedly decreased after 2 hours; after 3 hours normally no spermatozoa are found. Menstruation often prolongs motility in the vagina to as long as 4 hours compared with the normal period of 30 to 45 minutes.[5]
- Spermatozoa remain motile in the vagina for 2 to 3 hours and in the cervix for 48 to 110 hours[6]
- Normally 10% of the spermatozoa are alive in the vagina at the end of 2 hours post coitum. Variations in number and motility depend upon the pH of the vagina and semen, quantity of semen deposited, bacteria and flora of the vagina and the time examined post-coitally. The author has seen motile spermatozoa in the vaginal pool after 8 hours.[7]
- In several cases in which repeated examinations were possible before conception occurred, all motility ceased within one hour after intercourse. A fall of motility to 10% within 30 minutes is compatible with fecundity. On the other hand, spermatozoa may continue to move for 3 hours in a normal untreated vagina.[8]
- The motility of the spermatozoa in the specimen may give a clue to their length of stay as they remain motile from 30 to 60 minutes after deposition in the vagina.[9]

Literature provides a range of time periods for the persistence of spermatozoa in the oral cavity

- One study shows that the expectation of observing a sperm-positive oral swab is very low 15 hours post assault, with the longest time period being 27 hours, and no positives at 48 hours.[10]
- Other studies have shown a maximum time of 6 hours[11] and 24 hours (with one example of >48hours in deceased person with time since intercourse based on time of death).[12]

---

[1] O.J. Pollack. 1963 Arch. *Pathology* 35 p140-184
[2] Gordon, Turner and Price 1965 *Medical Jurisprudence*
[3] Morrison 1972 *Brit. J. Vener. Dis* 48 p141
[4] Gordon, Turner and Price 1965 Medical Jurisprudence
[5] O.J. Pollack. 1963 Arch. *Pathology* 35 p140-184
[6] Weisman 1941 *Spermatozoa and Sterility*
[7] Wm.Heinmann Medical Books Ltd 1945 *Fertility in Women*
[8] Hamish Hamilton Medical Books 1948 *Sterility and Impaired Fertility*
[9] Gonzales, Vance, Helpern and Umberger 1954 *Legal Medicine*
[10] Casey et. al. 2016 Journal of Forensic Sciences p1-8
[11] Willott & Allard 1982 Forensic Science International p135-154
[12] Nittis et al 2016 Journal of Forensic and Legal Medicine p92-97

Literature provides a range of time periods for the persistence of spermatozoa in anal and rectal swabs.

- One study shows that spermatozoa with tails are rare to find (observed at 4 and 6 hours post intercourse) and sperm heads were observed up to 46 hours post intercourse (with one example of 65 hours).[13]
- Another study indicates sperm can persist for up to 48 hours post intercourse, with the longest recorded time period being 85 hours, however it is unlikely that sperm will be detected on internal swabs beyond 24 hours.[14]

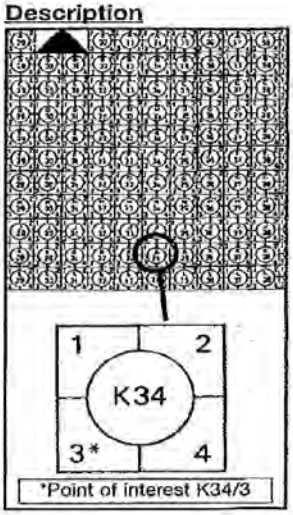
[13] Willott & Allard 1982 Forensic Science International p135-154
[14] Casey et. al. 2016 Journal of Forensic Sciences p1-8

11.3 Appendix 3: England Finder Package Insert

The England Finder

The England Finder is a glass slide marked over the top surface in such a way that a reference position can be deduced by direct reading, the relationship between the reference pattern and the locating edges being the same in all finders. The object of the Finder is to give the microscopist an easy method of recording the position of a particular field of interest in a specimen mounted on a slide, so that the same position can be re-located using any other England Finder on any microscope.

Description



The England Finder, a section of which is illustrated, consists of a glass slide 3" x 1" marked with a square grid at 1mm intervals. Each square contains a centre ring bearing reference letter and number, the remainder of the square being subdivided into four segments numbered 1 to 4. Reference numbers run horizontally 1 to 75, and letters vertically A-Z (omitting I). The main locating edge is the bottom of the slide which is used in conjunction with either the left or right vertical edge of the slide, according to the fixed stops of the stage of the microscope, all three locating edges being marked with arrow heads. The label on the finder should always appear visually at the bottom left corner when through most microscopes the reference image will appear correct.

In the illustration (part shown), the point of interest is marked with a cross, and will be seen to lie in the third segment of the square of reference K34, hence the England Reference is K34/3.

Method of Use

1. Mark the specimen slide with a label on the left indicating with arrows which sides are to be used for location. Place the slide on the stage of the microscope bringing the bottom long edge in contact with the base stops of the stage and then sliding either left or right into contact with the vertical fixed stops as appropriate. It is important always to obtain the main location of the slide and finder on the base stops first.

2. Having examined the specimen in the normal way and found a point of interest, bring this to the centre of the field of view (a crosswire in the eyepiece is useful in this respect).

3. Taking care not to alter the position of the fixed stops of the stage, remove the slide and replace with the England Finder, again bringing the bottom edge in contact first and sliding to the appropriate vertical stop, the label of the Finder being at the bottom left corner.

4. The reference pattern of the Finder will now be seen through the microscope (adjusting the focus if necessary). The reference number of the main square is recorded followed by an oblique stroke and the number of the segment in which the centre of the field of view lies (1 to 4 or 0 if in the centre circle). The boundary lines of the main squares are easily distinguishable as these are the only continuous straight lines of the pattern.

5. The reverse procedure is adopted to re-locate the point of interest, The England Finder is placed on the stage as outlined above and the stage is adjusted until the appropriate reference square and segment appear in the centre of the field of view. Remove the finder and replace with the specimen slide with label to left and appropriate vertical slide in contact with the fixed stop, when the point of interest will appear in the centre of the field of view.

11.3.1 England Finder Graticule Use

Before use ensure stage slide holder is in correct position (slide holder should be in the correct position as it is not removed on cleaning but if not-hold with one hand push holder back to full extent against the screws, tighten screws while holding and check for correct positioning).

1. Place graticule on stage with labelled corner at LHS front and clear edge against back of slide holder
2. Using the 10x objective (and Kohler illumination) – locate co-ordinates
3. Proceed to 40x or 50x objective and adjust focus as required (using oil if applicable). Locate co-ordinates and revert back to the 10x objective.
4. Taking care not to alter the position of the fixed stops of the stage, remove the graticule and replace with the slide of interest.
5. Proceed stepwise to 40x or 50x objective (oil or dry as applicable)
6. Adjust focus and locate sperm

NB: If the stage has moved repeat from step 1.

CA-70

Queensland Health

Forensic and Scientific Services

Examination of in-tube samples

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1 Purpose

To describe the actions involved in the processing of in-tube samples in Forensic DNA Analysis using the Forensic Register.

2 Scope

This standard operating procedure applies to all in-tube samples submitted for analysis to Forensic DNA Analysis, Forensic and Scientific services. All in-tube samples shall be dealt with in the manner described below.

3 Definitions

In-tube sample:	An item that has been sub-sampled and submitted to the laboratory in a 1.5/2mL tube. Also known as an 'In-tube(s)' or 'Tube(s)'
ERT:	Evidence Recovery Team
CSSE:	Crime Scene Sample Envelope (packaging used by QPS to store items collected at a scene)
PPE:	Personal Protective Equipment
SSLU:	Scientific Services Liaison Unit
SMU:	Sample Management Unit
QPS:	Queensland Police Service
FR:	Forensic Register (a laboratory information management system)
WATB:	What Appears To Be
FSS:	Forensic and Scientific services
FPP:	Forensic Property Point

4 Actions

4.1 Overview

Image check

During this stage the QPS images of the exhibit are assessed in the Forensic Register. If the image does not meet requirements further photography is required and will be completed at this time. This can be completed by Clinical Assistants, Technical or Scientific Officers.

In-Tube check

During this stage the nature of the packaging is recorded, the substrate is assessed for suitability and any quality issues are highlighted. This can be completed by Clinical Assistants, Technical or Scientific Officers.

Validation

During this stage the review and validation of the information recorded from the in-tube check is completed on each exhibit. The sample is assigned a specific extraction process, before being transferred to the Analytical Section for DNA profiling. This can be completed by a Technical or Scientific Officer.

Destruction of Packaging

This process involves the destruction of the in-tube packaging submitted for Forensic DNA Analysis. This step has been agreed upon by both Forensic DNA Analysis and the clients (QPS). This can be performed by Clinical Assistants, Technical or Scientific Officers.

Anti-contamination
Full PPE is a requirement when performing all processes of in-tube examination. All benches and equipment utilised in this process, along with any plastic storage containers are to be cleaned with bleach and ethanol solutions; the computer monitor and camera are to be cleaned with ethanol solution only (see QIS 22857).

Sterilisation of the workspace and items utilised during examination is to be performed before and after each process and as applicable during examination, as often as necessary.

4.2 Tracking of storage boxes

1. To see if in-tubes have arrived from FPP check the shelves [redacted]) in the Exhibit Room (6106B) for new in-tube boxes received; these are delivered on a daily basis, Monday to Friday.

2. It is also necessary to monitor whether additional tubes have been received by FPP throughout the day. To do this, click the equipment and supplies icon and select "Storage Box Search". Enter 'in-tube' into the storage box description (see Figure 1) and click submit or press enter (see Figure 2).



Figure 1 – FR in-tube storage box search



Figure 2 – FR storage box search results

3. To transfer storage boxes to the Evidence Recovery laboratory, follow the steps outlined below:

    a. Click the equipment and supplies icon and select "Storage Box Search" (see Figure 3).

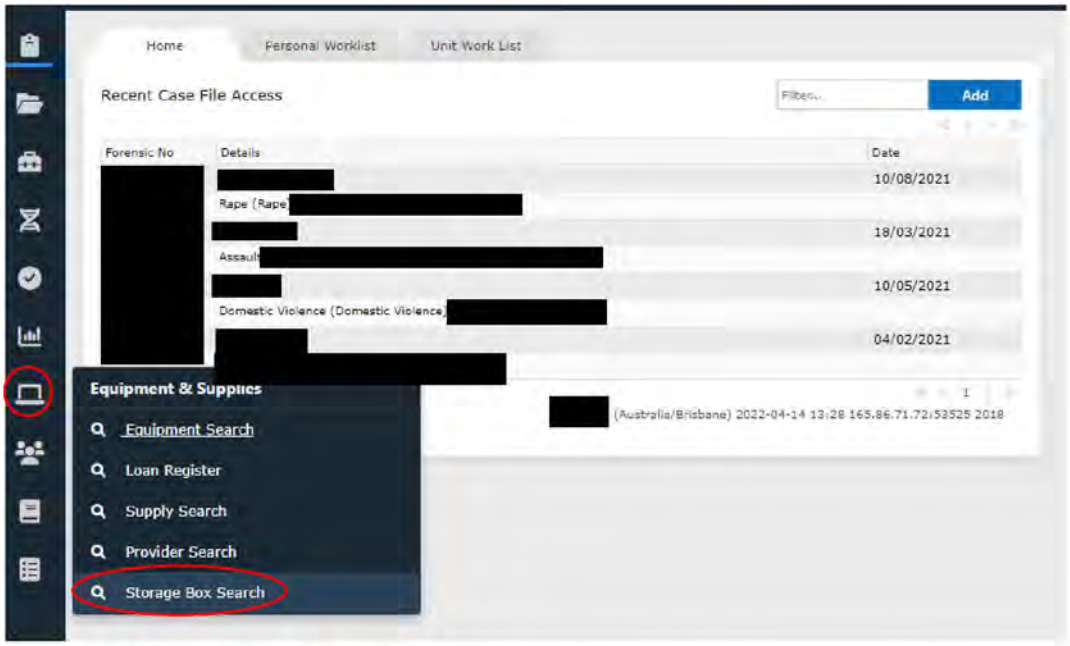


Figure 3 – Equipment and supplies icon

b. In the Storage Box No field scan the barcode of the box and click submit or press enter (see Figure 4).



Figure 4 – Storage box search table

c. In the box movement table click the plus icon (see Figure 5).

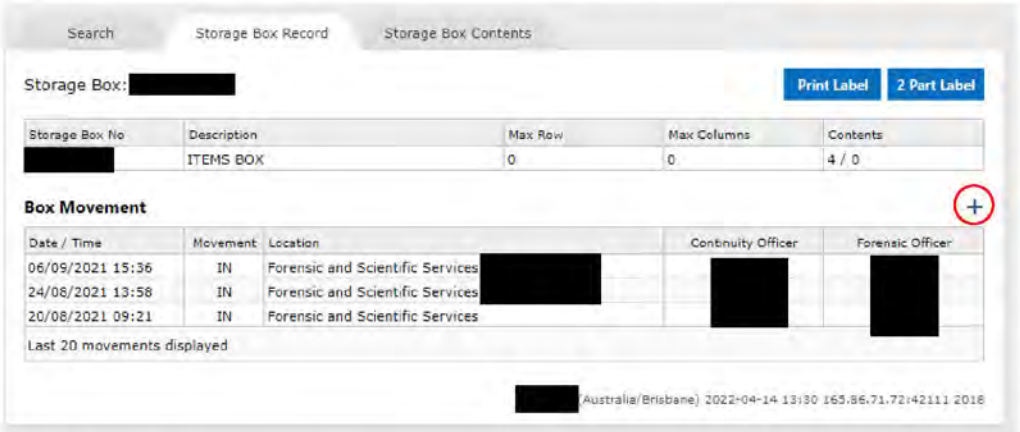


Figure 5 – Box movement table

d. In the storage location field either scan the room location ([redacted]) from a location sheet or type "EVI" and from the drop-down list select "DNA Evidence Recovery Evidence Recovery".

e. Click on the save button.

4.3 Tracking of individual samples

1. On any page, click the key identifier search icon and scan the exhibit barcode and press enter or click search.

2. Scroll to the exhibit movement table and click the plus icon (see Figure 6).



Exhibit Movement

Date / Time	Status	Location Details	Continuity Officer	Forensic Officer
01/10/2021 16:44	IN	Forensic and Scientific Services [redacted]	[redacted]	[redacted]
01/10/2021 16:44	REC	MAJOR CRIME UNIT		
30/09/2021 16:40	IN	Major Crime Unit		

Figure 6 – Exhibit Movement Table

3. If the exhibit is to be tracked to a fixed location enter the location into the "Shelf / Bench" field, if the exhibit is to be tracked to a storage box enter or scan the box barcode into the "Storage Box ID" field (see Figure 7).

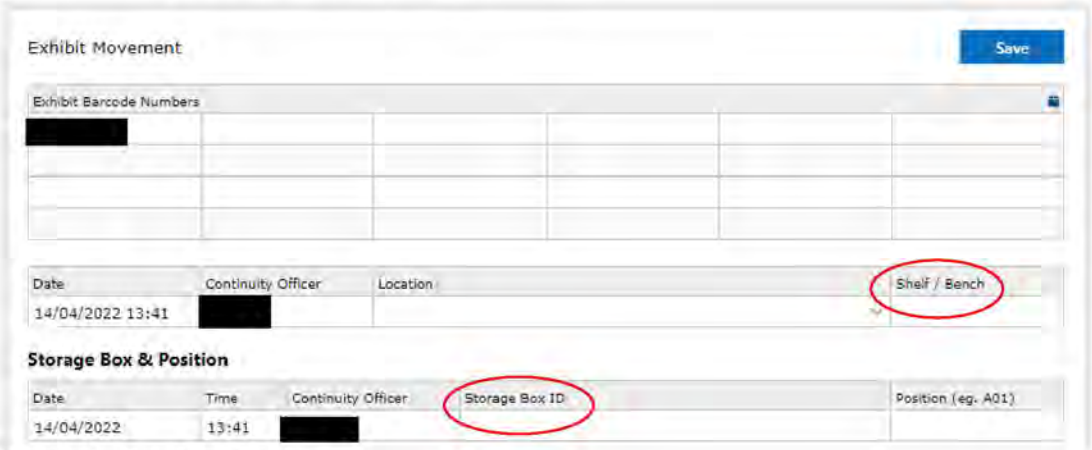


Exhibit Movement — Save

Exhibit Barcode Numbers [redacted]

Date	Continuity Officer	Location	Shelf / Bench
14/04/2022 13:41	[redacted]		

Storage Box & Position

Date	Time	Continuity Officer	Storage Box ID	Position (eg. A01)
14/04/2022	13:41	[redacted]		

Figure 7 – Exhibit Tracking

4. Click on the save button.

4.4 In-tube check

1. Log in to the Forensic Register.

2. Retrieve an empty ERT-AS box from the shelf in the Evidence Recovery laboratory, ensure the box contents are empty and track it to your bench ([redacted]) as per procedure listed in section 4.2. The contents of a box is visible on the storage box record page (Figure 5). If the ERT-AS box is not empty, consult a Technical or Scientific Officer.

3. On any page, click the key identifier search icon and scan the barcode on the CSSE, click search or press enter.

4.4.1 Image Check/Additional Photo

1. If the exhibit record is not visible, check the description on the CSSE to ensure that the exhibit is for Forensic DNA Analysis. Contact the QPS Forensic Reception Centre on (0) 3364 6208, identify yourself and explain that you have a sample that is not visible in the FR that requires the Forensic DNA Analysis box to be ticked.

2. Once in the exhibit record screen, scroll down and click on the thumbnail image of the CSSE, a larger image will open in a new window (see Figure 8 and Figure 9).



Figure 8 – Image thumbnail

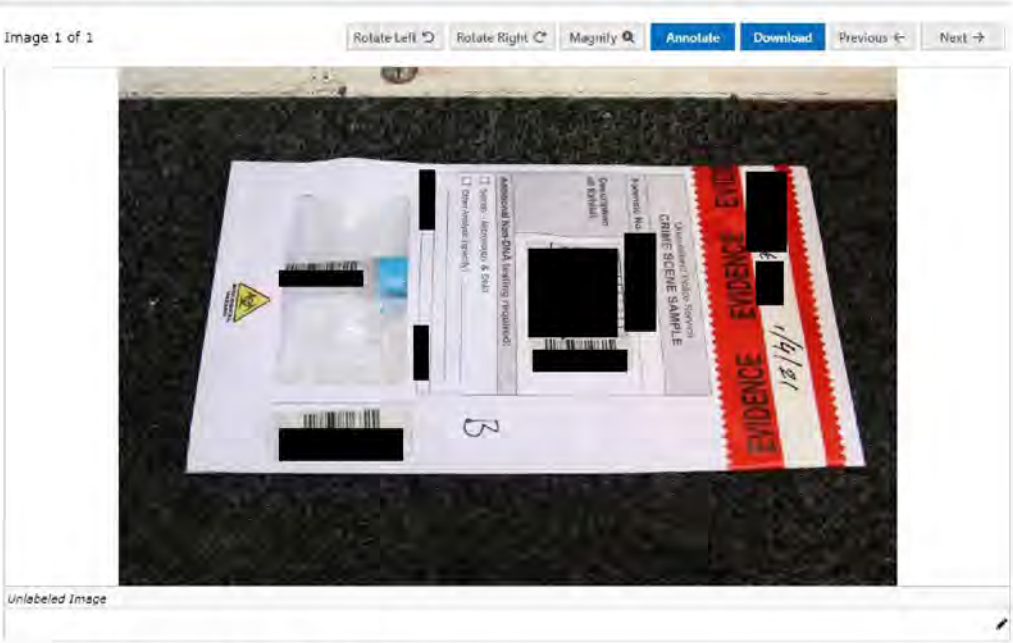


Figure 9 – Example image of CSSE

Note: One or more images for the exhibit may be considered explicit by the QPS. In these instances, the thumbnail images will not be visible in the images table. There will be text indicating that the images are explicit. In these instances, proceed with taking a new photo.

3. Check to ensure all details on the image match the packaging (CSSE) that has been received and check the image quality. As a guide, the following general principles apply:

    a. Ensure barcode/s affixed to the CSSE and tube and other labelling are legible and match.

    b. The entire CSSE is visible in the image and there is a clear border around the image (no part of the CSSE can be obscured or cut off).

c. Ensure that the CSSE is the main subject of the image. It is acceptable for other objects to be present within the image as long as there are no identifiers visible (barcode number). If unsure consult a Technical or Scientific Officer.

d. An additional photo must be taken if any of the following applies:

   i. If the packaging is damaged in any way, a photo must be taken of the damage to the CSSE.

      1. If an additional image is required of damage to the CSSE, this must also be noted in the in-tube check, see section 4.4.4.

   ii. If there is any additional information recorded on the rear of the CSSE an additional photo of the rear of the CSSE is required.

   iii. If the image does not match the physical CSSE it must be re-photographed.

e. If the barcode/s, FR number or the description on the CSSE does not match what is recorded in FR, the in-tube must be put on hold, see section 4.10.

Note: If there are multiple images of the same CSSE and requirements are met across all images (e.g. one image shows the CSSE without an FR number and the second image shows the CSSE with an FR number), then this is acceptable. If unsure whether an additional photo is required, it is better to take one.

4. Close the window containing the image.

5. If an additional photo is required, take the photo and upload to the PC (refer to section 8.1.1).

6. If the image meets requirements, go to section 4.4.2.

4.4.2 Assessment of testing requirements

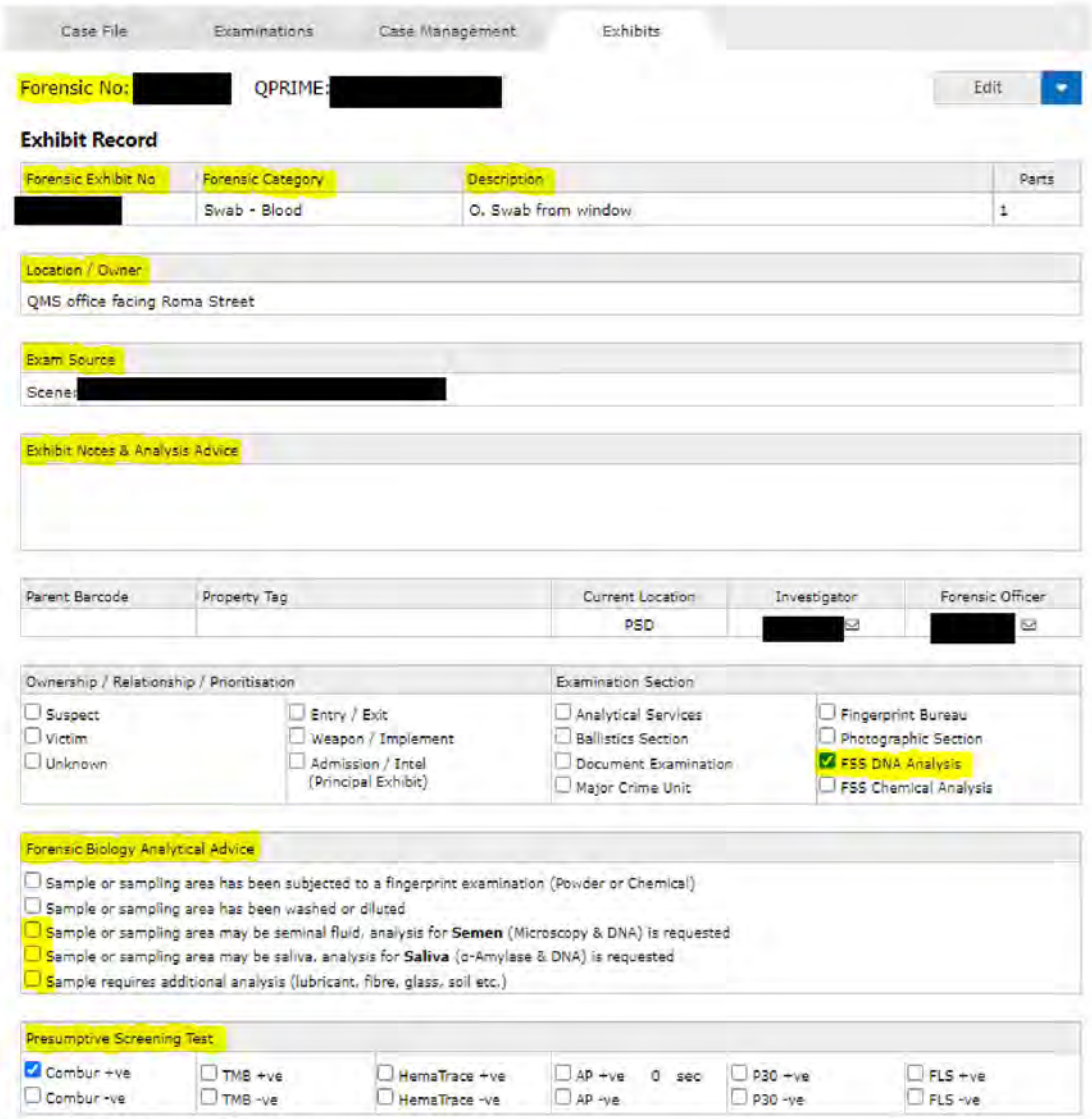
1. In the exhibit record screen, review the highlighted fields as per Figure 10, ensure any details on the CSSE and tube match the QPS image and FR. The following are the minimum labelling requirements:

   a. Forensic Register number

   b. Forensic Exhibit number (barcode) on both the CSSE and tube

   c. A brief description of item/s, either from or combination of information recorded in the "Description" and "Location/Owner" fields.

   d. The CSSE may contain additional information such as a batch/lot number or QP number. Although these details are not a minimum requirement if they are present on the CSSE they must match the details in FR.



Case File | Examinations | Case Management | Exhibits

Forensic No: [redacted] QPRIME: [redacted] Edit

Exhibit Record

Forensic Exhibit No	Forensic Category	Description	Parts
[redacted]	Swab - Blood	O. Swab from window	1

Location / Owner: QMS office facing Roma Street

Exam Source: Scene: [redacted]

Exhibit Notes & Analysis Advice

Parent Barcode	Property Tag	Current Location	Investigator	Forensic Officer
		PSD	[redacted]	[redacted]

Ownership / Relationship / Prioritisation

- ☐ Suspect
- ☐ Victim
- ☐ Unknown
- ☐ Entry / Exit
- ☐ Weapon / Implement
- ☐ Admission / Intel (Principal Exhibit)

Examination Section

- ☐ Analytical Services
- ☐ Ballistics Section
- ☐ Document Examination
- ☐ Major Crime Unit
- ☐ Fingerprint Bureau
- ☐ Photographic Section
- ☑ FSS DNA Analysis
- ☐ FSS Chemical Analysis

Forensic Biology Analytical Advice

- ☐ Sample or sampling area has been subjected to a fingerprint examination (Powder or Chemical)
- ☐ Sample or sampling area has been washed or diluted
- ☐ Sample or sampling area may be seminal fluid, analysis for **Semen** (Microscopy & DNA) is requested
- ☐ Sample or sampling area may be saliva, analysis for **Saliva** (α-Amylase & DNA) is requested
- ☐ Sample requires additional analysis (lubricant, fibre, glass, soil etc.)

Presumptive Screening Test

Combur	TMB	HemaTrace	AP	P30	FLS
☑ Combur +ve	☐ TMB +ve	☐ HemaTrace +ve	☐ AP +ve 0 sec	☐ P30 +ve	☐ FLS +ve
☐ Combur -ve	☐ TMB -ve	☐ HemaTrace -ve	☐ AP -ve	☐ P30 -ve	☐ FLS -ve

Figure 10 – Exhibit record page

2. If the item is ticked for **FSS Chemical Analysis** in addition to FSS DNA Analysis or FSS Chemical Analysis is ticked but not FSS DNA Analysis, the tube is to be given to a Technical or Scientific Officer who will send a task request to QPS and place the CSSE on hold pending advice/clarification from QPS.

3. Check Forensic Biology Analytical advice box for "**Sample or sampling area may be seminal fluid, analysis for Semen (Microscopy & DNA) is requested**" and the semen testing required box on the CSSE. If these boxes are ticked, the in-tube should not be removed from the CSSE. Track the CSSE to the bench as per section 4.3 and attach a note to the CSSE identifying the reason (i.e. semen testing). A Technical/Scientific officer will add the exhibit to the examination worklist and track it to a items box. This will be actioned by a Technical or Scientific officer. This process is also to be completed in instances when an entire cigarette butt is submitted in an in-tube.

4. Clinical Assistants, Technical or Scientific officers should be aware of trigger phrases/words that may be present in the FR or on the CSSE, refer to Table 1 for

examples. If these trigger words are present, click the case file tab. If the "General Offence Class" field contains rape, sexual offences or child offences a Technical/ Scientific officer or the Evidence Recovery Senior Scientist must be notified.

Table 1 – Trigger wording for possible additional screening

Words/phrases	Possible Examination Required
Semen, seminal fluid, AP pos, PSA/p30 pos, polilight pos, condom, genital swab, sampling from clothing or bedsheets.	Semen testing

Note: The above table is for guidance purposes only and is not an exhaustive list. If unsure consult a Technical/Scientific officer or the Evidence Recovery Senior Scientist.

5. If a Scientific officer or the Evidence Recovery Senior Scientist determines clarification is required from QPS, the exhibit must be placed on-hold as per section 4.10 and a request/task be sent as per section 4.9.1.

6. If a Scientific officer or the Evidence Recovery Senior Scientist advises no further screening is required a notation must be added to state "INITIALS advised no semen testing required" or "INITIALS advised cells only".

7. If the "**Sample or sampling area may be saliva, analysis for Saliva (α-Amylase & DNA) is requested**" box is ticked, process the exhibit as normal.

8. If the "**Sample requires additional analysis (lubricant, fibre, glass, soil etc**)" box is ticked, track the exhibit to the bench as per section 4.3, with a post-it note stating "additional analysis". The Technical or Scientific Officer will then send a task request to QPS and place the CSSE on hold pending advice/clarification from QPS.

9. If the "**No testing required**" box is ticked (this box will not be visible unless it has been ticked), track the exhibit to the bench as per section 4.3, with a post-it note stating "no further work". The Technical/Scientific Officer will complete the necessary process.

10. If further screening for biological fluids is not required, proceed to section 4.4.3.

4.4.3 Check in-tube integrity and assessment for processing

1. Stamp the rear of the CSSE with the correct date and initial. Open the CSSE by popping the tube through the rear of the CSSE.

2. Inspect the tube and lid for damage and if evident, advise a Scientific Officer of the issue, who will transfer the substrate to a new tube.

3. Assess the individual substrate within the in-tube to ensure it is compatible with downstream processing. If the sample requires manual intervention this must be done by a Scientific or Technical Officer prior to submission to the Analytical team. In-tubes requiring manual intervention are to be stored to a separate box once the in-tube check is complete. Some samples that do not meet requirements are listed below:

    a. Swab stick too long (maximum length of swab and stick is ~12 mm measured from the swab tip to the stick).
    b. Excess substrate, if the sample size is too large. Maximum size for a piece of fabric is ~7.5mm x ~7.5mm and for chewing gum is ~5mm x ~5mm x ~5mm. Ask a Scientific or Technical officer if unsure of sample sizes.

c. Hair located outside of an in-tube. If hair is found, place the in-tube into a small clip seal plastic bag and store to an ERT-AS box. Alert a Technical or Scientific Officer.

d. Cracked tube.

4. If you pop the tube out of the CSSE and realise that a photo is required, take a photo of the tube beside the CSSE. When uploading the image following section 4.4.4, make a note in the in-tube check "CSSE and tube photographed after opening".

5. Place a length of clear sticky tape around the barcode and if the tube cap is pierced, adhere a tough spot over the hole.

6. Wipe the tube with bleach and ethanol (cleaning with bleach and ethanol is not conducted on damaged tubes to avoid contact with the substrate within the tube).

4.4.4 In-tube processing

1. Scroll down to the exhibit analytical/testing table (see Figure 11 – Exhibit analytical/testing table), click the create exhibit test icon.



Figure 11 – Exhibit analytical/testing table

2. Go to "Testing/Analysis" and in the process field use the dropdown menu to select in-tube check (see Figure 12).

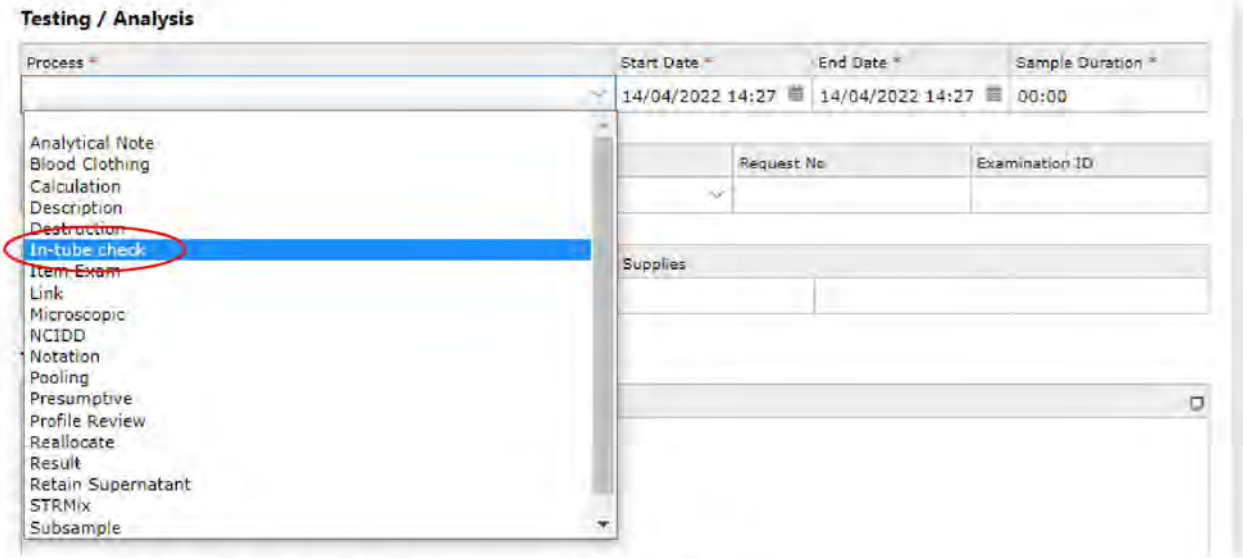


Figure 12 – Testing/Analysis table - process dropdown menu

3. Tick any quality issues identified with the sample (see Figure 13). **Note:** If there is no barcode on the sample or the barcode is stuck to the inside of the CSSE, go to section 4.6.

Testing Detail

Quality Issue	
☐ Hair located on the outside of tube	☐ Additional information on reverse of CSSE
☐ Tape-lift rolled incorrectly	☐ Labelling Discrepancy
☐ Excess substrate	☐ No Barcode on Sample
☐ Swab stick too long	☐ Other manual intervention required

Figure 13 – Quality Issue table

a. If a labelling discrepancy is noted, depending on the discrepancy, the tube may need to be put on-hold.

   i. Typographic labelling discrepancies:
   This type of problem is where the difference between the CSSE and the FR record represents a typo or handwriting equivalent of a typo (for example, one record states "Vehicle Rego 123ABC" and the other record states "Vehicle Rego 123ACB"). For these samples, proceed with testing, ensuring that the "Labelling discrepancy" check box is ticked and details of the discrepancy is noted in the notes field.

   ii. Description or other type of discrepancy:
   Some examples may be; two different barcodes on the one CSSE; CSSE states "swab of right shoe" but FR record states "swab of left shoe" or FR record indicates the sample is a swab, but there appears to be a tape-lift in the tube. In these instances, do not process the exhibit any further as it will need to be placed on-hold and the discrepancy be resolved.

   iii. Samples that have been on-hold prior to the completion of an in-tube check can be restarted once clarification has been sought from QPS. Technical or Scientific officers will place CSSE's into the Evidence Recovery in-tube hatch with a note indicating testing can restart. Clinical Assistants or Technical/Scientific officers can proceed with standard processes (in-tube check). Ensure the "Labelling discrepancy" check box is ticked and a comment made in the notes field "Refer to notation, labelling discrepancy has been resolved".

b. If an additional photo was required for the rear of the CSSE, the "**Additional information on reverse of CSSE**" is to be ticked.

c. If the swab within the tube is too long and manual intervention is required, the "**Swab stick too long**" box is to be ticked.

d. If a hair is located on the outside of the tube, the "**Hair located on the outside of tube**" box is to be ticked.

4. Tick the "Packaging matches Exhibit image" only if an additional photo was not required (an exception is if a photo was required of the rear of the CSSE). The "Packaging matches Exhibit image" should only be used when the entire CSSE is visible in the QPS image and there are no visible differences. For example, if there are staples present in

the CSSE received, but these are not visible in the QPS image, this check box cannot be used as an additional photo is required.

a. If a CSSE is received with a property receipt attached, a photo of the CSSE and the attached property receipt is required and notes made to the in-tube check "Image taken of CSSE with Property receipt attached". The property receipt is then removed and an additional photo of just the CSSE is required with notes made "Image taken of CSSE without Property receipt". In this case, do not tick the "Packaging matches exhibit image" tick box.

    i. If the property receipt is a printed copy, batch up with the completed CSSE's to be retained for 3 months.

    ii. If the property receipt contains additional information i.e. handwritten information. The property receipt must be given to the administration team to be scanned and uploaded.

5. Tick the "Seal and Packaging Intact" if the CSSE has been sealed, signed and dated and there is no visible damage present. If there are any exceptions the auto-generated text in the notes section can be edited to detail the nature of the packaging (e.g. "seal is signed but not dated").

6. Tick the "Sample meets requirements" box if the substrate is appropriate for analytical processing and does NOT require further manual intervention.

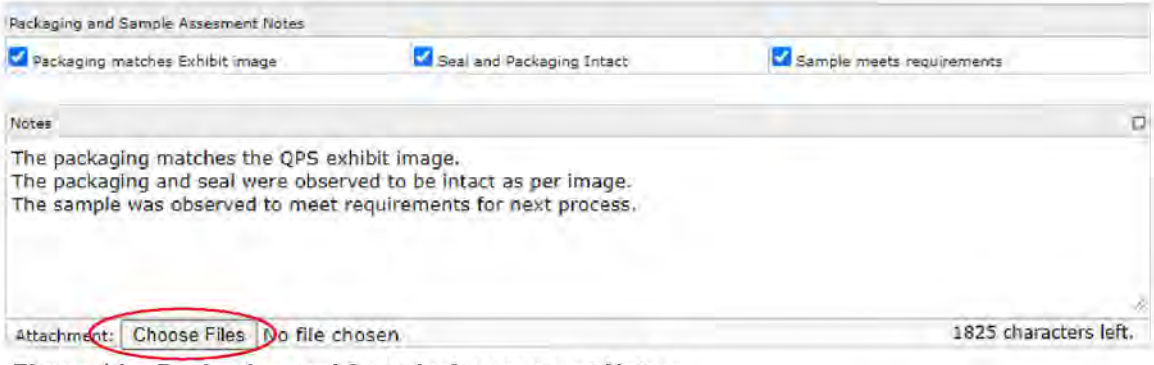


Figure 14 – Packaging and Sample Assessment Notes

7. Refer to appendix 8.1 to upload an image from a camera the PC. To upload a photo to the in-tube check, click on the "Choose Files" button (see Figure 14), scan the CSSE barcode into the search field of the folder window, select the image and click open. If you are uploading a photo due to damage to the CSSE, remember to note the damage in the notes field.

    a. If an error is noted after the image has been uploaded, you can override the old image by re-uploading the correct image.

    b. If you have taken a photo of the tube beside the CSSE, insert the comment "CSSE and tube photographed after opening".

8. Ensure that a priority is selected. This box should only be changed if a Senior Scientist or Team Leader has advised that the sample is priority 1.

9. If the CSSE has a correction and it has not been signed or dated, this should be noted in the notes field i.e. "correction not signed or dated noted".

10. In the storage box ID field scan the barcode of the ERT-AS box. Press tab and the position field will auto fill, if you want to store the tube in a different position this field can be manually over-ridden by typing the desired position into the field. Ensure a position is selected otherwise the sample will not store to the box (see Figure 15).



Figure 15 – Storage Box ID and position

11. Click on the save button. If the in-tube check requires changes after saving click the edit button, make any necessary changes and click save.

4.4.5 Temporary storage of CSSE (for destruction)

1. Bind CSSE's that have been processed by the same Clinical Assistant and on the same day together and place the CSSE's into a destruction box labelled with the correct month. Destruction boxes are to be emptied after 3 months as described in section 4.8. **Note:** CSSE's are not to be tracked electronically.

4.5 In-tube check validation

4.5.1 Retrieving in-tube ERT-AS boxes

1. Collect ERT-AS box(s) from shelves [redacted] in the exhibit room, freezer box 1 [redacted] or from an examination bench in the laboratory. Transfer the box(s) to the Evidence recovery laboratory as per section 4.2 if required.

4.5.2 Review and validation of the in-tube check

1. Click the equipment and supplies  icon and select "Storage Box Search", scan or type the ERT-AS box barcode into the "Storage Box No." field and click submit or press enter.

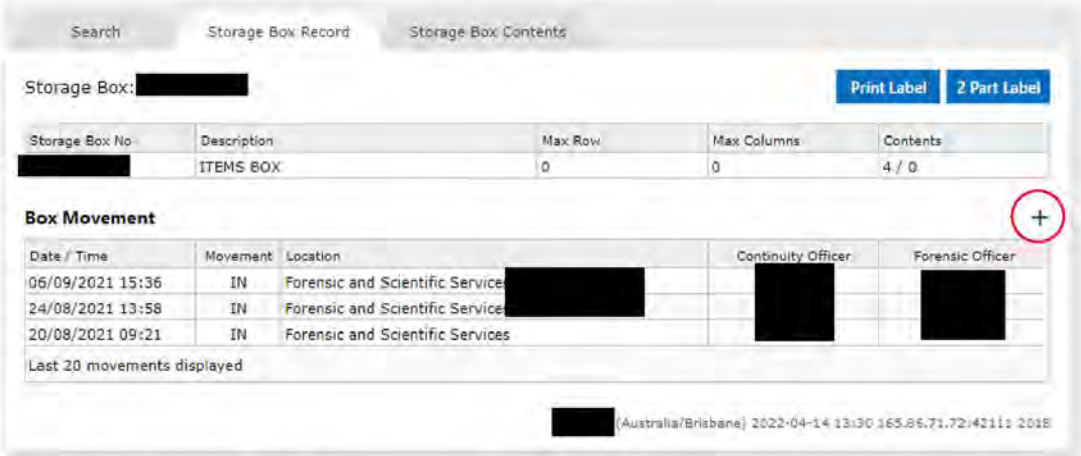


Figure 16 – Storage Box Record

2. Transfer the ERT-AS box to the examination bench in the Evidence Recovery laboratory.

    a. Click on the plus icon (refer to Figure 16).

    b. In the "Shelf/Bench" field, type "EVI" and select "DNA Evidence Recovery bench" from the drop down box. Enter the bench number and click save.

3. Click on the Storage Box Contents tab (see Figure 17).

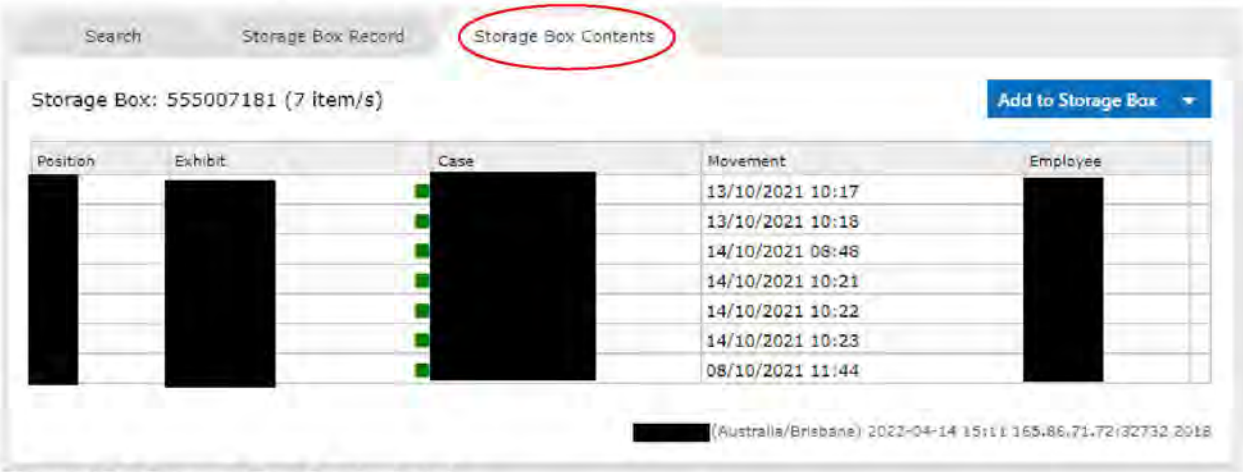


Figure 17 – Storage Box Contents tab

4. This will list the contents contained in the ERT-AS box. **Note:** The orange traffic light button indicates samples awaiting validation, once validation is complete this will change to green. Click on the first laboratory number in the ERT-AS box to perform individual review and validation.

5. Ensure that the barcode affixed to the in-tube matches the Exhibit Record in the FR.

6. Ensure that the "Category" in the FR is consistent with the exhibit received within the tube.

7. Scroll down and click on the thumbnail image of the CSSE or the thumbnail associated within the in-tube check. Check the image quality, ensuring barcodes affixed to the CSSE and tube and other labelling are legible and that the entire CSSE is visible in the image. If the image is not acceptable return the tube to the person who created the in-tube check for an additional photo.

8. Check the item description ensuring all details match. Check testing requirements – pay particular attention to the semen or saliva testing tick box, the sample requires additional analysis box and the no testing required tick box (if present) or any additional notes on the CSSE.

9. Close the image window.

10. If the FSS Chemical analysis box and/or Sample requires additional analysis boxes are ticked further advice may be required as the sample may require dual analysis or lubricant testing unless specific information is provided in the "Exhibit Notes & FSS

Advice" field. Inform the Evidence Recovery Senior Scientist in the instance where more information is required.

11. Once all details have been checked, scroll down to the "Exhibit Analytical/Testing" table and click the date/time hyperlink for the in-tube check.
12. Review the in-tube check notes field. **Note:** If the labelling discrepancy box is ticked, a Request/Task may be required to be sent to the QPS Forensic Officer as per procedure listed in section 4.9.1. If the exhibit cannot be processed refer to section 4.10.
13. If the in-tube check is incorrect or incomplete return the tube to the person who created the in-tube check for correction. **Note:** The person who edits the record cannot validate it.
14. If the sample requires manual intervention refer to section 4.5.3.
15. It is important not to validate the in-tube check at this stage as the extraction must be ordered prior to validation to trigger an automatic result line.
16. Scroll down to the exhibit analytical/testing table and click the create exhibit test icon.
17. Under "Worklist" use the dropdown menu in the "Technique" field to select DNA Extraction. In the "Method" field use the dropdown menu to select the relevant extraction method (e.g. QIAsymphony Pre-Lysis). If the sample requires saliva testing select Retain Supernatant DNA IQ. If the sample is a **Priority 1** or "chewing gum", select the Maxwell 16 extraction method unless instructed otherwise (see Figure 18).

Note: The retain supernatant worklist should not be selected for an exhibit where saliva is likely to be present (i.e. bottle or can opening). Consult with the Evidence Recovery Senior Scientist if you are unsure.

Worklist

Technique	Method	Source Batch / Rack ID	Position
DNA Extraction	QIAsymphony Pre-Lysis		

Figure 18 – Worklist selection table

18. Click on the save button.
19. Scroll down to the exhibit analytical/testing table and click on the date/time hyperlink for the in-tube check
20. If all details are correct click the [CLICK TO VALIDATE] bar (Figure 19). Once validated, this bar will turn green.

[CLICK TO VALIDATE]

Figure 19 – Validate Bar

Note: The process of selecting a DNA Extraction worklist and validating the in-tube check will automatically generate the result line "Submitted Results Pending". If the automatic

result line does not automatically generate this will need to be completed manually refer to QIS 33800.

21. Close the window or tab and return to the storage box contents page, the traffic light button will turn green if the page is refreshed (F5) for the sample that was validated. Complete the above process for each tube in the ERT-AS box until all traffic lights appear green.

22. Once the box is completed, add a storage box movement to track the box to the Evidence Recovery laboratory [redacted] as per section 4.2. Attach a rubber band and place the ERT-AS box into the hatch for collection. If a box is completed towards the end of the day, transfer the box to freezer box 1 [redacted]). Any boxes that have unvalidated tubes are to be placed into freezer box 1 ([redacted]) at the end of the day with a note attached indicating the tubes are awaiting validation.

23. The awaiting review in-tube worklist can be checked at the end of the day to ensure that all in-tube validations have been complete, refer to QIS 34298.

4.5.3 Manual intervention

1. Set up the examination bench and clean required instrumentation with bleach and ethanol.

2. Complete sample manual intervention as per current laboratory procedures ensuring to change gloves and clean/sterilize equipment between samples if necessary. Examples of appropriate sample sizes are located in the laboratory for reference and training purposes.

3. Complete the standard in-tube check review, but do not validate the in-tube check.

4. Track the tube requiring manual intervention to the examination bench via exhibit movement as per section 4.3.

Note: Only in-tubes that need to be opened are required to be tracked to an examination bench.

5. In the exhibit analytical/testing table click the create exhibit test icon.

6. Under the "Testing/Analysis" table go to the process field and use the dropdown menu to select "Item exam" (see Figure 20).

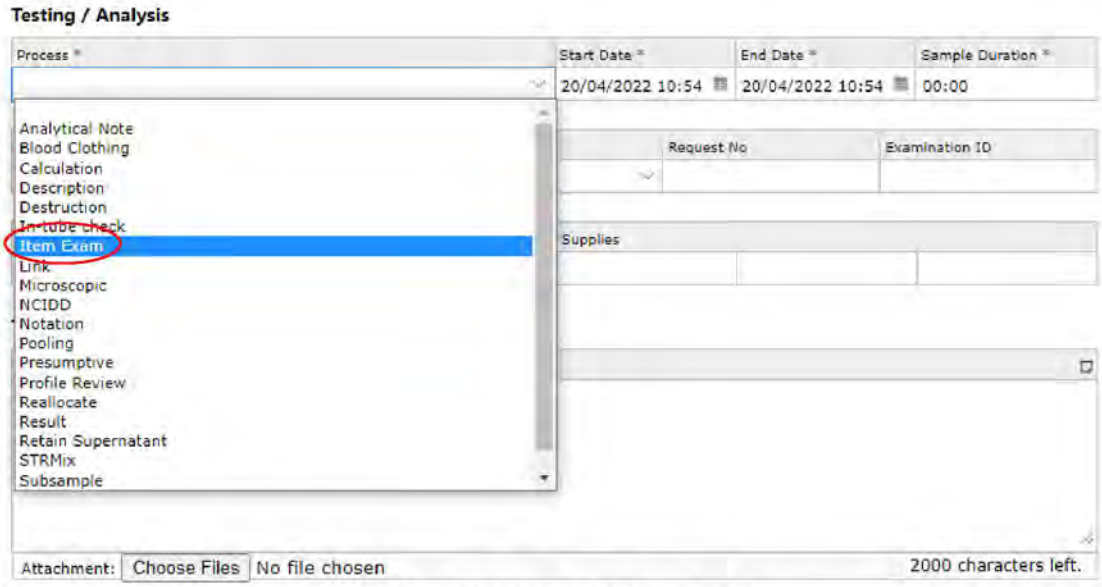


Figure 20 – Testing/Analysis table - process dropdown menu

7. In the notes field write a description of the manual intervention performed (see Figure 21).

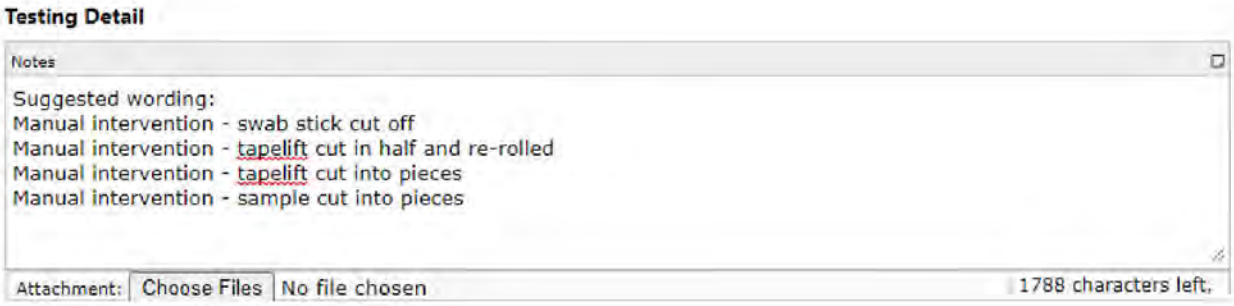


Figure 21 – Item exam notes field

8. Scroll down to the "Worklist" table and in the "Technique" dropdown menu select DNA Extraction (see Figure 22).

9. In the "Method" field use the dropdown menu to select the relevant extraction type (e.g. QIAsymphony Pre-Lysis) (see Figure 22).



Figure 22 – Worklist selection table

10. Click on the save button.

11. In the exhibit analytical/testing table go back to the in-tube check and click on the date/time hyperlink to open.

12. Click the [CLICK TO VALIDATE] bar (Figure 19). Once validated, this bar will turn green.

4.5.4 Manual intervention – retained portion

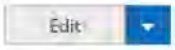
1. Complete section 4.5.3.
2. In the exhibit analytical/testing table click the create exhibit test icon.
3. In the "Testing/Analysis" table go to the process field and use the dropdown menu to select "Subsample".
4. In the SubID field, select the plus icon to auto assign a new barcode and in the "Subtype" field select "RETAIN" from the dropdown menu.
5. In the notes field add a brief description of the retained portion.
6. Enter the item retention storage box barcode into the Storage box ID field and press tab for the next available position.
7. Record the tube lot number (see Figure 23).
8. Click on the save button.



Figure 23 – Creating subsample for retained portion

9. In the exhibit analytical/testing table click on the date/time hyperlink for the subsample. Follow section 4.6 to print a tube label for the retained portion. Label the tube and place it in the item retention box in the position allocated.
10. Validation of manual interventions is to be completed by Scientific officers only, refer to section 4.7.

4.6 Printing sample tube labels

1. On the exhibit record page click the arrow 

icon next to the edit button and select "3 Part Tube Barcode" (see Figure 24).

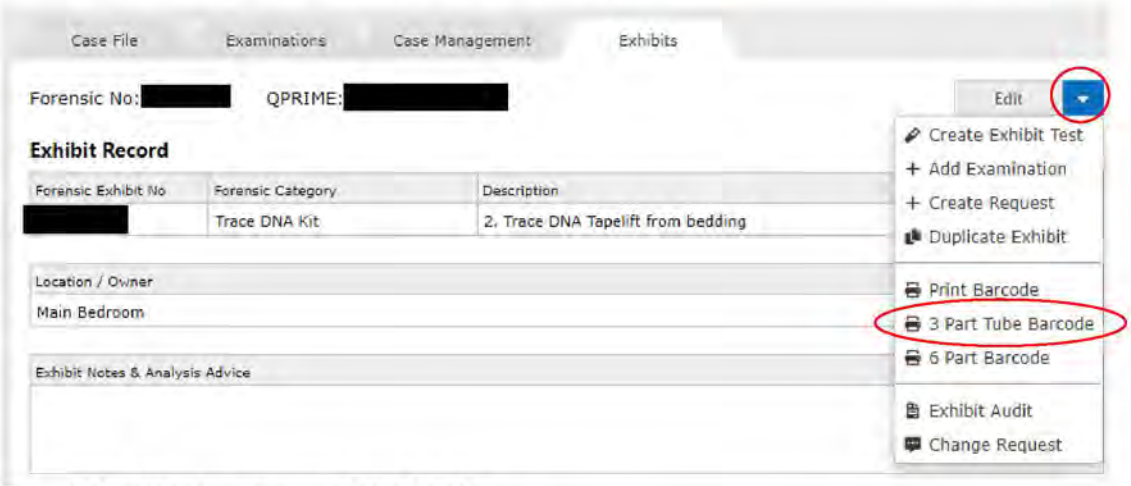


Figure 24 – Printing sample tube labels

2. A new window will open displaying the 3 part label, click the printer icon and select print.
3. To print a subsample barcode, click on the subsample hyperlink from the exhibit record page and follow the above steps (see Figure 24).

4.7 Validation of manual intervention

All manual interventions must be reviewed and validated by Evidence Recovery Scientific officers.

1. Click on the DNA  icon and select worklist.
2. Click on the worklist tab > awaiting review > item exam.
3. Click on the relevant barcode number and click the date/time hyperlink in the exhibit testing/examinations table (see Figure 25).



Figure 25 – Hyperlink to item exam

4. Review the item exam notes field and details of any subsamples if necessary (see Figure 26).

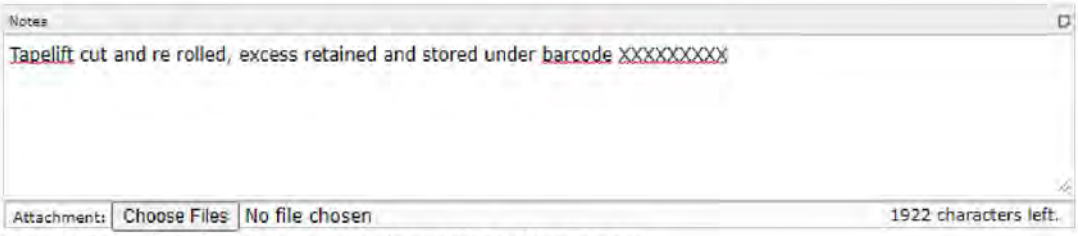


Figure 26 – Details of manual intervention item exam

5. If the item exam is incorrect or is incomplete the Technical or Scientific officer will need to correct or complete it before validation. **Note:** The person who edits the record cannot validate it.

6. If all details are correct click the [CLICK TO VALIDATE] bar (Figure 27). Once validated, this bar will turn green.

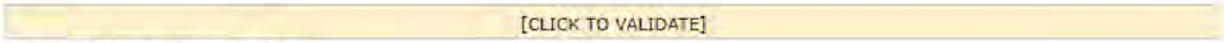


Figure 27 – Validate bar

7. Ensure the in-tube check has been validated, an extraction worklist has been selected and there is an automatic result line as per section 4.5.2.

4.8 Destruction of packaging

1. This is performed every month for CSSE's that were processed 3 months prior (**Note:** CSSE storage boxes will be labelled according to the month they were processed).

2. Empty the CSSE's into a biohazard bin bag.

3. Clean the empty destruction box/s with bleach/ethanol.

4.9 Labelling discrepancy procedure

4.9.1 Creating a Request/Task

1. On the exhibit record page, right click on the FR tab and select duplicate, a duplicate window will appear as a new tab to be used when completing a request/task.

2. From the "Exhibit Record" page, click the arrow 

icon next to the edit button and select "Create Request" (see Figure 28).



Figure 28 – Creating a new request/task

3. Alternatively, click on the case management tab and click the add button.

4. Ensure the "Report Type" field is selected as Request/Task.

5. Refer to the duplicated screen and enter the QPS Forensic Officer's number into the Action Officer field of the request/task.
6. Select "Review" in the "Request Type" field.
7. Ensure Forensic DNA is selected in the Job/Request Type field.
8. In the comments field type the details of the request, refer to appendix 8.3 for standard wording. Refer to Figure 29 for request/task requirements.
9. Click on the save button.

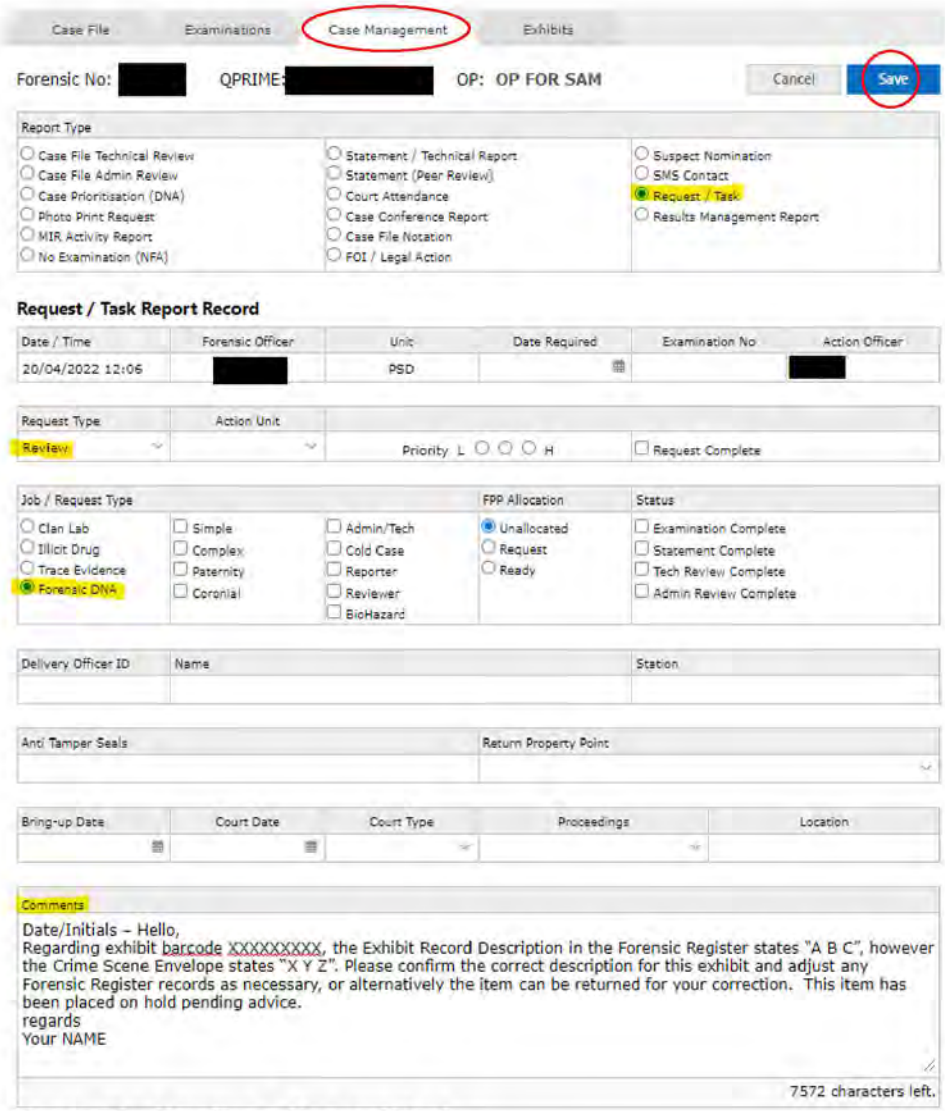


Figure 29 – Creating a Request/Task

10. Once saved, navigate to the Exhibit/Item table and click the add exhibits + icon.
11. Scan the barcode of the item/s that the request/task refers to. Alternatively, a list of the related exhibits will be visible in the "All Related Exhibits" table, select the forensic exhibit no barcode/s that apply. The selected barcode/s will highlight green and will appear in the case report - exhibit/items table.

12. Click on the save button.

This request will be sent to the Forensic Officer for action. Once actioned, the Forensic Officer will edit the request/task and enter the FR number of the person that sent the original request and add any comments into the comments field. This will return the request/task to the unit worklist and the individuals personal worklist.

4.9.2 Completing a Request/Task

1. Staff are to complete request/tasks that have been returned to them.
2. The validator is responsible for completing outstanding request/tasks for absent staff using the unit worklist tab on the main screen of the FR, refer to QIS 34298.
3. Once the QPS Forensic Officer has sent a request/task back to the original creator the Forensic or Technical Officer will be alerted by the bell icon on any page on the FR see Figure 30.



Figure 30 – Notification of request/task

4. Click on the bell, select assigned reports and click on the request to open.
5. Alternatively, click on the "bdna" logo at the top of the screen to return to the main home page. Request/tasks that have been returned will appear in the personal worklist tab. Click the tab and click the FR number to open the request/task.
6. Review the comments from the QPS Forensic Officer and ensure that any changes to the FR have been completed if necessary.
7. If the exhibit/s were on-hold refer to section 4.11 to restart testing.
8. If the exhibit/s were not on hold and the request has been completed, click the edit button, click the "Request Complete" box and click the save button.

4.10 On-hold procedure

1. If a sample is to be put on hold pending further advice from QPS, validate the in-tube check if it has been completed as per section 4.5.2 but do not add an extraction type. Create a request/task as per section 4.9.2.
2. Scroll down to the exhibit analytical/testing table and click the create exhibit test icon.
3. Go to "Testing/Analysis" and in the process field use the dropdown menu and select result.
4. In the Police Report field select "SOHAA – Sample on hold, awaiting advice" from the dropdown menu (see Figure 31).

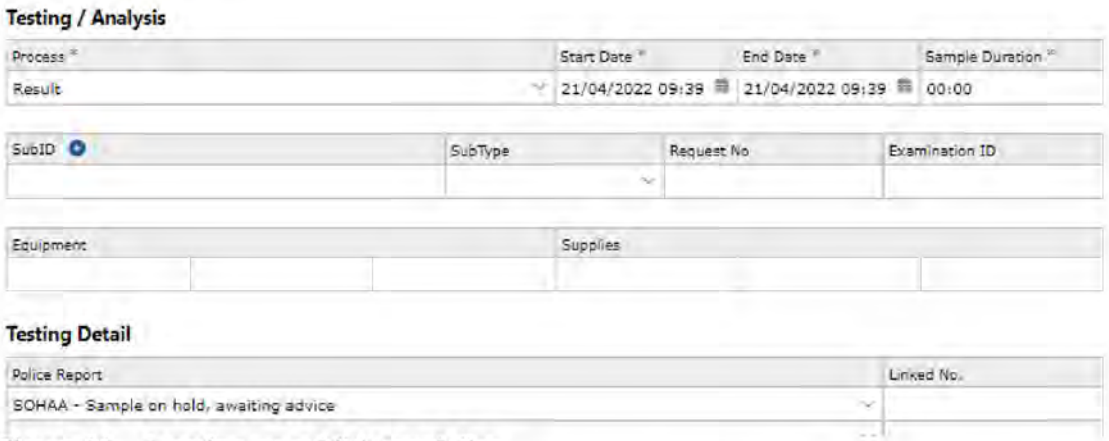


Figure 31 – Creating an exhibit result line

5. Go to the "Worklist" table and in the "Technique" field use the dropdown menu to select "On Hold".
6. In the method field use the dropdown menu to select "Awaiting Advice" (see Figure 32).



Figure 32 – Worklist table - "On-hold"

7. Click on the save button.
8. Transfer the CSSE to the on-hold box using exhibit movement.
9. Have a colleague check and validate the "SOHAA" result line.

4.11 Testing restarted procedure

1. Follow section 4.9.2 to view and complete the request/task.
2. In the exhibit analytical/testing table, click the create exhibit test icon.
3. Go to "Testing/Analysis" table and in the process field use the dropdown menu to select "Notation".
4. Indicate in the notes field if testing can be restarted and note where communication with QPS can be found (see Figure 33).

Note: Creating a new notation will trigger removal from the on-hold worklist.

Testing / Analysis

Process *	Start Date *	End Date *	Sample Duration *
Notation	21/04/2022 10:23	21/04/2022 10:23	00:00

SubID	SubType	Request No	Examination ID

Equipment			Supplies		

Testing Detail

Notes

Restart testing as per advice from QPS, see case management reports.

Attachment: Choose Files No file chosen 1931 characters left.

Figure 33 – Notation for testing restarted

5. Click on the save button.
6. Create an exhibit movement as per section 4.3 and transfer the CSSE to the evidence recovery laboratory [redacted]. Place the CSSE into the in-tube hatch in the evidence recovery laboratory and attach a note to the CSSE to indicate that testing can be restarted. **Note:** If an in-tube check had already been completed and validated, refer to section 8.2.7.

4.12 No further testing procedure

1. If testing is no longer required, QPS will tick on the "No Testing Required" box on the exhibit record page. This will auto generate an exhibit result line "No further work required as per advice from QPS" and will highlight red in the exhibit analytical/testing table (see Figure 34). **Note:** The no testing required box is only visible when ticked.
2. Locate the CSSE from the storage boxes within Evidence Recovery and return the tube to the CSSE, seal with evidence tape, sign and date.

Exhibit Anaytical / Testing

Date / Time	Technique	Testing Summary -	P3	Employee	Reviewer
20/04/2022 10:08	In-tube check			[redacted]	
20/04/2022 10:19	In-tube check				
20/04/2022 10:24	Result	No further work required as per advice from QPS			

Figure 34 – No Further Work - Exhibit analytical/testing table

3. Create an exhibit movement as per section 4.3 and transfer and place the CSSE in the exhibit room returns box [redacted].
4. Click on the date/time hyperlink of the result line and validate.

Note: If a sample has not undergone any testing (i.e. exhibit analytical/testing table is blank), then a notation stating that testing is no longer required must be entered in order to

remove it from the Received Worklist. The no further work result line will also need to be added manually.

4.13 Correcting errors in worklist selection

If the wrong technique and/or method are selected in the worklist table and the record has already been saved, check the exhibit analytical/testing table to establish whether the sample is already on a batch, if it is contact the Analytical Senior Scientist.

If the sample is not on a batch:

1. Navigate to the exhibit analytical/testing table and click create exhibit test icon.
2. In the "Process" field select "Reallocate" from the dropdown menu.
3. In the worklist table, select the correct technique and method.
4. Click on the save button.

5 Associated Documentation

QIS: 17117 – Procedure for Case Management
QIS: 22857 – Anti-Contamination Procedure
QIS: 23849 – Common Forensic DNA Analysis Terms and Acronyms
QIS: 23959 – Storage Guidelines for Forensic DNA Analysis
QIS: 30800 – Investigating Adverse Events in Forensic DNA Analysis
QIS: 33800 – Examination of Items
QIS: 34298 – Validation of Examinations

6 References

AS2243.1:2005 Safety in Laboratories Part 1 - General

Workplace Health and Safety Act 2011

Workplace Health and Safety Regulation 2011

Workplace Health and Safety Advisory Standards – various

Health, safety and wellbeing | HSQ staff site

7 Amendment History

QIS² Edition			
Version	**Date**	**Updated By**	**Amendments**
1	19/05/2016	A. Houlding	First issue.
2	09/06/2017	A. Ryan	Added storage, and photography Updated screenshots. Added request/task procedure. Added label printing. Amended on-hold procedure. Added section 4.3 tracking of individual samples. Amended no further testing procedure. Added subsample procedure for manual interventions requiring retention.
3	12/07/2017	A McNevin	Amended imaging procedure to reflect use of notation, added further information on CSSE labelling requirements and image quality and procedure for labelling discrepancies
4	15/12/2017	A McNevin	Addition of extra troubleshooting as Appendix 2, other minor changes to reflect current practice using FR
5	10/07/2019	C. Angus	Amended in-tube pick-up procedure, update of screenshots, update of Appendix 1 to include iPad photo procedure and Windows 10 updates. Addition of additional troubleshooting (10.2.2, 10.2.10), addition of Appendices 3 and 4.
6	18/03/2021	M Margetts	Complete review of SOP, updated procedure for uploading additional images. Adjustments made to some formatting.
7	22/04/2022	K Morton	Updated template, updated content/screenshots to reflect current procedures. Added procedure for completing request/tasks and added new standard wording.

8 Appendices

1 Appendix 1: Uploading Images
2 Appendix 2: Example Problem Scenarios
3 Appendix 3: Standardised Wording for Task Requests
4 Appendix 4: Correspondence Between QPS and Forensic DNA Analysis

8.1 Appendix 1: Uploading Images

8.1.1 Uploading images with a camera

1. Refer to individual camera manuals for specific functionality, manuals are stored in I:/Equipment/Equipment Manuals/Canon.

Note: Regularly check the camera date/time stamp so that the image meta data is reflective of contemporaneous record keeping. The camera date/time should closely match the PC date/time.

2. Capture the photo.
3. Plug the camera into the computer via a USB cable.
4. Right click on the camera shortcut on the desktop and select "Import pictures and videos" (see Figure 35).

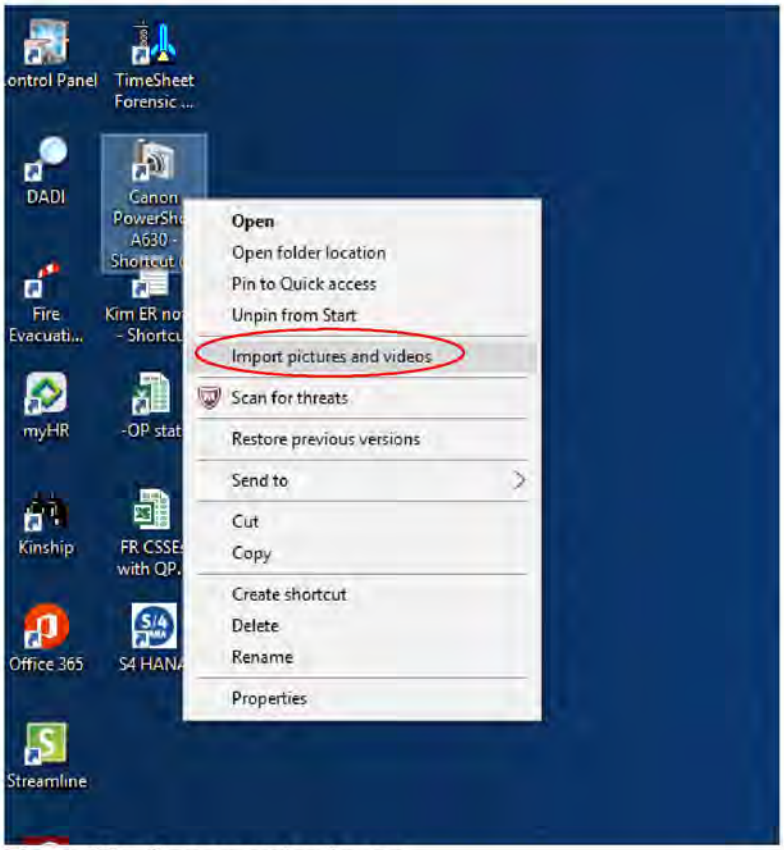


Figure 35 – Camera upload page

5. The import window will open, scan the item barcode into the tag field and click import (see Figure 36).

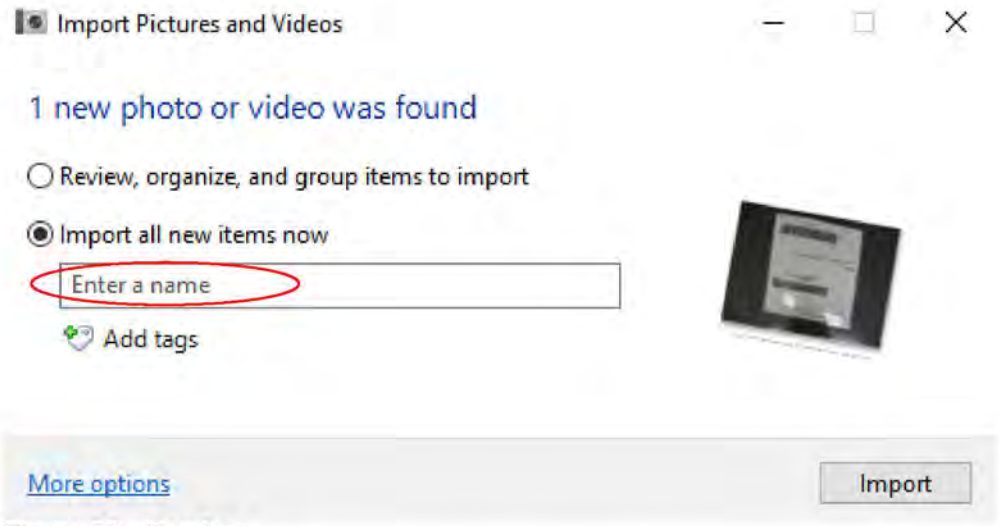


Figure 36 – Tag box

Note: The import settings should not need to be adjusted (see Figure 37). The image will upload to I:\FR Images into folders sorted by date. Additionally, "Open Windows Explorer after import" may not be applicable to all processes and can be unchecked if desired.

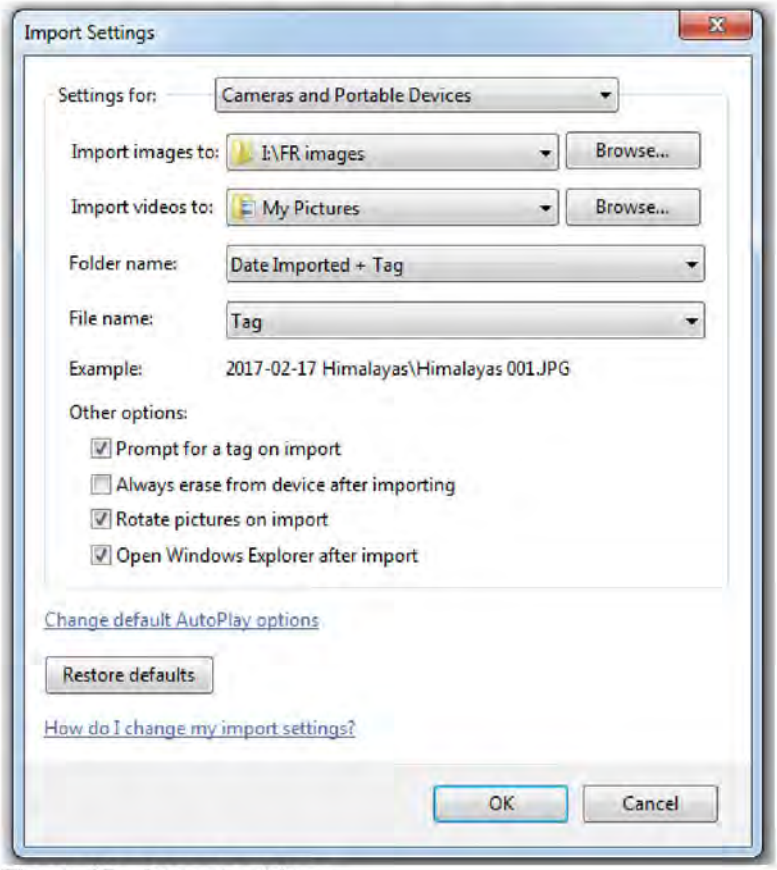


Figure 37 – Import settings

8.1.2 Uploading images using the iPad

1. Open the safari icon on the iPad homepage to login into the FR (see Figure 38).



Figure 38 – iPad main screen - safari

2. Follow the prompts and sign into the FR.
3. Click into the key identifier search icon and scan the barcode, click search.
4. In the Process drop down menu, select “Notation”.
5. Click on “Choose File” and then “Take Photo or Video”.
6. Once the photo has been taken, select “use photo” or “retake” if another is required.
7. Complete the notes field as required.
8. Click on the save button.

Note: Once you have finished using the iPad, it is important that you correctly sign out of FR.

8.2 Appendix 2: Example Problem Scenarios

8.2.1 No Testing Required ticked by QPS prior to sample submission

For these items, the entry of the "No further work …" result line is not automatic so needs to be entered manually prior to tracking to the returns box. A colleague will need to validate the result line.

8.2.2 No Testing Required ticked after validation of in-tube check

If Analytical testing has not yet begun on an in-tube (e.g. Sample has been pulled onto an extraction batch but not processed), the Clinical Assistants will track the sample to an ERT-AS box and deliver it back to the Evidence Recovery hatch or exhibit room shelf. The Technical Officers will find the corresponding CSSE, reseal the in-tube and track it to the returns box in the Exhibit Room ([redacted]).

If the in-tube has been processed for semen testing but is now no longer required, it must be transferred to the no further work box located in the Extracting Sorting freezer ([redacted]).

8.2.3 QPS image is of a completely different CSSE

A photo must be taken of the CSSE that was received, the sample can then be processed as normal (as long as there are no further problems such as a labelling discrepancy). The Technical or Scientific Officer must inform the Evidence Recovery Senior Scientist who will organise to have the issue corrected.

8.2.4 Partial QP on the CSSE

Although the QP number is not a required identifier on a CSSE, if the QP number is present, then it needs to be correct. A request/task must be sent as per section 4.9.1.

8.2.5 Multiple CSSE's attached together

If two or more CSSE's are received stapled or otherwise attached together, this must be noted in each in-tube check. Additional images may also be required.

8.2.6 Substrate within in-tube is different to category in FR

If an in-tube contained a swab, however the FR category field states "Trace DNA Kit" and the Description states "Swab of …" the exhibit will need to be placed on-hold (section 4.10) and a request/task must be sent (section 4.9.1).

8.2.7 In-tube placed on hold after In-tube check performed, tube returned to CSSE

If an in-tube check has been performed and the in-tube has then been returned to the CSSE and placed on-hold, a notation stating that the tube has been returned to the CSSE must be added. Refer to section 4.9.1 for request/task creation and section 4.10 for the on-hold process.

Refer to section 4.9.2 to complete a request/task and section 4.11 to restart testing. **Note:** Another in-tube check is not required. Transfer the CSSE to the Evidence Recovery laboratory, remove the in-tube from the CSSE, sign and date the opening. Track the tube to an ERT-AS box, add the relevant extraction type and manually add the submitted result pending result line (SRP). Another colleague must validate the SRP result line.

8.2.8 No Testing Required previously checked and subsequently un-checked

If the "No testing required" check box is unchecked, the "No Testing …" result line highlighted colour will change to a neutral colour. Check the date / time stamp of the "No

Testing …" result line, this will likely be some days prior, indicating that the previously unrequired exhibit now requires testing.

8.2.9 Testing re-started on returned in-tubes

1. If a CSSE is still located within Forensic DNA Analysis, testing can be restarted as per section 4.11. If an in-tube check had already been completed testing can restart as per section 8.2.7.

2. If the exhibit is not located within Forensic DNA Analysis (with FPP or QPS); the exhibit requires an in-tube check to be completed as it has left the custody of Forensic DNA Analysis. Note: A new in-tube check is required even if one had already been completed.

3. If the exhibit has a validated SRP (submitted results pending) result line prior to the validation of the NWQPS (No further work required as per advice from QPS) result line, then when the exhibit is restarted a TRQ (Testing restarted on advice from QPS) result line must added and validated.

8.3 Appendix 3: Standardised Wording for Task Requests

8.3.1 Discrepancy for exhibit record description (Item placed on-hold):

Date/Initials – Hello,
Regarding exhibit barcode XXXXXXXXX, the Exhibit Record Description in the Forensic Register states "A B C", however the Crime Scene Envelope states "X Y Z". Please confirm the correct description for this exhibit and adjust any Forensic Register records as necessary, or alternatively the item can be returned for your correction. This item has been placed on hold pending advice.
regards
Your NAME

8.3.2 Discrepancy for location/owner field (Item NOT placed on-hold):

Date/Initials – Hello,
Regarding exhibit barcode XXXXXXXXX, the Exhibit Record Location / Owner field in the Forensic Register states "A B C", however the Crime Scene Envelope states "X Y Z". Please confirm the correct description for this exhibit and adjust any Forensic Register records as necessary.
regards
Your NAME

8.3.3 Discrepancy for exam source field (Item NOT placed on-hold):

Date/Initials – Hello,
Regarding exhibit barcode XXXXXXXXX, the Exhibit Record Exam Source field in the Forensic Register states "A B C", however the Crime Scene Envelope states "X Y Z". Please confirm the correct description for this exhibit and adjust any Forensic Register records as necessary.
regards
Your NAME

8.3.4 FR number discrepancy (Item placed on-hold):

Date/Initials – Hello,
Regarding exhibit barcode XXXXXXXXX, the exhibit is registered in the Forensic Register under FR number "1 2 3", however the Crime Scene Envelope states "3 2 1". Please confirm the correct FR number for this exhibit and adjust any Forensic Register records as necessary, or alternatively the item can be returned for your correction. This item has been placed on hold pending advice.
regards
Your NAME

8.3.5 No FR number on CSSE (Item placed on-hold):

Date/Initials – Hello,
Regarding exhibit barcode XXXXXXXXX, the exhibit is registered in the Forensic Register under FR number "1 2 3", however the Crime Scene Envelope has no FR number present. Please confirm the correct FR number for this exhibit and adjust any Forensic Register records as necessary, or alternatively the item can be returned for your correction. This item has been placed on hold pending advice.
regards
Your NAME

8.3.6 Discrepancy for collection description (Item NOT placed on-hold):

Date/Initials – Hello,
Regarding exhibit barcode XXXXXXXXX, the Exhibit Record Description in the Forensic Register states "A B C", however the Crime Scene Envelope states "X Y Z". Please confirm the correct description for this exhibit and adjust any Forensic Register records as necessary.

regards
Your NAME

8.3.7 Discrepancy in forensic category (Item placed on-hold):

Date/Initials – Hello,
Regarding exhibit barcode XXXXXXXXX, the Exhibit Record Forensic Category in the Forensic Register states "A B C", however the exhibit received with the Crime Scene Envelope is a "X Y Z". Please confirm the correct exhibit type and adjust any Forensic Register records as necessary, or alternatively the item can be returned for your correction. The item has been placed on hold pending advice.
regards
Your NAME

8.3.8 Sample requires additional analysis confirmation (Item placed on-hold):

Date/Initials – Hello,
Regarding exhibit barcode XXXXXXXXX, this item has been ticked as "Sample requires additional analysis (lubricant, fibre, glass, soil etc.)" with no additional information provided as to what form of additional analysis is required. Please advise the nature of the additional analysis required, or alternatively, if none is required, please uncheck. The item has been placed on hold pending advice.
regards
Your NAME

8.3.9 Sample requires semen or saliva testing confirmation (Item placed on-hold):

Date/Initials – Hello,
Regarding exhibit barcode XXXXXXXXX. Due to the nature of this case could you please confirm whether semen or saliva testing is required. This item has been placed on hold pending advice.
regards
Your NAME

8.4 Appendix 4: Correspondence Between QPS and Forensic DNA Analysis

8.4.1 Semen Testing

If Technical/Scientific Officers have considered that semen testing may be required due to the details available for the case, a request/task needs to be sent to the Officer for clarification as per section 4.9.1. If there is no response within a reasonable time (agreed time of at least one week) the Evidence Recovery Senior Scientist (or in their absence, the Evidence Recovery & Quality Team Leader) must be notified via email with the exhibit barcode/s details. An email will be sent to the Inspector for follow up and a case file notation will be added to show that it has been actioned.

8.4.2 Labelling Discrepancies

In the first instance, seek clarification from the Forensic Officer. If this does not resolve the issue, or if it is not followed up within a reasonable time (agreed time of at least one week) the Evidence Recovery Senior Scientist (or in their absence, the Evidence Recovery & Quality Team Leader) must be notified via email with the exhibit barcode/s details. An email will be sent to the Inspector for follow up and a case file notation will be added to show that it has been actioned.

CA-71

Queensland Health
Forensic and Scientific Services

Forensic Register FTA Processing

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1 Purpose and scope

To describe the processing of FTA™ papers from reference buccal and blood samples to yield a DNA profile. The methods outlined below are applicable to all FTA Reference and Evidence samples that require Forensic DNA Analysis processing. This document applies to all Forensic DNA Analysis staff that process FTA samples.

2 Definitions

FTA	Flinders Technology Associates - paper used to store DNA
PCR	Polymerase chain reaction
DNA	Deoxyribonucleic acid
EDTA	Ethlyenediaminetetraacetate
SDS	sodium dodecyl sulphate
dNTP	Deoxyribonuceotide triphospate
BSD	Semi-Automated dried sample puncher
FRIT	Forensic Reporting and Intelligence Team
SSLU	Scientific Sciences Liaison Unit
QPS	Queensland Police Service
BSC	Biological safety cabinet

3 Principle

DNA Technology

FTA paper is a reagent impregnated paper for DNA-Storage that gives a positive kill of common blood-borne pathogens and DNAses and provides a long-term, broad-spectrum protection from saprophyte growth, particularly moulds, during storage in laboratory cabinets at ambient temperature and humidity (Whatman 2005; Whatman 2009). The protective reagents were specifically selected to have well known properties and to all be safe for human handling. They are mildly alkaline with uric acid/urate, sodium dodecyl sulphate (SDS), EDTA, and TRIS.

DNA source

The most common cell collection protocol used for DNA extraction are cells collected from inside the cheek which contain exfoliated buccal epithelial cells and other cells found in saliva. Human blood is a mixture of red blood cells, white blood cells and plasma. Only white blood cells and immature red blood cells contain DNA.

Collection of Material

Buccal FTA samples are collected using the foam rubber swabs supplied in collection kits. Gently rubbing of the internal cheek collects buccal cells on the foam swab. The swab is then applied to the FTA card and cells are transferred. Blood or post-mortem blood samples are applied directly to the FTA card and allowed to dry.

Queensland Police Service QPRIME

FTA samples that are taken by the QPS are registered in QPRIME. QPRIME sends the registration to Forensic Register. Once the sample is received at QHFSS Property Point the Forensic Register will allocate the sample to the Direct STR Amp FTA work list.

BSD600 Ascent A2

The BSD600 Ascent A2 (BSD Robotics, Australia) is a semi-automated dried sample punch instrument. The instrument in Forensic DNA Analysis is fitted with two punching dies; 1.2mm and 3.2mm. The 1.2mm punch is the standard punch size for direct amplification

FTA sample processing. The 3.2mm punch size is used for very low, very high concentration or inhibited FTA samples that require extraction.

Polymerase Chain Reaction
Polymerase chain reaction (PCR) is a method of selectively amplifying a particular region or regions of DNA. PCR utilises Bacterial DNA polymerase enzymes, region specific primers and dNTP's to replicate DNA.

4 Reagents and equipment

4.1 Reagents

1. 5% v/v Trigene-Advance solution.
2. 0.5% w/v Bleach solution
3. 100% v/v and 70% v/v Ethanol
4. Hamilton pierceable foil seals
5. PowerPlex® 21 System (Promega 2012):
   - Master Mix - PowerPlex® 21 5X Master Mix
   - Primer Mix - PowerPlex® 21 5X Primer Pair Mix
   - Liquid Positive Control - 2800M Control DNA, 10ng/µl
   - Water, Amplification Grade
   - PowerPlex® 21 Allelic Ladder Mix
   - WEN Internal Lane Standard 500

4.2 Equipment

1. BSD600 Ascent A2
2. Hamilton Plate Sealer
3. Labogene Scanspeed Centrifuge
4. Euroclone Safemate ECO ABC 1.2 Class II BSC

5 Safety

Personal Protective Equipment (PPE) including laboratory coats, masks, caps, gloves and safety goggles (where appropriate) must be worn by all staff when performing analytical procedures. Ensure instrument is turned off prior to cleaning.
To avoid possible injury from moving parts, ensure the BSD instrument is turned off prior to cleaning.

6 Procedure

6.1 Delivery of FTA samples

QPS deliver reference samples to the Forensic Property Point and FSS Property Point staff then deliver the samples to Forensic DNA Analysis. The samples are electronically stored to boxes which are stored on shelves in the Exhibit Room ([redacted]).

Blood FTA cards are stored to a separate box located in the Exhibit Room. At the present time, all blood FTA cards are sampled by the Evidence Recovery team.

6.2 Locating FTA cards for processing

6.2.1 Locating FTA Cards for rework batches

1. Click on the Worklist tab and select Direct STR Amp FTA

2. The list can be filtered for the batch type.
   Click on the appropriate filter: OSD 3500xl, RPT 3500xl or RUN 3500xl

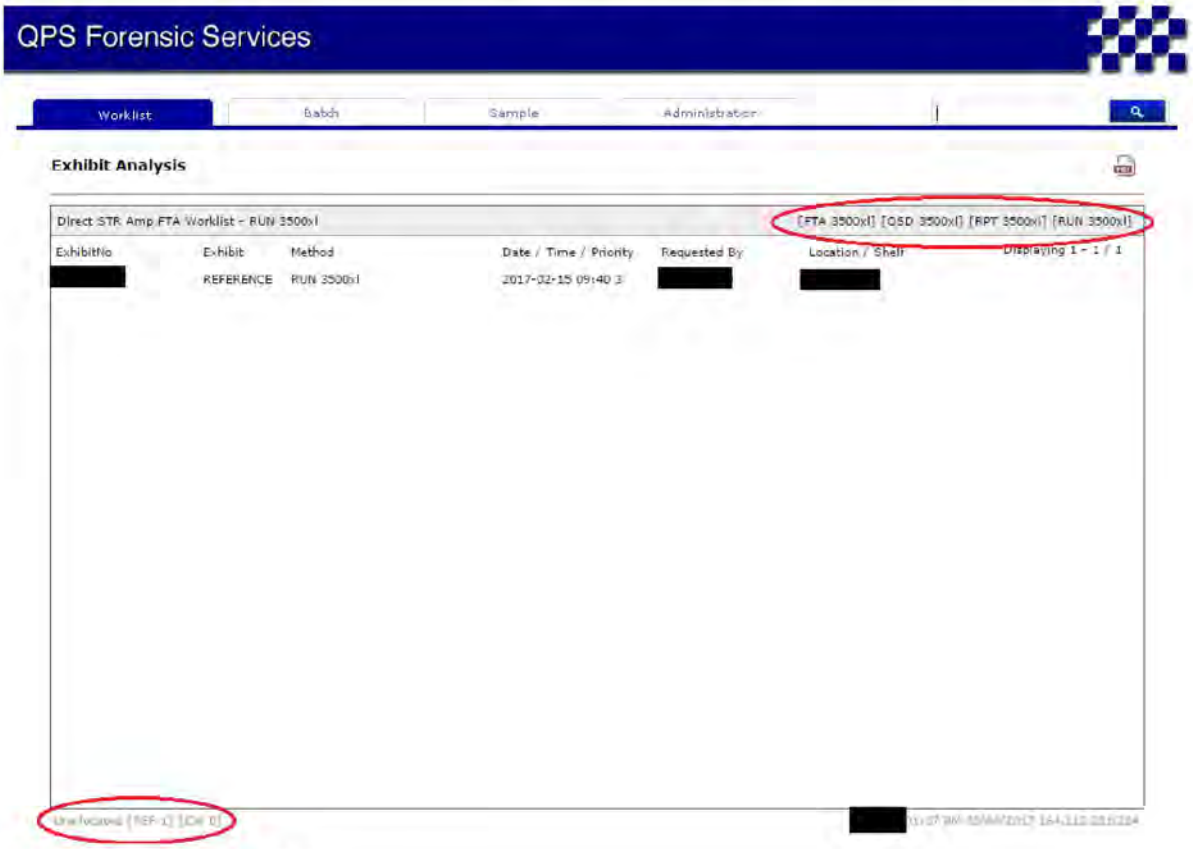


Figure 1 Worklist and Filters

3. The number of samples that have not been allocated to a batch (outstanding samples) is displayed at the bottom of the page.
4. From the filtered list; click on the PDF icon to generate a storage list which can be printed.
5. The storage list includes the storage location as well as the previous Direct STR Amp FTA batch ID.

Worklist	Method	Printed
Direct STR Amp FTA Worklist	RUN 3500xl	[redacted]

Barcode	Previous Batch	Storage Box / Position	Description	Storage Box Location
[redacted]	[redacted]	[redacted]	Non-grided Tube (unlimited positions)	[redacted]

[redacted] PSD 01:15 PM 03/04/2017 164.112.251.224

Figure 2 Storage location sheet

6. Print the list and locate required samples.
7. Move exhibit storage to FTA transfer boxes. (refer to section 6.8.1).

6.2.2 Instructions for Using DADI Program to Locate Samples

1. Log in to **DADI** using your Novell log-in. If you do not have a DADI login, consult the Quality Team for assistance
2. Go to **Tools - Results Management**
3. In **Search Sample** -Type in connected barcode or lab no/old DNA Number.
4. Click **Search** by double clicking the lab no.
5. Note down the RUN ID e.g. FTA# 44 and log out of DADI.

6.3 Reference samples other than buccal FTA cards

Reference samples which are not FTA cards (e.g. hair, blood, FTA blood card) will be sampled by the Evidence Recovery Team and submitted for extraction.

If a sample is received is a hair sample, please notify the quality team so they can change the sample type in the Forensic Register.

1. **Add a Notation as per section 9.1.1**
   Add details such as "Reference swab received", "Reference hair received" or "Reference blood received".
2. Save the record.
3. **If the sample is a swab or hair continue to section 9.1.3.**
4. **If the specimen is a blood FTA card proceed to section 9.1.4.**

5. Transfer the swab/hair/FTA blood card sample to the box labelled Evid Sample – Manual (FR rack ID [redacted]) located on a shelf in the Exhibit room.

6. Transfer the ESMP box to location corresponding to that day's shelf.

6.4 Preparing FTA cards for punching on the BSD.

The following steps can be performed in rooms [redacted] (Exhibit Room) or in room [redacted].

1. Open the FTA cards using a letter opener.

2. Stamp and sign the envelopes with the date and user's initials, or print off "FTA Opened By " stickers using the Zebra Designer software and affix to the back of the FTA envelope. FTA cards should be opened just before processing.

Note: Rework samples will have been previously opened and possibly re-sealed. These cards should be as per steps 1 and 2 listed above.

3. Retrieve the FTA Transfer box from the pass-through hatch in Extraction sorting and wipe down the outside of the FTA transfer box/es with 0.5% w/v bleach solution and 70% ethanol solution.

4. In the Forensic Register move the storage location of the FTA Transfer Box from the Exhibit Room to the FTA Processing Bench in room [redacted].

6.5 FTA samples with missing/discrepant barcodes

When the envelope has been opened and the card is found to be missing a barcode or the barcode does not match the envelope; then refer to section 9.1.1.
Move the sample storage to the FTA problem box located in the Exhibit Room.

6.6 BSD Daily Maintenance

Refer to QIS 35692 BSD600 Ascent A2 Operator Manual for the BSD operating instructions.

6.7 Direct Amplification FTA Processing

1. Turn on the biological safety cabinet. Clean BSC surfaces with 70% ethanol.

2. In the BSC; hand label a new PCR plate using a permanent marker with the batch type (e.g. FTA, RPT, RUN, OSD) on the front skirt (longer side) of plate.

   Leave enough room to affix the batch ID label once the batch has been created in the Forensic Register.

3. Add 7.5uL of Amplification Grade Water to each well that will contain either a sample or control. (The wells that will contain ladders do not require Amplification Grade Water.)

4. Use a new blank FTA card for cleaning punches. For small batches, the blank FTA cards used for blanks can be cut in half using scissors that have been cleaned with

bleach and ethanol first.

5. Operator tasks during punching:
   The first operator is to remove the FTA card from envelope, check barcodes match on the envelope and the sample and pass the card to the second operator. After the sample has been punched the operator ensures the correct card has been stored to the FTA envelope.

   The second operator runs the BSD. They scan the barcode on the FTA paper, checking the BSD software to ensure that the barcode has scanned correctly (if not, delete the scanned barcode from the field and rescan barcode) and punch sample.

6. Refer to QIS 35692 BSD600 Ascent A2 Operator Manual for the BSD operating instructions.

7. When the punch run is complete, place the plate into the biohazard cabinet adjacent to the BSD to add the Amplification mix.

8. Proceed to section 6.6.3.

6.7.1 Creating Direct Amplification FTA batches in Forensic Register

After punching samples using the BSD, the batch can now be created using the BSD output file.

1. Open Forensic Register and type SM into the search field. This will load the sample management page.

2. Navigate to the Direct STR Amp FTA batch type.

3. Click on the Add Record button 

4. Enter details for Batch Template, Technique, Method and Type as per Table 1.

Table 1 Batch creation details for FTA Direct Amplification

Batch type	Batch Template	Technique	Method	Type
PP21 FTA	FTAAMP_FTA 3500xl	Direct STR Amp FTA	FTA 3500xl	RF
PP21 OSD	FTAAMP_FTA 3500xl	Direct STR Amp FTA	OSD 3500xl	RF
PP21 RPT	FTAAMP_FTA 3500xl	Direct STR Amp FTA	RPT 3500xl	RF
PP21 RUN	FTAAMP_FTA 3500xl	Direct STR Amp FTA	RUN 3500xl	RF

5. Select Batch/Rack/File for Sample Source type.

6. Click on Choose File button to select BSD file to be imported.

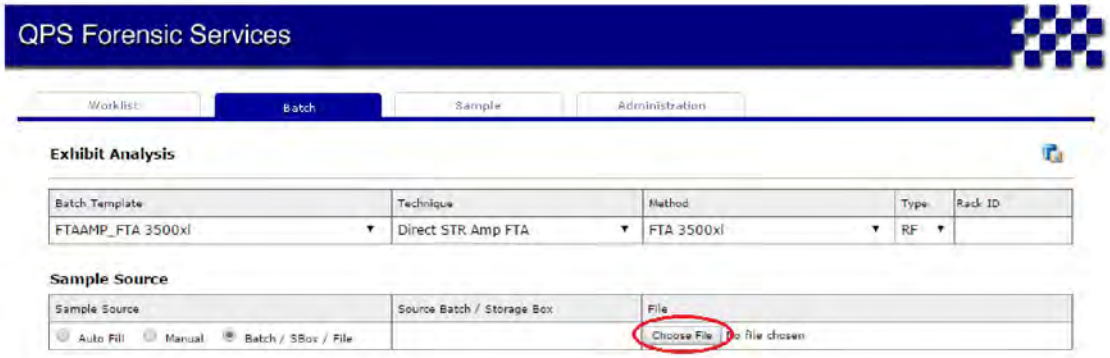


Figure 3 FTA batch creation from BSD file

7. Navigate to I:/BSD/Plate maps/ and select file that the batch is to be created from and then click on Open.

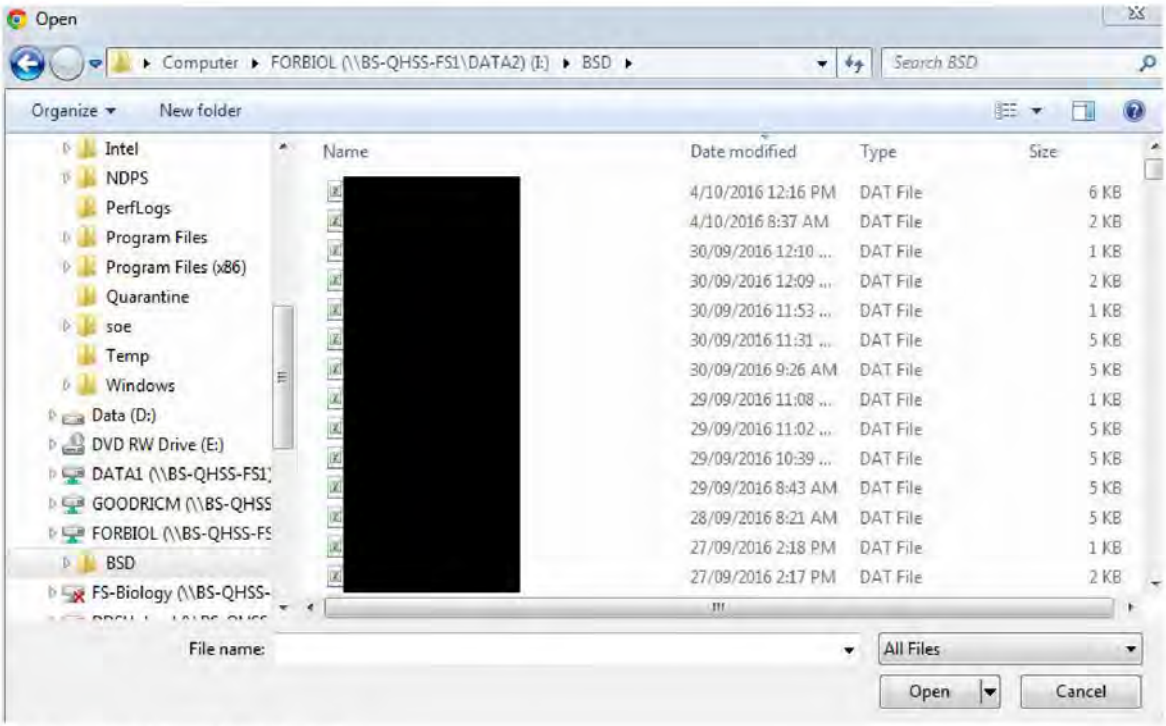


Figure 4 Navigate to BSD file location

8. Click on save record icon.

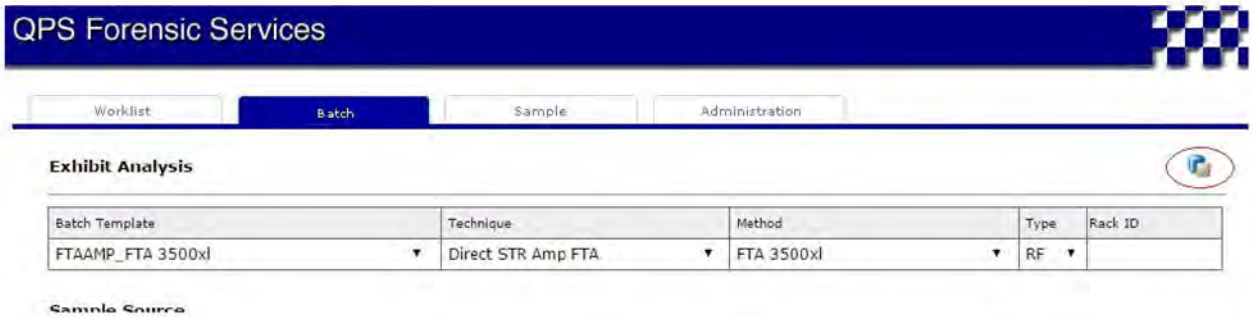


Figure 5 Create Batch

When batch is created, the batch details screen looks like

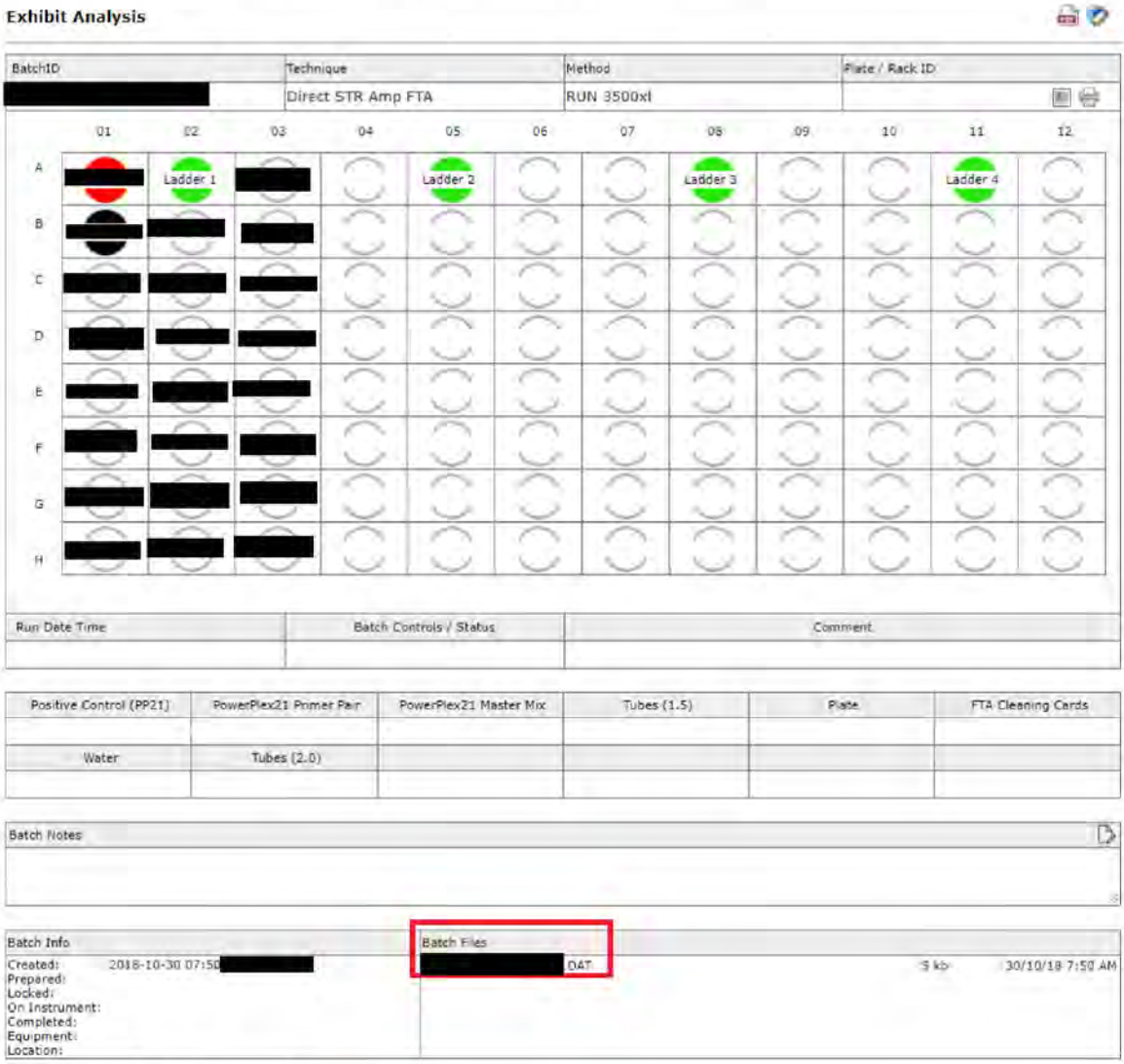


Figure 6 Batch details screen

9. Save the record .

10. Check that the BSD instrument file is listed in the Batch Files section and ensure the samples from the BSD output file (as shown in Figure 6) match those in the Forensic Register.

    To do this, double click on the file from the Batch Files to open.

    If the Forensic Register samples do not match the BSD instrument file (.dat), it could mean that the incorrect file was used to create the batch. Refer to section 9.1.5. to mark the batch as Not Required. Then recreate the batch with correct BSD output file as per Section 6.6.1.

6.7.2 Samples not recognised by the Forensic Register

1. If any of the sample wells are highlighted as this means that the barcode is not recognised/registered in the Forensic Register.
2. Delete the barcode from the batch.
3. Enter a batch note detailing which sample was removed from the batch such as "Sample XXXXXXXXX removed from position XY – sample not registered in FR".
4. Move the sample to the FTA Investigation Box and inform the Laboratory Assistant Supervisor/Quality Team.

6.7.3 Preparation of Amplifcation Mix for PowerPlex® 21 Plates

To be performed in the clean reagent room biohazard cabinet (Room 3188). **Amplification Mix is only to be made after the plate has been punched by the BSD.**

1. Clean pipettes, racks, tip containers with 0.5% v/v bleach solution followed by 70% v/v ethanol.
   Clean work bench and biohazard cabinet stainless steel surfaces 70% v/v ethanol.
2. Remove required amount of PowerPlex ® 21 5X Master Mix and PowerPlex® 21 5X Primer Pair Mix from the freezer and thaw.

   Note: Master Mix and Primer Pair Mix vials may be kept in the refrigerator for subsequent use for up to and not exceeding five days. Any remaining reagent in the refrigerator must be returned to the freezer by the Friday of that week.

   Centrifuge tubes briefly then vortex each reagent for 15 seconds before use.
3. Use FTA Mastermix calculator (QIS 32930) to calculate reagent volumes and to record lot numbers of the reagents used.
   This is located in I:\AAA Operational Staff\FTA MasterMix
4. Vortex the Amplification Mix thoroughly for 5-10 seconds at half speed, taking care to minimise splashing under the lid.
   Label the tube with the batch ID and put into the pass through hatch between rooms 3188 and 3189.

   Note: Each Batch is to have an individual tube of PowerPlex® 21 Amplification Mix.

6.7.4 Finalising FTA plate and Forensic Register batch

1. Clean all work areas with 0.5% v/v bleach solution followed by 70% v/v ethanol. The BSD machine is to be cleaned with 100% ethanol inside and outside. Refer to Section 6.
2. Dispense 5µL of prepared Amplification Mix into each well containing sample. Make sure to add Amplification Mix to the Positive and Negative control wells (A1 and B1). Please note, the control wells will not contain FTA™ spots.

3. Add 1uL of 2800M Control DNA (10ng/µL) to the positive control well (A1).
4. Seal the plate with the Hamilton plate sealer or by hand. Take care to seal plate well as evaporation can occur during the amplification cycles.
5. Hand label the back of the plate with the batch type (FTA, OSD, RUN or RPT).
6. From the batch screen in the Forensic Register
7. Edit the record , enter in reagent/equipment details (Operators, PP21 reagents, PCR plate, FTA cleaning card, BSD etc),

Run Date	Run Time	Batch Controls / Status	Comment
		PASS FAIL INV N/R CEQ	

Positive Control (PP21)	PowerPlex21 Primer Pair	PowerPlex21 Master Mix	Tubes (1.5)	Plate	FTA Cleaning Cards
Water	Tubes (2.0)				

Batch Notes

Location	EquipmentID	EquipmentID	EquipmentID	Batch File
				Choose File No file chosen

Figure 7 Add consumables and reagents

8. Enter initials of both operators into batch notes.

   If there are any comments to record for the batch, enter "See batch" in the comment field, then enter the details in the batch notes table.

   When entering batch notes, enter operator initials followed by the date and then the notes. (e.g. XYZ 01/01/2017 – notes)

Run Date Time	Batch Controls / Status	Comment
01/06/2016 14:25		see batch

Positive Control	PowerPlex21 Primer Pair	PowerPlex21 Master Mix	Tubes	Plate	FTA Cleaning Cards
	t	t			t
Water					

Batch Notes
Repunch of samples from batch [redacted]

Figure 8 Add batch comment

9. Check that the Forensic Register Batch matches the samples from the BSD instrument file. To do this, double click on the file from the Batch Files to open.

   If the Forensic Register samples do not match the BSD instrument file (.dat), it could mean that the incorrect file was used to create the batch. Refer to section 9.1.5.

10. Print batch labels. One label is to be attached to the PCR plate (Batch ID on front of plate, Barcode on the end of the plate) and one label to be attached to the FTA card storage ID.

11. Lock the batch

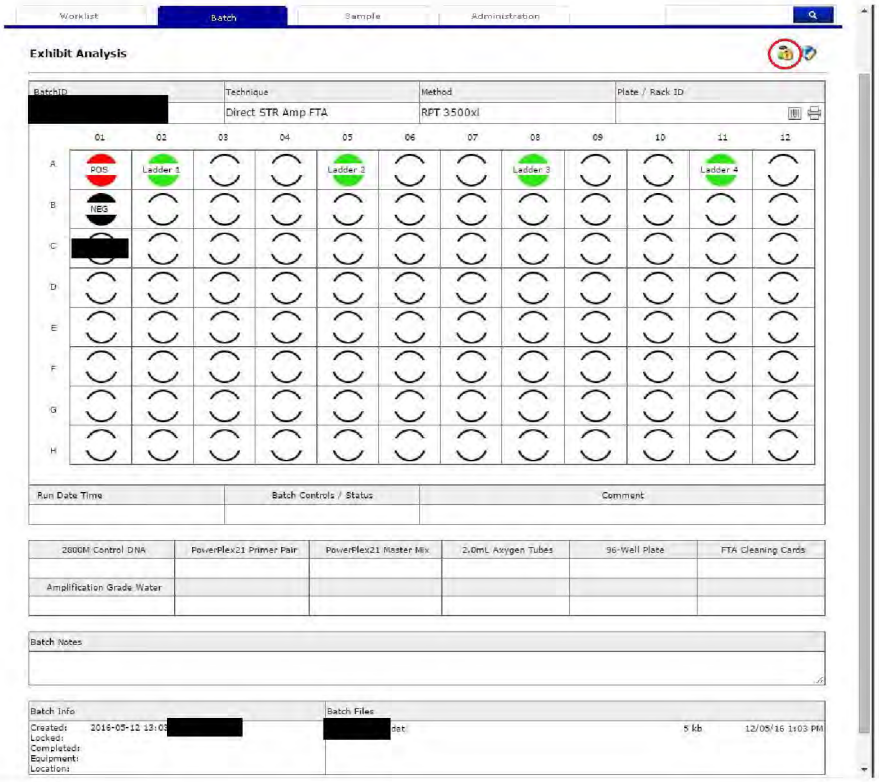


Figure 9 Lock batch

12. Then click on the Complete Sequence Check (check box) then save  .

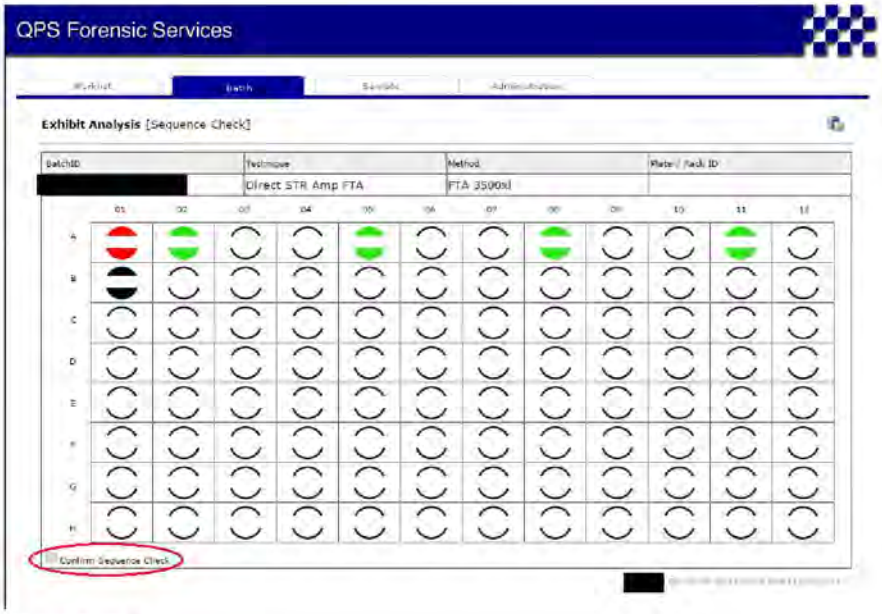


Figure 10 Sequence check batch

13. Pulse spin the FTA plate, place in pass through hatch to CE and notify CE staff.

14. Store FTA cards as per section 6.8

6.8 Processing of FTA for extraction

Sections 6.7.1 and 6.7.2 are to be performed in room 6106B (Exhibit Room)

6.8.1 Locating FTA Cards for Extraction

1. Proceed to the DNA Extraction worklist

   The list can be filtered by clicking one of the batch types at the top of the table.

2. Click on [BSD Prep].

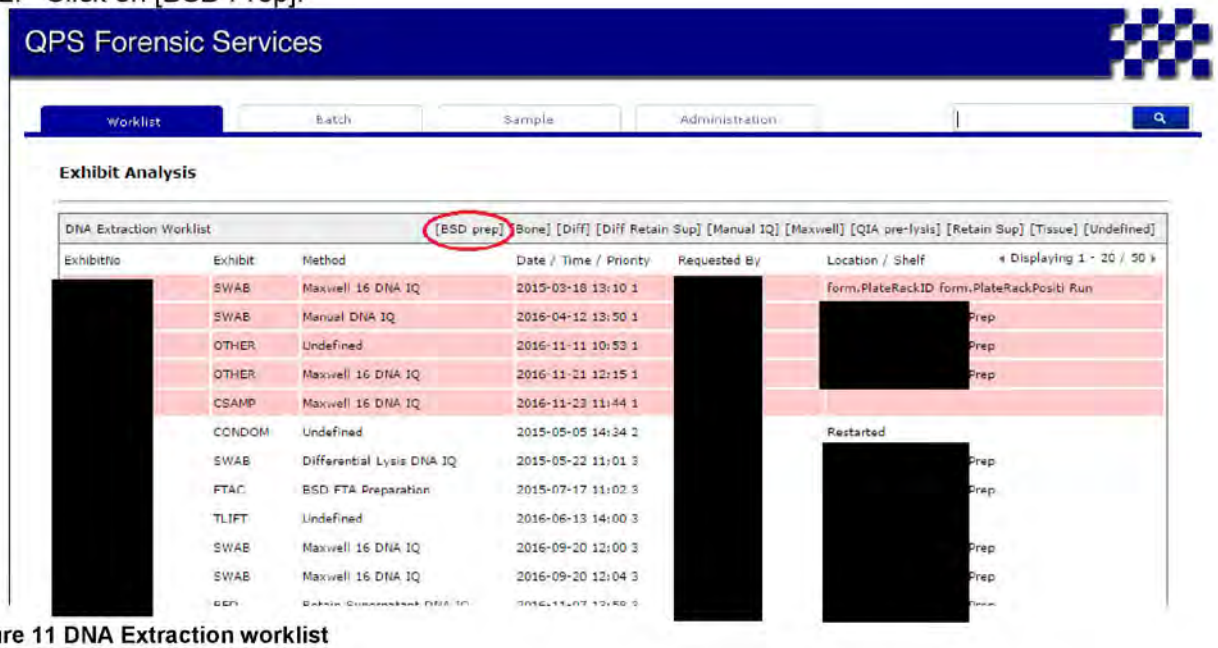


Figure 11 DNA Extraction worklist

3. Click on the PDF button to display the storage locations for the BSD Prep worklist.

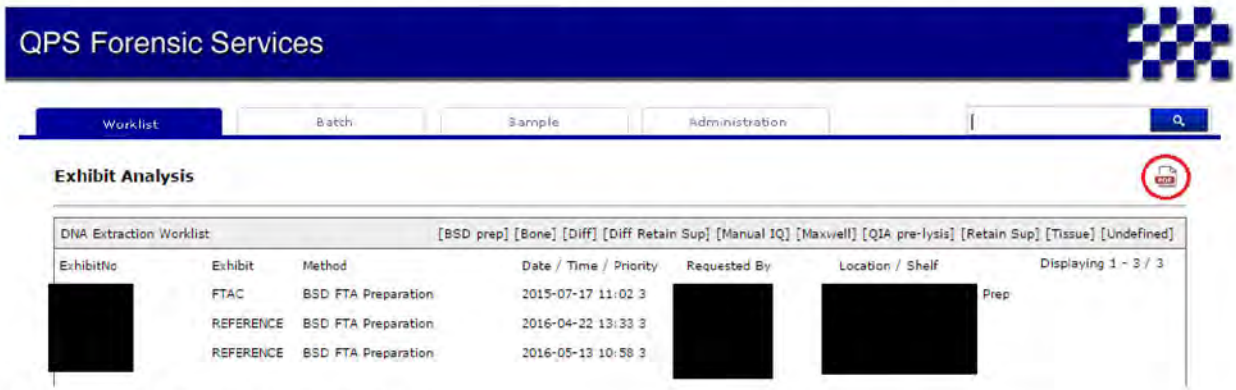


Figure 12 Filtered BSD Prep extraction worklist

Storage sheet will appear similar to

Worklist	Method	Printed
DNA Extraction Worklist	BSD FTA Preparation	06-10-2017 [redacted]

Barcode	Parent	Previous Batch	Storage Box	Description	Storage Box Location
[redacted]	[redacted]		[redacted]	FTA Box 711	
		[redacted]	[redacted]	FTA Box 715	[redacted]
		[redacted]	[redacted]	FTA Box 716	[redacted]
		[redacted]	[redacted]	FTA Box 715	[redacted]
			[redacted]	FTA Box 722	

Figure 13 Sample storage sheet

4. The Parent ID is the barcode that the FTA card was submitted with.
   The Barcode (left hand column) is the Subsample ID that was created for processing and storage by the Forensic Register.

5. After locating the card, the envelope will need to be labelled with the subsample barcode (refer to section 6.8.2).

6.8.2 Label FTA envelope with SubID barcode

1. In the Exhibit Testing table, click on the Subsample (EREF) link (date/time).

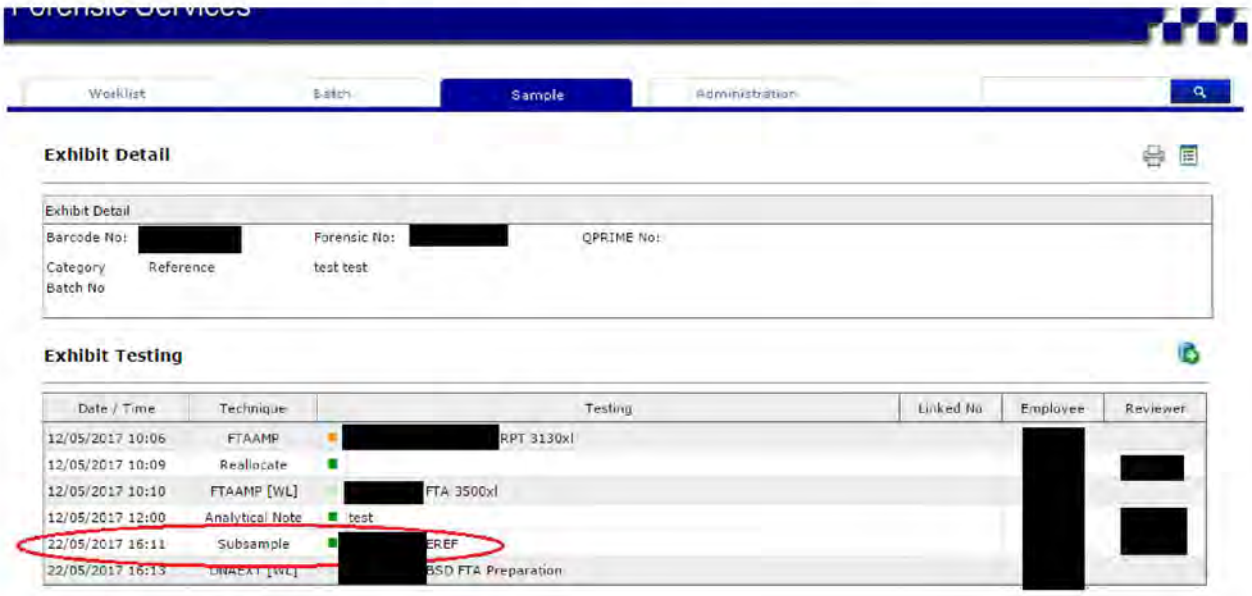


Figure 14 SubID hyperlink

This page shows information regarding the SubID which has been created.



Figure 15 SubID page

2. Click on the button to view and then print the SubID barcode.

The SubID barcode also has the Exhibit number on the label. This can be used to check that the correct label has been attached to the FTA envelope.

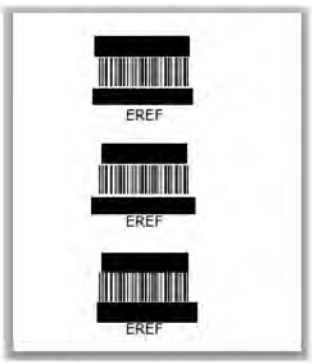


Figure 16 SubID sample label

3. Print the 3-part label (either by clicking on the blue printer icon or by pressing Ctrl+P).



Figure 17 Label print icons

4. Attach the label to the FTA envelope and date and sign.
   Second operator to check the correct SubID label has been attached to the FTA envelope.

5. Move exhibit storage to FTA transfer boxes. (refer to section 6.8.1).

6.8.3 Punch FTA cards

Refer to QIS 35692 BSD600 Ascent A2 Operator Manual for the BSD operating instructions.

When punching BSD Extraction Preparation Batches, scan the EREF SubID barcode.

6.8.4 Create extraction batch in Forensic Register

1. From the Analytical page, click on the Batch tab, then select DNA Extraction from the drop-down list.

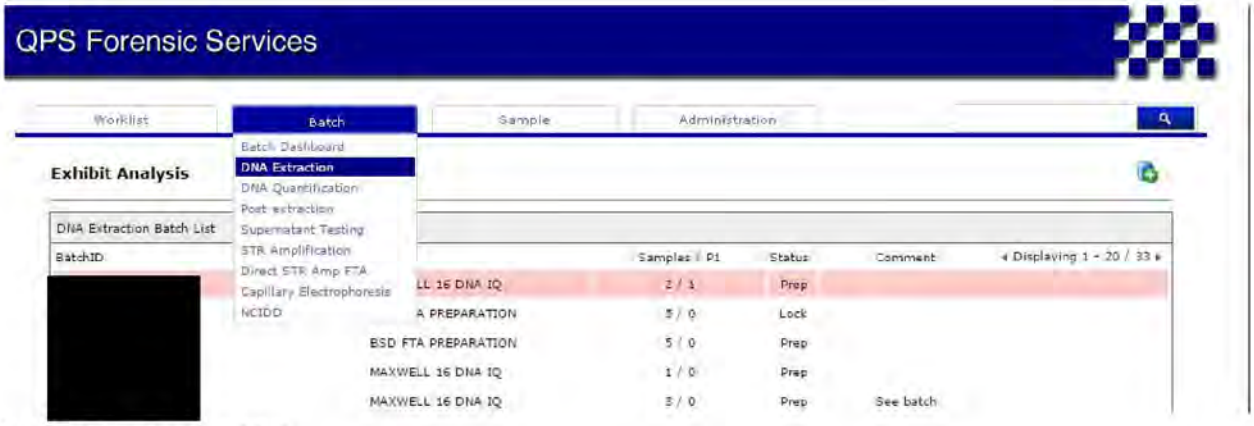


Figure 18 DNA Extraction worklist

2. Click on the Add record button 

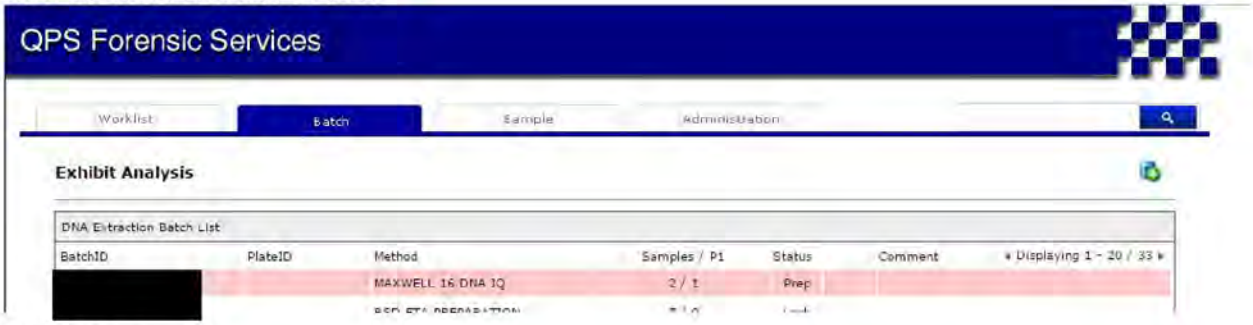


Figure 19 Add record

3. Complete the Exhibit Analysis table as below to select batch to be created.

Batch template: Select **DNAEXT_BSD FTA Preparation**

Technique: **DNA Extraction**

Method: **BSD FTA Preparation**

Type: **RF**

In the Sample Source table, select Batch/Rack/File. This tells the Forensic Register that the batch will be created from an external BSD file.

4. Click on the Choose File button.

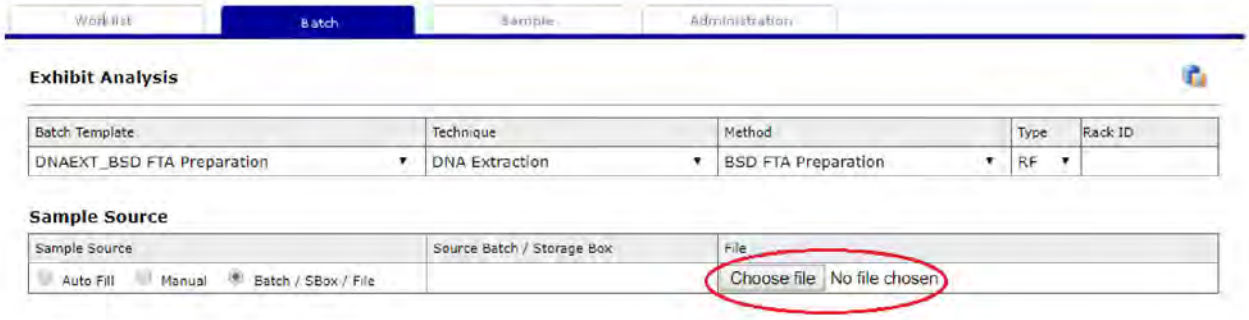


Figure 20 Choose file to create batch from

5. Navigate to I:/BSD/Logs and select file that the batch is to be created from and then click on Open.

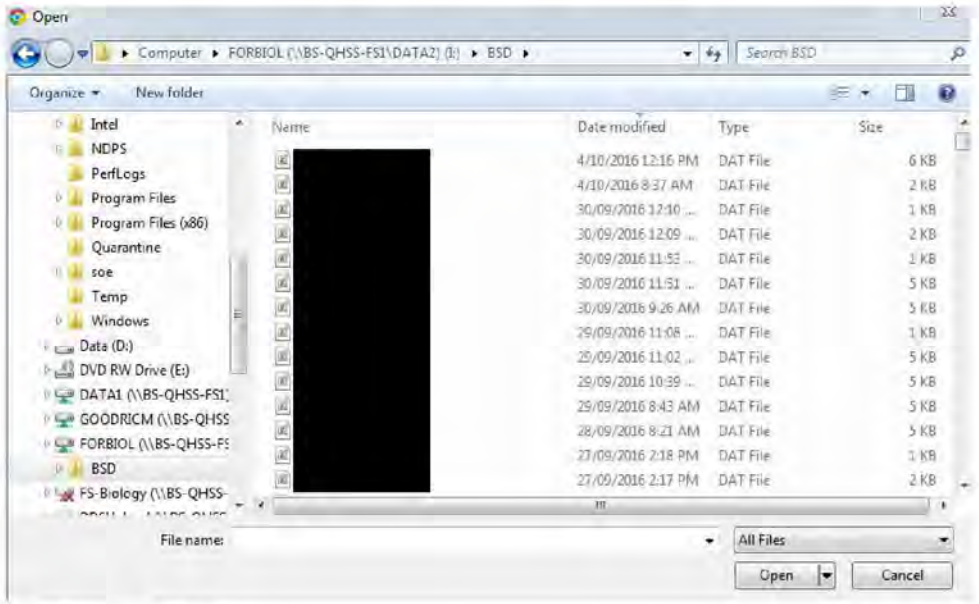


Figure 21 Locate BSD file

6. Click on the save record button  .

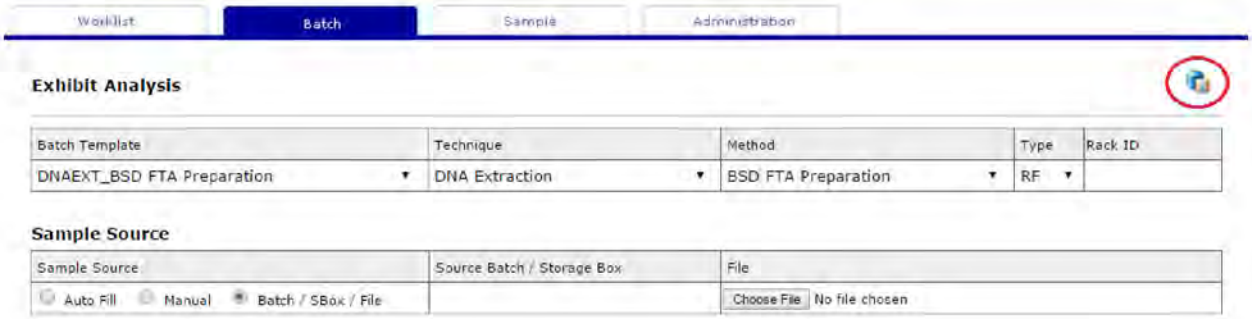


Figure 22 Save record

7. Then, from the batch details screen, click on the save record button .
8. Edit the record to enter in reagent/equipment details (2mLtubes, FTA cleaning card, BSD etc) and then save .
9. Check that the BSD instrument file is listed in the Batch Files section and ensure the samples from the BSD output file (as shown in Figure 23) match those in the Forensic Register.

   To do this, double click on the file from the Batch Files to open.

   If the Forensic Register samples do not match the BSD instrument file (.dat), it could mean that the incorrect file was used to create the batch. Refer to section 9.1.5. to mark the batch as Not Required. Then recreate the batch with correct BSD output file as per Section 6.7.4.

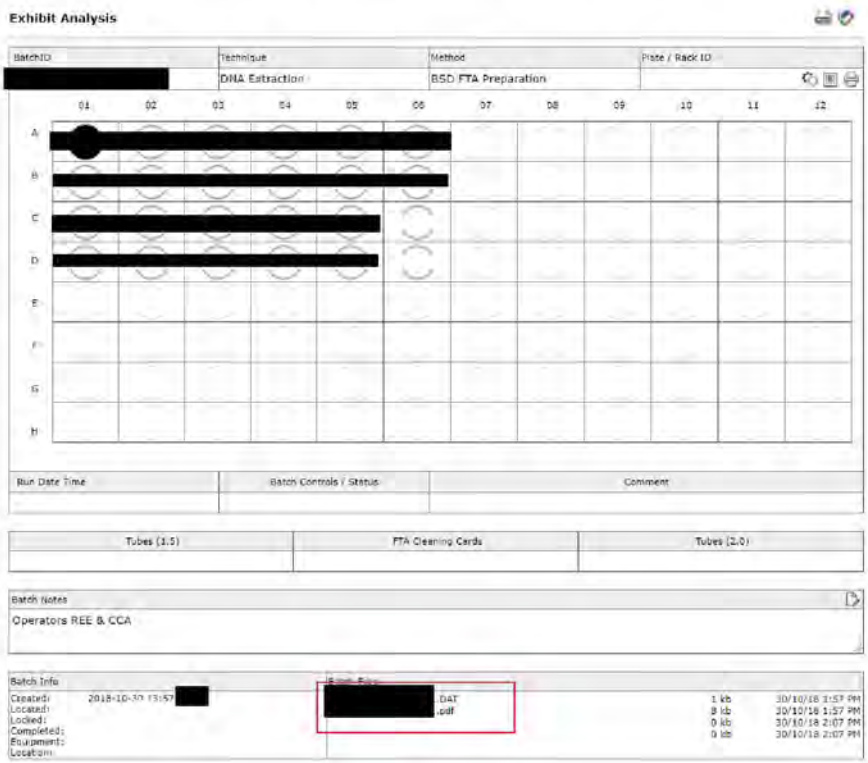


Figure 23 Check BSD files

10. Enter initials of both operators into batch notes.

    If there are any comments to record for the batch, enter "See batch" in the comment field, then enter the details in the batch notes table.

    When entering batch notes, enter operator initials followed by the date and then the notes. (e.g. XYZ 01/01/2017 – notes)

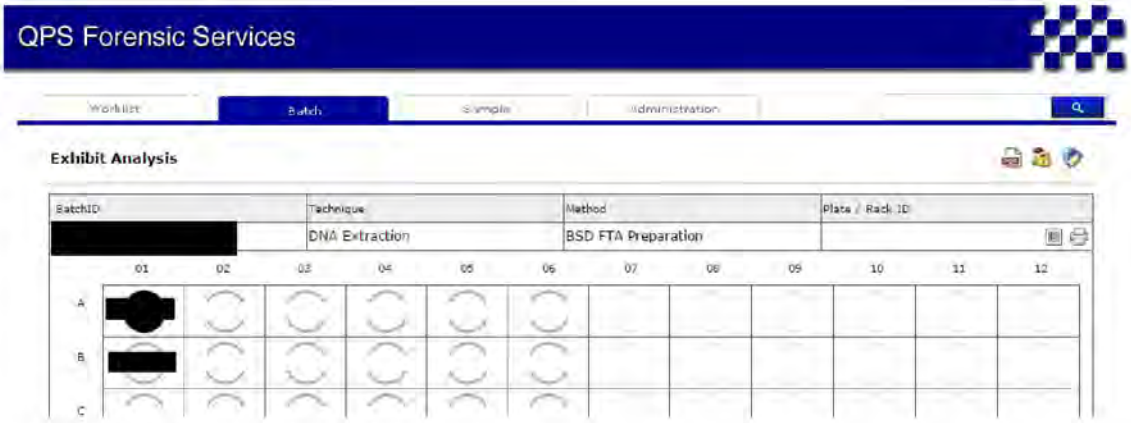


Figure 24 Batch details screen

After saving the page, the print icons will display at the top of the page.

11. View tube sample labels by clicking on the icon.

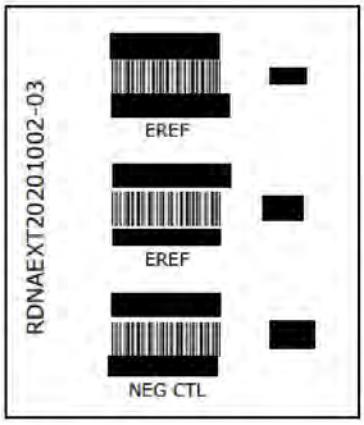


Figure 25 Sample label

12. Then click on the printer icon to print tube sample labels.



Figure 26 Label print icons

13. Print two batch labels. One is used to label the PCR plate and the other is used as the FTA storage ID.

6.8.5 Tube labelling and sequence check procedure for BSD FTA Preparation batch

1. Label the tubes one at a time from left to right starting at position A1 (top left), placing the labelled tube back into the BSD rack.
2. Proceed to the next row and continue labelling tubes left to right for each row until all tubes are labelled.
3. Check the labelled tubes match the plate map as displayed in the FR.
4. Perform a sequence check of all tubes for the batch by clicking the **Sequence Check & Lock** icon.



Figure 27 Lock batch

5. Scan all tubes in the order they are positioned in the rack corresponding with the FR plate map. The cursor will move down the column after a sample ID is successfully scanned.

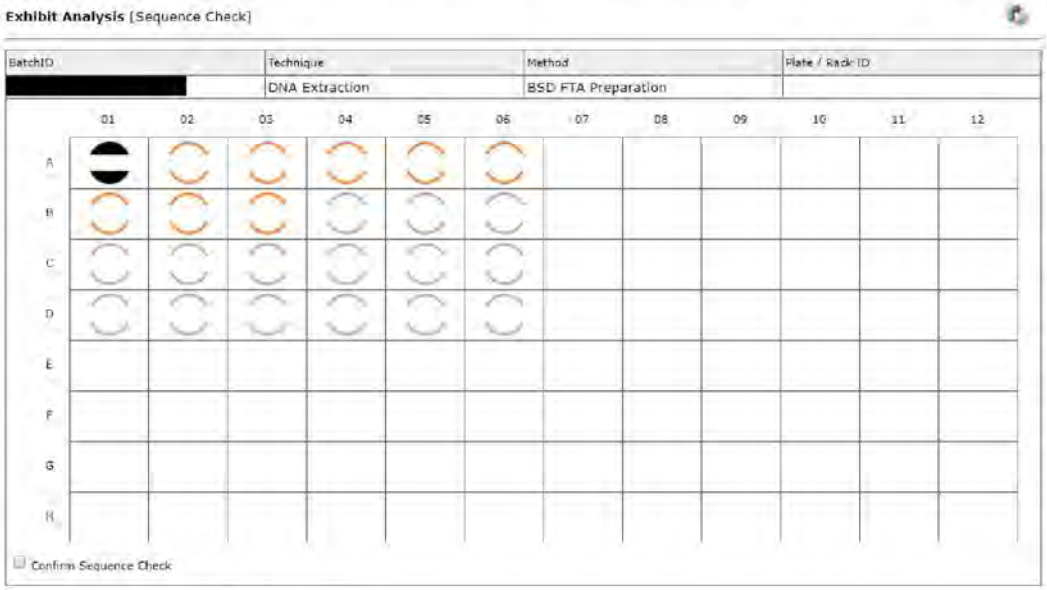


Figure 28 Batch sequence check entry

Note: If a barcode is scanned incorrectly during the sequence check a pop-up error message will appear and the position with the error will be highlighted in red. If this occurs refer to section 9.1.6.



Figure 29 Sequence check error

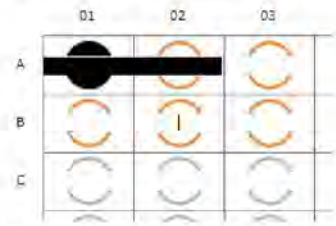


Figure 30 Position with error indicated by red

6. Once all tubes have been scanned, check there are no positions highlighted in red.
7. Click on the Confirm Sequence Check checkbox.

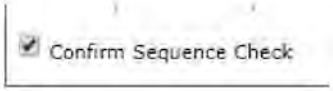


Figure 31 Sequence check

8. Save  record.
9. After the sequence check has been saved there will be an entry on the batch details screen. The sequence check entry displays how many samples were scanned, and the log can be viewed by clicking on the hyperlink illustrated in the red circle below.

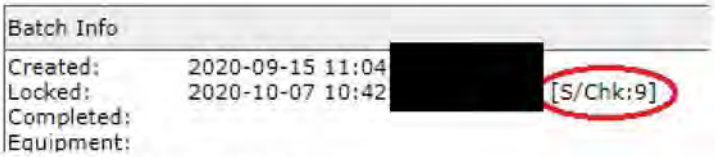


Figure 32 Sequence check record

6.8.6 Extraction preparation batch sample transition page

1. Before completing the extraction batch, the sample transition table needs to be saved. To do this, click on the sample transition button on the batch details screen.

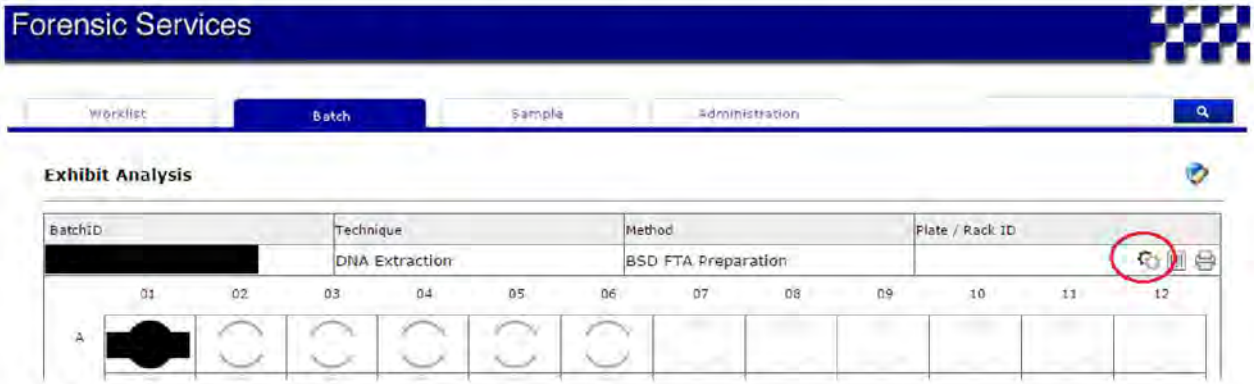


Figure 33 Sample Transition Button

This opens a screen which looks similar to



Figure 34 Sample Transition Table

2. The Technique should default to DNA Extraction and the Method to Maxwell 16 DNA IQ for all samples.
3. Save the sample transition page by clicking on the save record button .

6.8.7 Batch Completion

4. To complete the batch, enter in the Run Date Time by clicking on the calendar button and selecting the date. If the current date is selected it will automatically update the time.

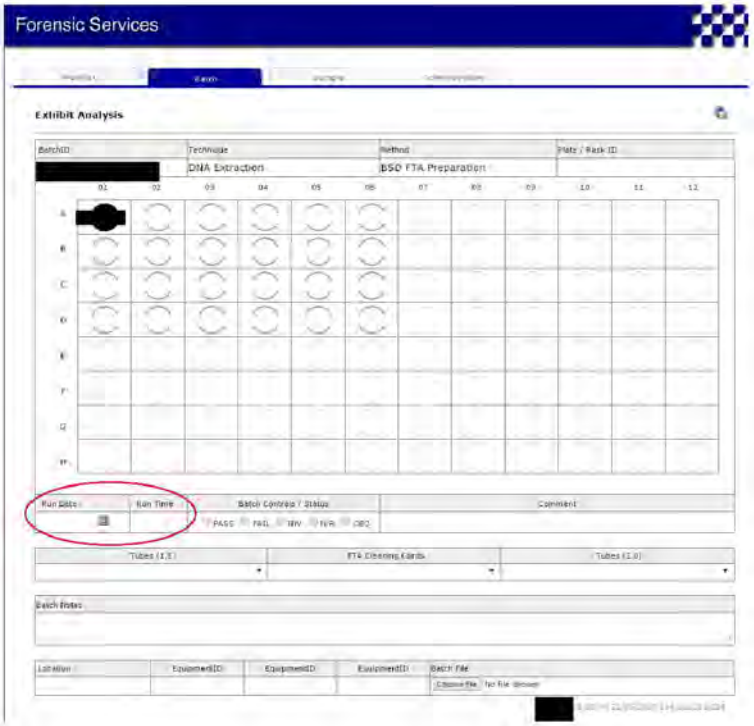


Figure 35 Batch completion

5. Save the batch details page by clicking on the save record button .

6.9 Storage

6.9.1 FTA card storage

FTA cards are stored to the FTA storage boxes which are located in the Exhibit Room (6106B).

All FTA cards must be sealed prior to storing. Seal must include the date and the initials of the person/s sealing the card.

1. FTA cards can be stored by using the Batch Exhibit movement form or by scanning a storage box ID into the Equipment section and using the Contents – Add to storage box function.

6.9.2 BSD Extraction FTA Preparation Tube storage

The tubes containing FTA punches for extraction are stored under the SubID barcode to the tube ERT-AS storage boxes located in the Extraction Sorting Freezer.

1. Scan the tube ERT-AS box ID into the Equipment section and use the Contents – Add to storage box function.

2. After storing the tube, the page will refresh and display the next empty position in the rack.

7 Validation

1. In house validations have been completed for the processing of buccal cells on FTA™ papers (refer F22186 and F23713).

2. In house validations have been completed for the preparation of FTA papers for DNA extraction; please refer to "*Reference Sample preparation using the BSD Duet 600 Series II 3.2mm die*".

3. In house validation has been completed of FTA processing using the PowerPlex® 21 System.

8 Quality assurance/acceptance criteria

FTA paper sampling is performed in the Room 3189 using the BSD600 Ascent A2 punching instrument. PPE (hats, gown, mask and gloves) must be worn during FTA punching.

In circumstances where a reference plate does not pass CE Quality check (refer to QIS 34131) the plate should be referred to the Senior Scientist Quality and Projects for investigation and actions (as per QIS 30800).

The amplification reagents are tested on known samples prior to use. Refer to QIS document 34103 *Receipt, Storage and Preparation of Chemicals, Reagents and Kits in Forensic Register.*

9 Troubleshooting

9.1 FTA troubleshooting instructions for Forensic Register

9.1.1 Laboratory assistant actions – adding Notation test

1. Enter exhibit barcode and scroll down to the Exhibit Testing table.
2. Click on the add record icon .
3. Add a "Notation" from the Process dropdown list.



Figure 36 Add notation test

4. Add details to the Notes field.

If the sample is to be placed on hold, proceed to section 9.1.2

If the sample is to be processed by the Evidence recovery Team proceed to section 9.1.3 to reallocate the sample (remove from the FTA worklist).

9.1.2 Laboratory assistant actions – placing sample on hold

1. While on the Notation page, add the Worklist Technique "On Hold" work list, and select "Awaiting advice" for the Method.



Figure 37 Exhibit Testing page - Method dropdown list

2. Save the record by clicking on the save icon .
3. Store the sample to the FTA Investigation box ([redacted]).

9.1.3 Laboratory assistant actions – Reallocating samples

1. Enter exhibit barcode and scroll down to the Exhibit Testing table.
2. Click on the add record icon .
3. From the Process dropdown list select Reallocate.

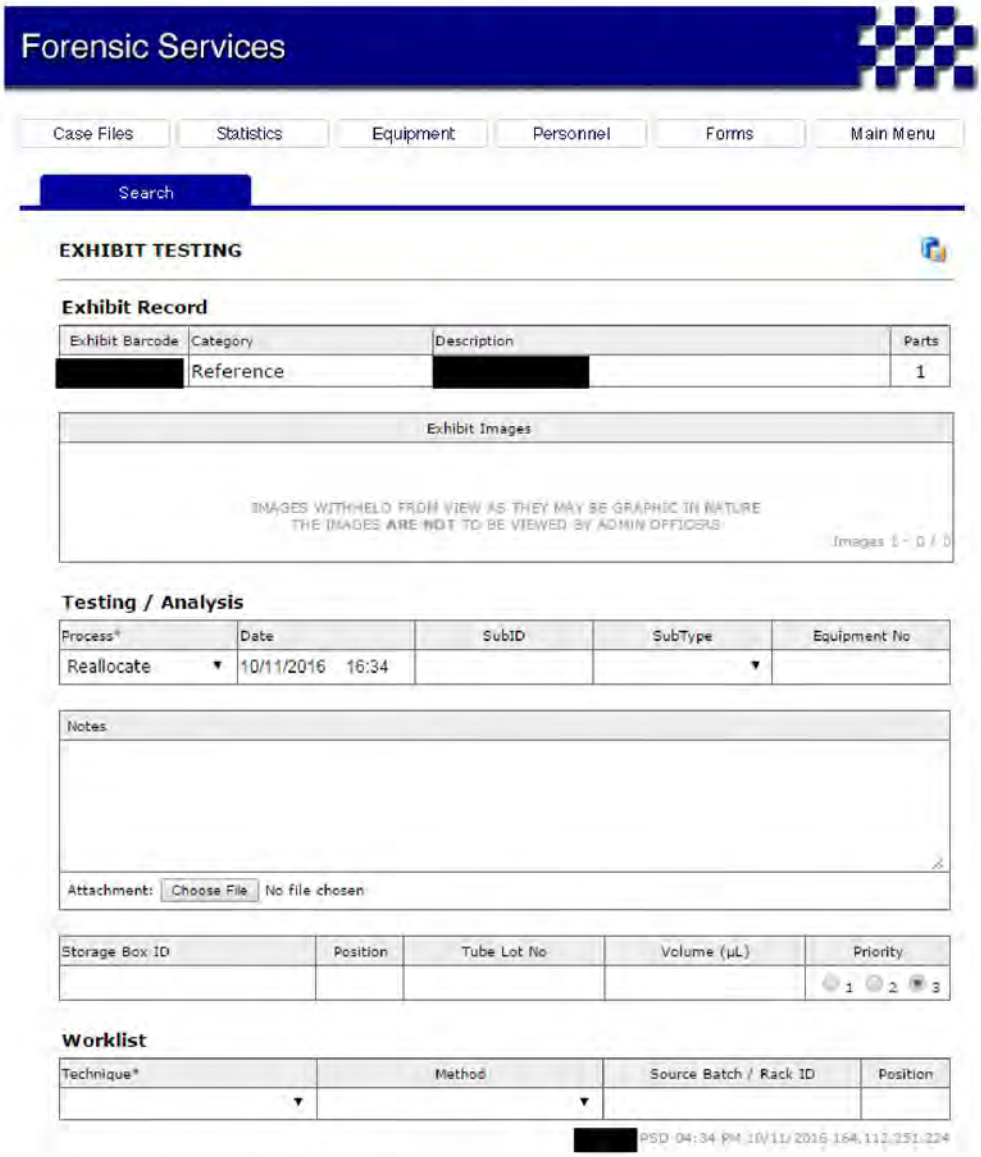


Figure 38 Add Process Reallocate

4. Add a reason why it is being removed from the worklist to the Notes section. (e.g. Reference hair sample to be processed by ER Team.)
5. Click on save record .

9.1.4 Add to Evidence recovery Examination worklist

1. Scroll down to the Exhibit Testing table.
2. Click on the add record icon  .

3. Add the sample to the "Examination" worklist, with the Item Exam method.
   This is so the Evidence Recovery Team can see what exhibits need to be processed.

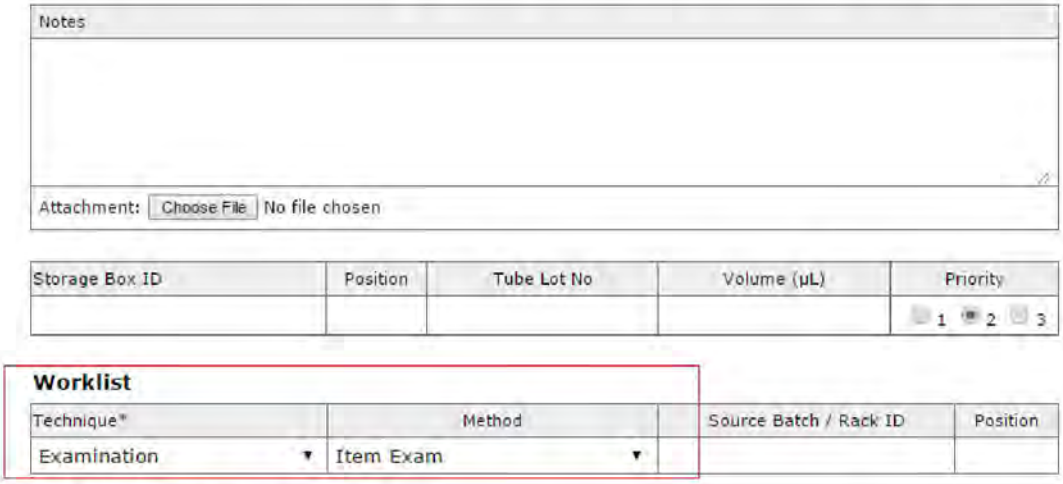


Figure 39 Add to Examination worklist

4. Click on save record  .

9.1.5 Batch Not Required

If a batch has been created in error, edit the batch and change the batch Status to Not Required (N/R).
Also enter a batch note to briefly explain the issue and save the batch.

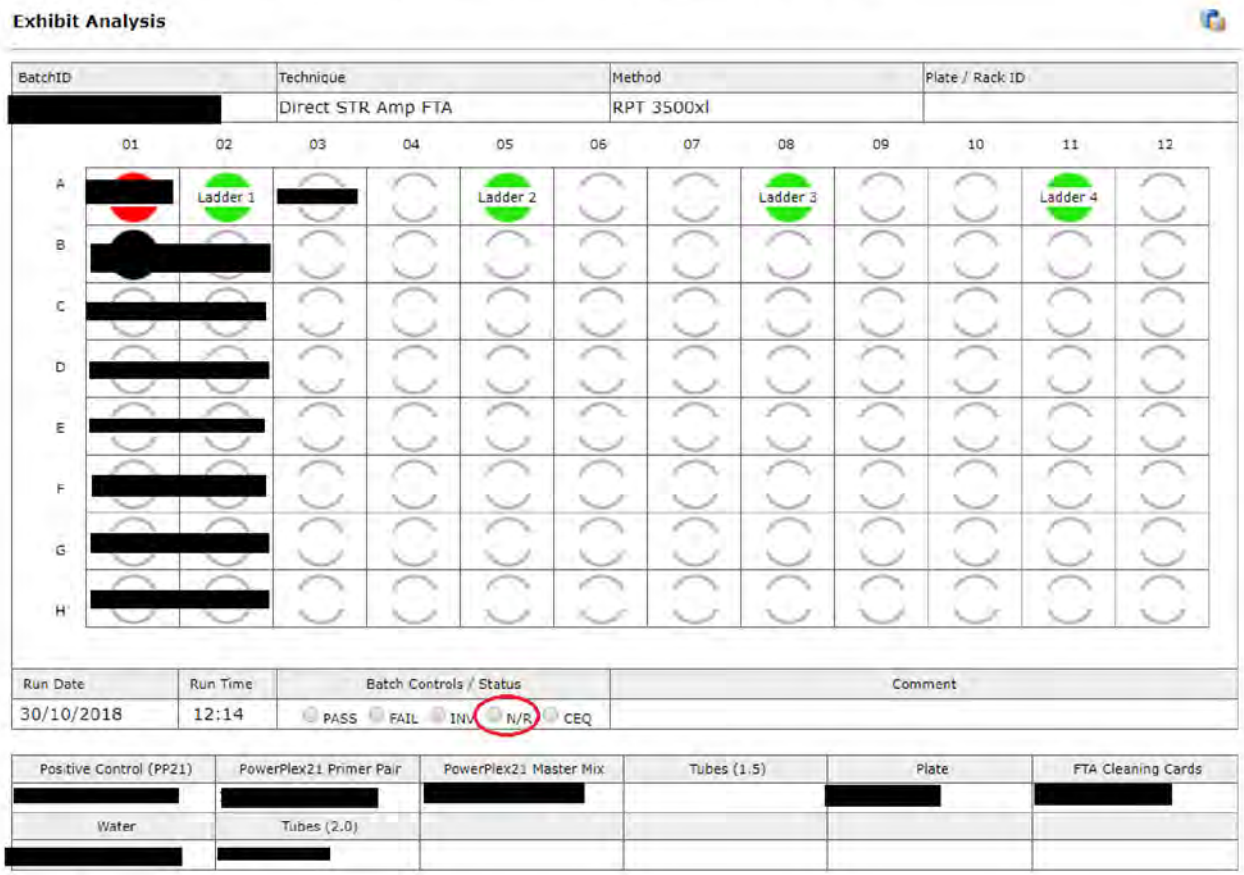
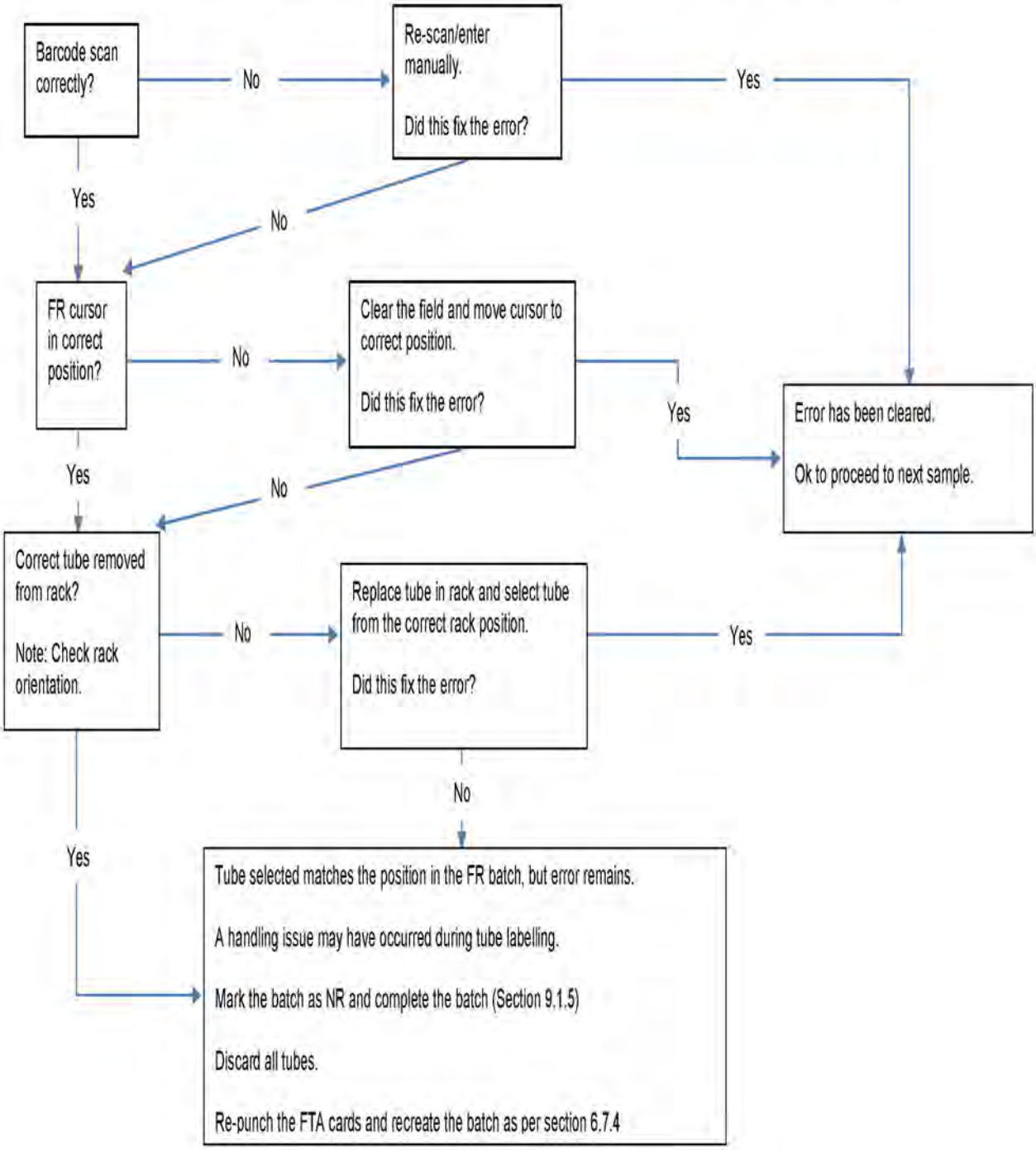


Figure 40 Update Batch Status to N/R

Any samples that were listed on this batch remain on the worklist so the batch can be recreated if required.

9.1.6 BSD extraction preparartion batch sequence check errors

If an error is encountered during the Forensic Register sequence check procedure please work through the flowchart:



9.1.7 Laboratory Assistant Supervisor/Quality Team actions

If sample is to be processed:

1. Go to the Analytical Work list and select On Hold work list.
2.  add a Notation test, add details and supporting information.
3. Save the record.
4. If the sample is to be processed on the existing worklist, move the sample to a FTA Box/FTA Transfer Box to be processed, and notify staff.

   If the sample requires processing on a different batch type:
   Add reallocate test, and record what batch type the sample is to be processed on.
   Add to appropriate work list.



Figure 41 Exhibit testing page – Reallocate

If the sample is not for processing:

1. Go to Analytical Work list and select On Hold work list.

2. Add a notation with details and supporting information.

3. Save.

4. **If sample is to be stored (coronial samples):** Go to On Hold test page and add Notation test with details of why the sample is not to be processed.
   Also add the Result **IPNE** (Items prioritised not examined at this time).
   This removes the sample from the 28-Audit reference list.
   The result line will need to be validated by another member of the quality team.

5. **If sample is to be returned (QPS reference samples)**: Request QPS to tick "No Further Testing", and quality must validate this result line.
   Also add the Result **FBRET** (Returned to QPS).
   This removes the sample from the 28-Audit reference list.
   The result line will need to be validated by another member of the quality team.

   Go to On Hold test page and add Reallocate test then use exhibit movement to transfer to Exhibit Room Returns.

   For FTA samples returned to QPS add the result line "FBRET - returned to QPS".

   This will have attached email from QPS, and exhibit movement to returns

6. **If sample is to be destroyed (QPS reference samples)**: Ask QPS to request through FR or return sample to QPS for disposal.

9.2 Punch batch troubleshooting

If there are problems during the punching of samples, clear notes are to be entered against the batch in the Forensic Register.

Table 2 Punch batch troubleshooting

Problem	Possible cause	Remedy
Punch error		**** In the event of punching errors – consult with Quality Senior Scientist before undertaking any remedial actions****
	The spot has passed through the chute undetected and fallen into the correct well.	If spot is visible in the camera image – select *Disk in Well* and proceed. If spot is not visible in camera image, select *Inspect Plates* and try to locate the spot. If the spot is located on top of the plate, carefully remove the spot and select *Re-Punch*.
	The spot has passed through the chute undetected but not fallen in the correct well	If the spot has fallen into another well, *Re-Punch* the current sample. If the spot went into a punched well, edit comment on the well with the extra spot to say *Extra spot – remove well from batch*. Scan the barcode of the sample with extra spots and re-punch that sample as a duplicate. After the batch is completed, open the DAT file and delete the sample barcode that has the added *remove well from batch* comment. If the spot went into an empty well, disable that well. (If the spot cannot be located, try removing the chute. Clean the chute and spot detector.) If punch error occurs whilst punching the cleaning card, try to locate the spot by inspecting the plate or checking the chute. *Re-Punch* the cleaning card. If the spot went into a punched well, edit comment on the well with the extra spot to say *Extra spot – remove well from batch*. Scan the barcode of the sample with extra spots and re-punch that sample as a duplicate. After the batch is completed, open the DAT file and delete the sample barcode that has the added *remove well from batch* comment. If the spot went into an empty well, disable that well.
FTA card barcode does not match envelope barcode	Labelling error	Do not process, report to or email Quality Team and refer to section 9.1, store FTA in the investigation box located in the exhibit room and also write on the envelope.
Added too much or too little reagent to well	Pipetting error Reagent added to well in duplicate	Remove reagent from well with pipette and add correct volume of reagents.

Spot sticking to side of tube	Static	Push into bottom of well with clean pipette tip.
Batch failed to create in Forensic Register	1. Incorrect file and path entered. 2. Mis-scanned barcode. 3. Sample punched but not on Forensic Register Batch Worklist.	1. Check the filename and path and retry creating in the Forensic Register. 2. Open BSD output file using EXCEL and check for mis-scanned barcodes, correct any mis-scanned entries and then retry batch creation in Forensic Register. 3. Check the samples ID's against the outstanding samples list for that batch type for any discrepant samples. Put any discrepant FTA samples to the side, open the BSD output file and delete the corresponding Lab ID's, then resave the file and create batch. Once batch is created, enter batch notes to explain why the BSD DAT file was altered.
Plate has evaporated after PCR	Plate not sealed adequately	Re-punch and seal

10 References

Promega Corporation. 2017. *PowerPlex-21-system-protocol*. [ONLINE] Available at: https://www.promega.com.au/-/media/files/resources/protocols/technical-manuals/101/powerplex-21-system-protocol.pdf. [Accessed 22 August 2017].

Whatman (2009) *Whatman FTA for the protection and storage of DNA.*

Whatman (2005) *FTA Datasheet.*

11 Associated documents

17125 Processing of FTA Reference Samples Training Module
33733 Reference Blood Processing in Forensic Register
17154 Procedure for Quality Practice in DNA Analysis
34103 Receipt, Storage and Preparation of Chemicals, Reagents and Kits in Forensic Register.
34042 Procedure for the use of the STORstar unit for automated sequence checking
30800 Investigating Adverse Events in Forensic DNA Analysis Unit
32930 FTA MasterMix Calc
35692 BSD600 Ascent A2 Operator Manual

12 Amendment history

Version	Date	Author/s	Amendments
1	Dec 2016	M. Goodrich	First Issue
2	Apr 2017	M. Goodrich	Updated with reviewer comments, removed CE batch creation.
3	Oct 2017	M. Goodrich	Added instructions for paperless processing, updated troubleshooting section and with reviewer comments. Updated EREF processing.
4	Oct 2018	M. Goodrich	Updates to sections 6.5 6.6. Added Subsection 9.1.5. Updated with minor changes from reviewer comments.
5	Oct 2020	M. Goodrich	Removed operating instructions for BSD600 Duet Series II. Replaced use of STORstar with Forensic Register sequence check procedure. Updated with references to BSD600 Ascent A2. Updated troubleshooting section.
6	November 2021	M Mathieson M Goodrich	Updated Thermal Cycler Operating Instructions. Replaced 9700 with Proflex. Updated with minor changes and reviewer comments.

13 Appendices

Appendix A. Thermal Cycler Operating Instructions

Appendix B. Direct Amplification Batch Completion

Appendix C. Manual creation of EREF SubID

Appendix D. Form 6 authorisation for coronial sample destruction

13.1 Appendix A. Thermal Cycler Operating Instructions

1. In the PCR/CE room (3196) retrieve plate from the pass through hatch.

2. Turn on the ProFlex™ thermal cycler and log in to the Fleet Control server using personal log in (Figure 19).

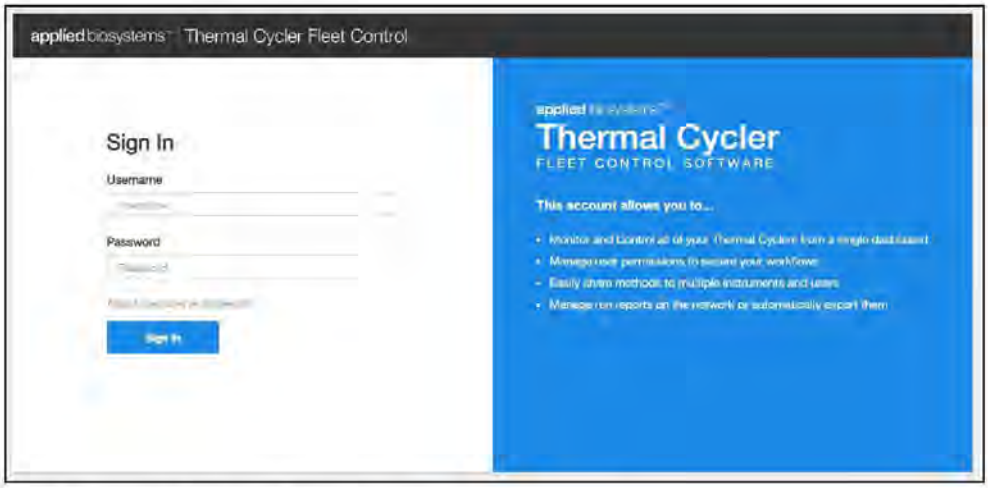


Figure 42 ProFlex™ fleet control log in screen

Note: Alternatively, fleet control can be accessed via a web browser on a PC using the address 10.96.49.238. The fleet control server must be turned on to access it via web address.

3. From the Instrument dashboard screen select the Methods options at the top of screen (Figure 20).

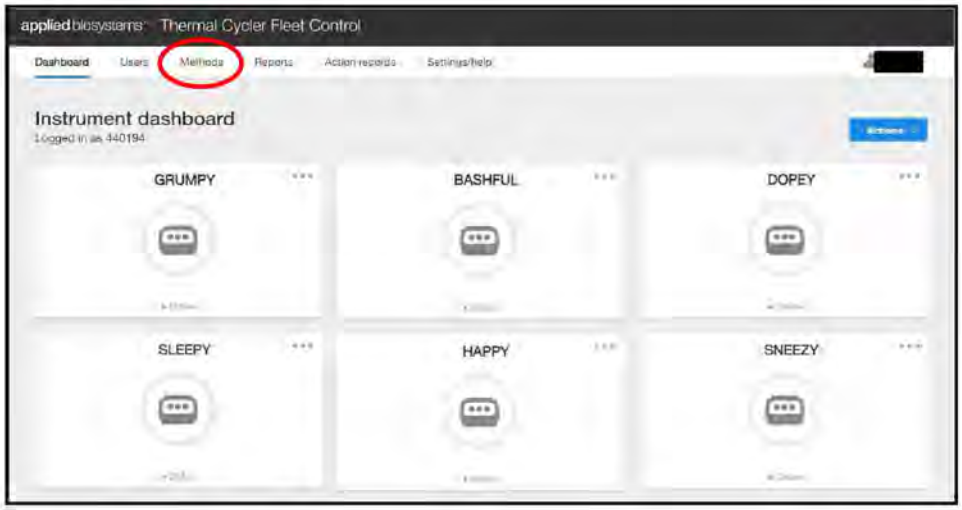


Figure 43 Instrument Dashboard screen

4. In the Method Folders tree drop down into Instruments and select the Synced files folder (Figure 21).

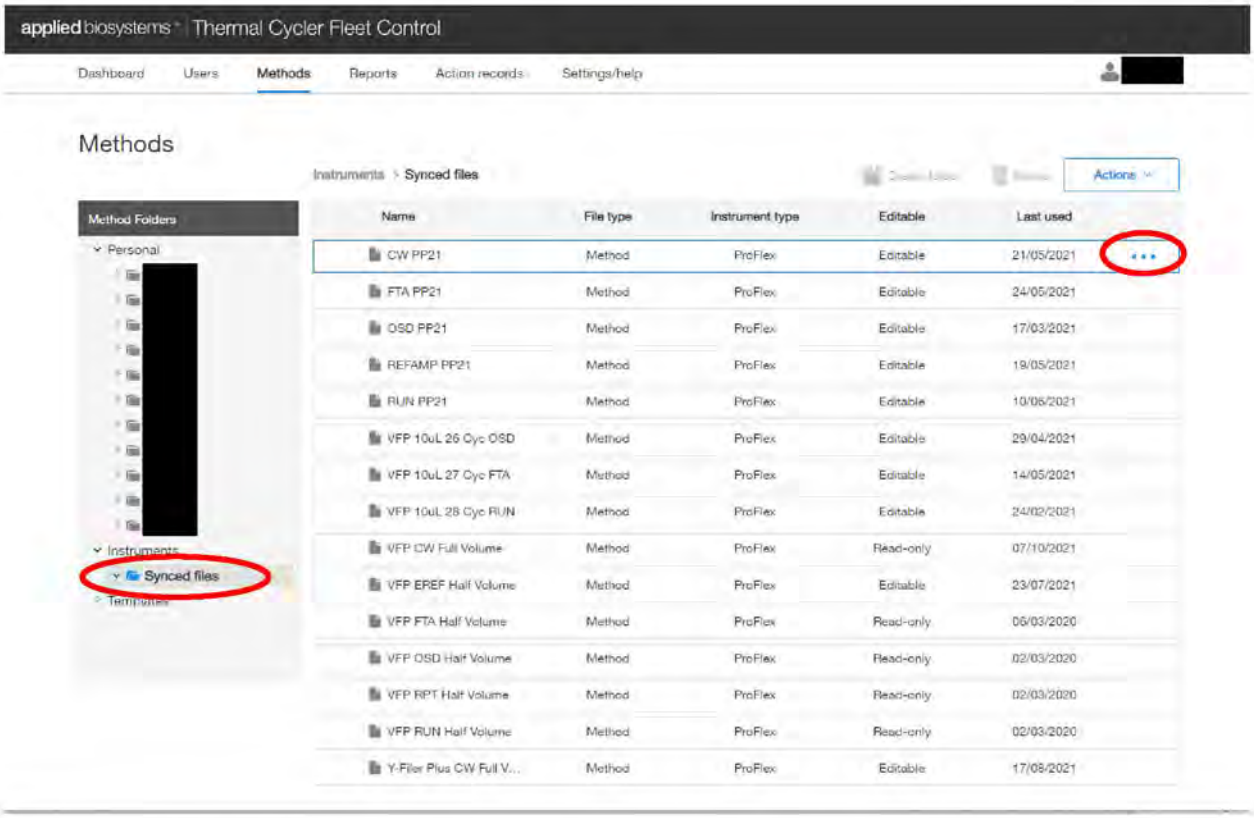


Figure 44 Select method screen

5. Check in the FR for the correct amplification method required then select the "…" to the right of the corresponding method type (Figure 21) and select Open Method from the drop down box (Figure 22).

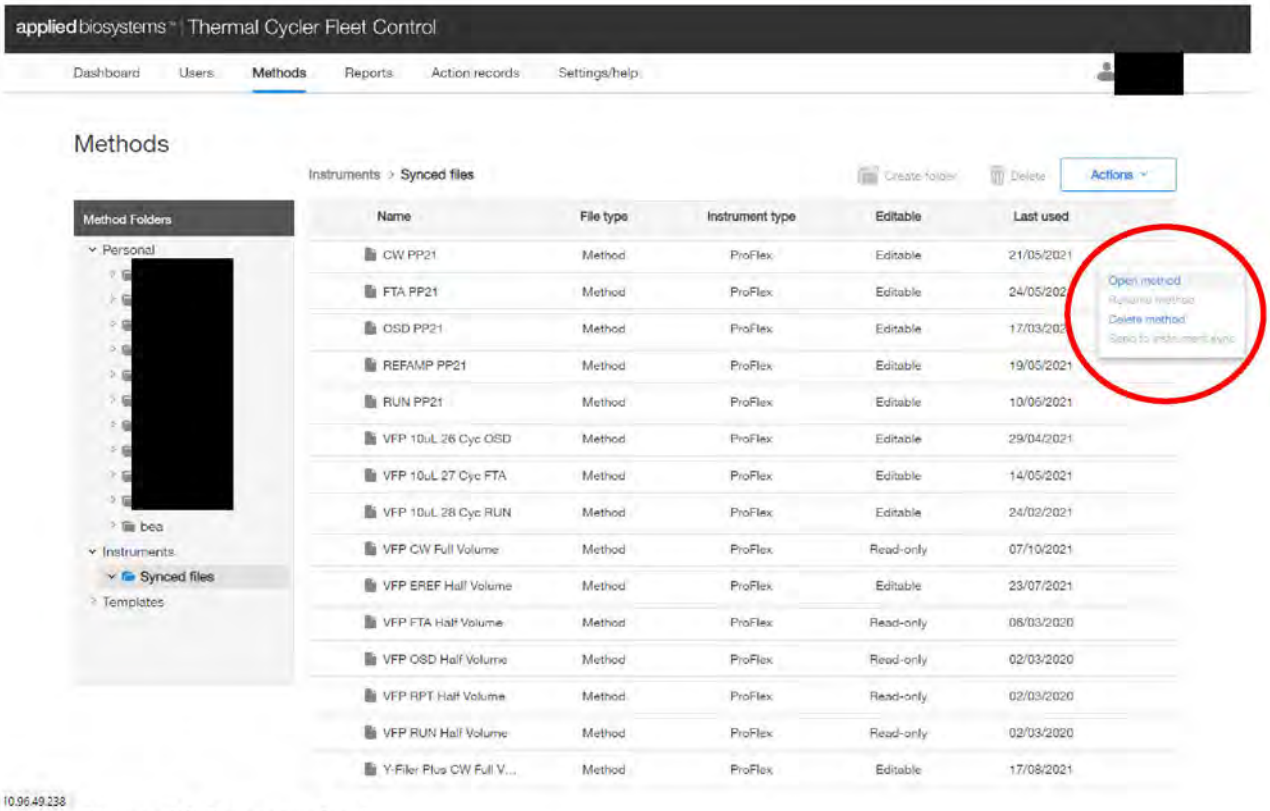


Figure 22 Open method

6. The Method details screen will appear with the details of the cycles for the method selected. Select the Set up run… icon (Figure 23).

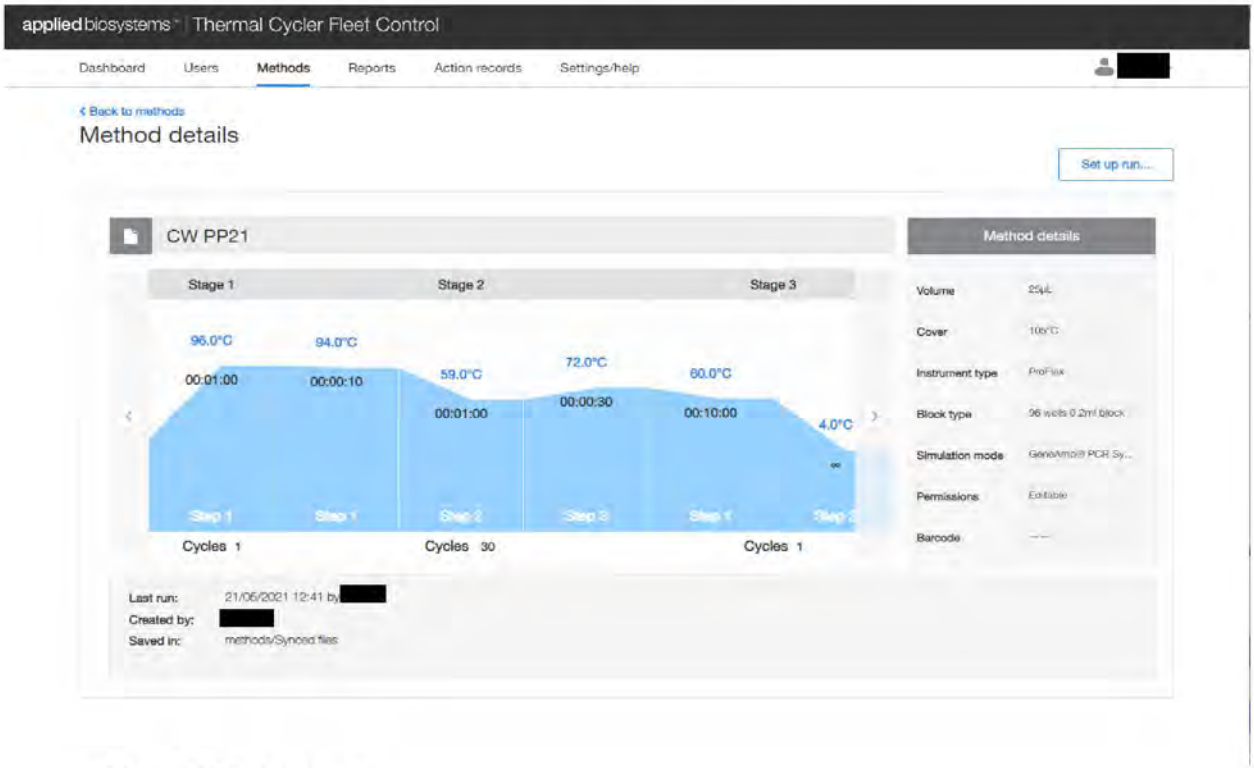


Figure 23 Set up run

7. On the Select instrument screen, select by clicking inside the grey circle of an available instrument, when the instrument has been selected the circle will turn blue and a green tick will appear on the instrument icon (Figure 24).

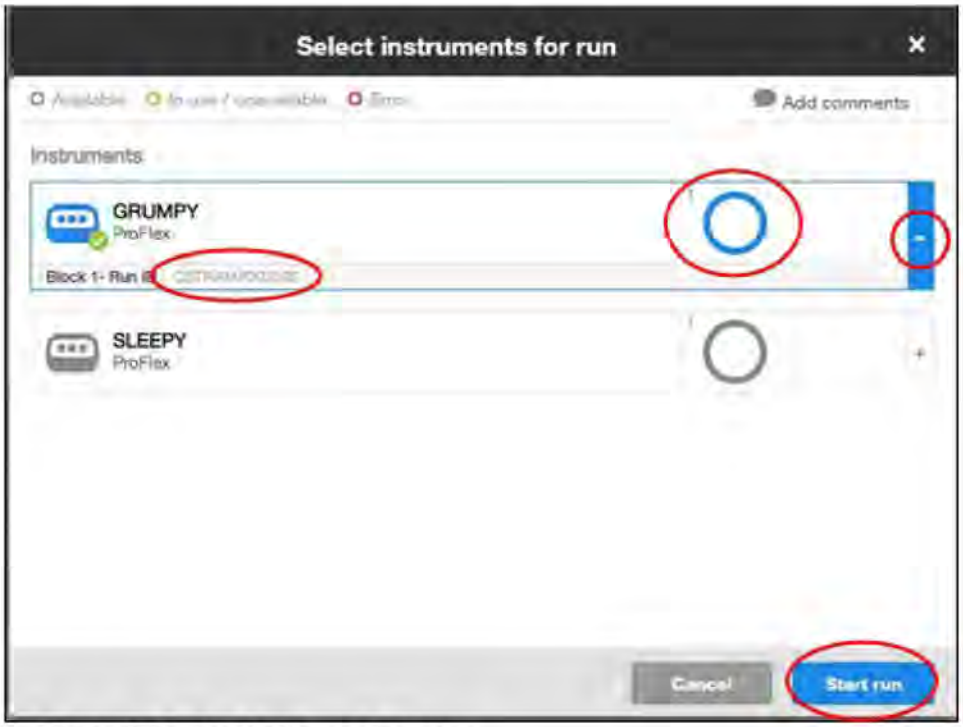


Figure 24 Select instrument screen

8. Select the + on the right side of the instrument box so it drops down the Run ID field (Figure 24).

9. Enter the Batch ID and user initials into the Run ID field to replace the generated ID (Figure 24).

10. Place the amplification plate on the sample block of the ProFlex™ orientated so that well A1 is at the upper left corner and close the heated cover.

11. Select the Start run button on the Select instrument screen (Figure 24).

12. Ensure the method is running before walking away (Figures 25 and 26).



Figure 25 Method started on Fleet Control screen



Figure 26 Method started on instrument

13. In the FR record the ProFlex™ ID in the equipment field and select On Instrument as per Section 4.4.

14. Record the thermal cycler ID in the equipment field and select **On Instrument** as per Section 4.4.

15. Enter a note in the **Batch Notes** field in FR with the details of the thermal cycler method sequence check, e.g. 28/02/2019 TJD – Thermal cycler protocol checked by SCN.

16. Complete the **Run Date & Run Time** fields (Figure 27) (manually enter and date and time, or select the current date from the calender which autofills the time field upon batch completion).

Run Date	Run Time
09/05/2017	08:12

Figure 27 Run date and Run Time field.

13.2 Appendix B. Direct Amplification Batch Completion

1. From the batch details screen, complete batch by clicking on Edit Record, then add Run Date and Time by clicking on the calendar icon and select the date. If the current date is selected it will automatically update the time.



Figure 45 Batch completion

2. Save the record .

13.3 Appendix C. Manual creation of EREF SubID

Once the cards have been located SubID's need to be created to process and store the extracts.
The SubID will be attached to the FTA envelope, and the Extraction Prep will be punched under this barcode.

1. Scan/type sample barcode into the search bar at the top of the analytical page to bring up the exhibit page.



Figure 46 Exhibit number search

2. Click on the add record button  under the exhibit testing section.

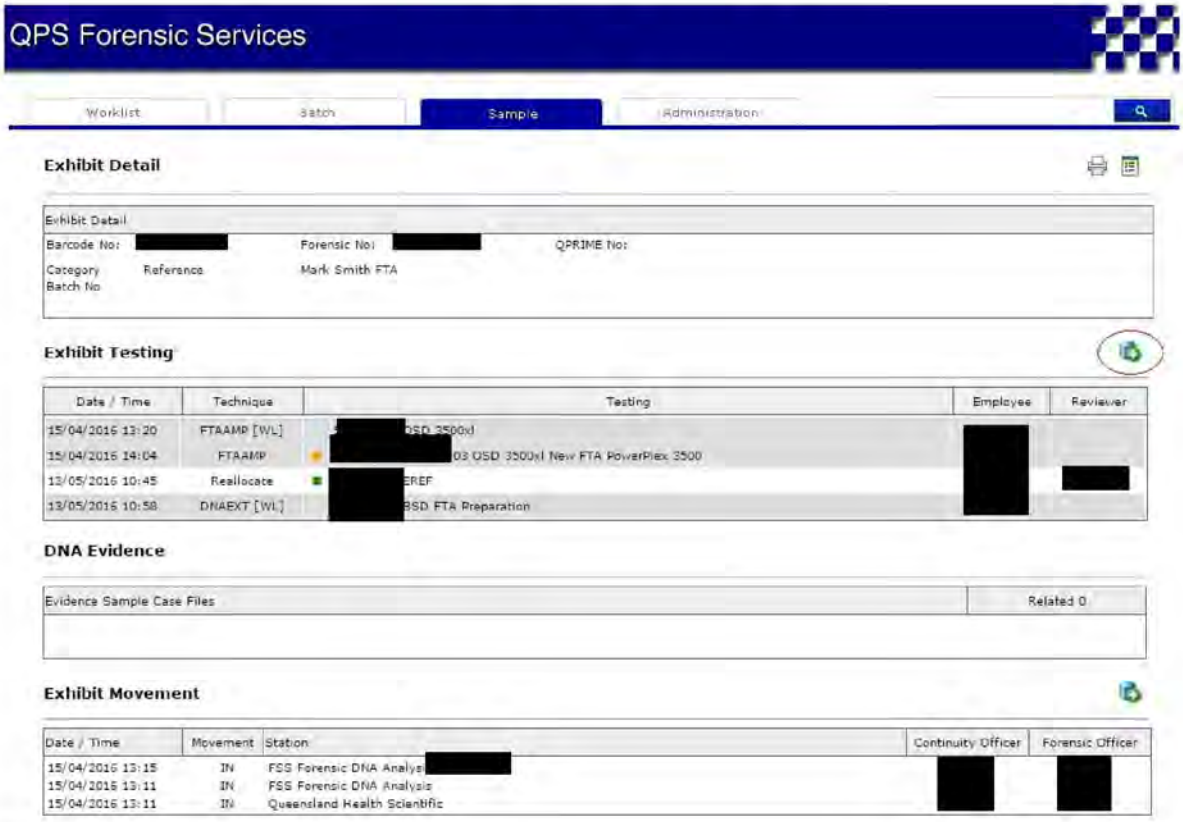


Figure 47 Add test

A new window will open.

3. In the Testing/Analysis Table:
   For the "Process" select **Subsample** from the drop down list.
   Scan/type a barcode into the SubID field.
   For SubType, select **EREF** from the drop down list.

4. In the Worklist table:
   For Technique, select **DNA Extraction** from the drop down list.
   For Method, select **BSD FTA Preparation** from the drop down list.

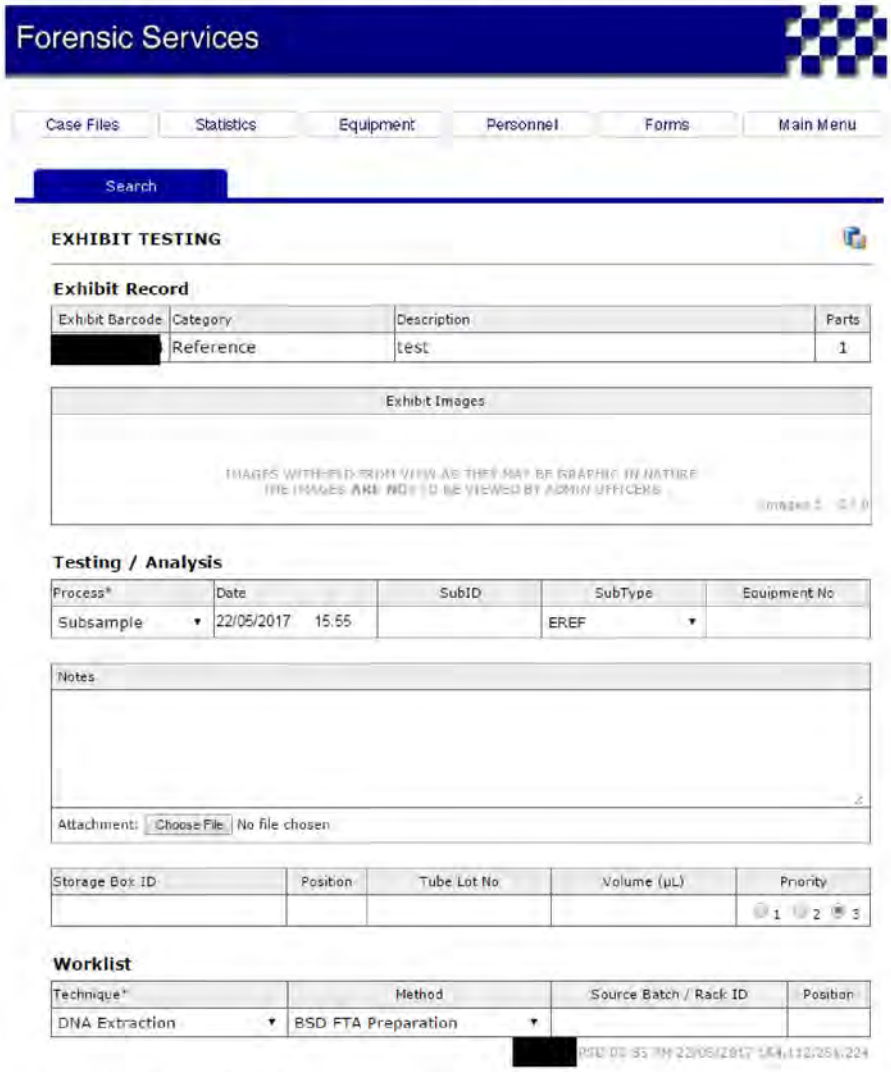


Figure 48 Create SubID and add to worklist

5. Click on the save record button .
6. Close the window.
7. Refresh the exhibit details screen (original barcode is displayed).



Figure 49 Refresh screen

After the exhibit details screen is refreshed, the Exhibit Testing table will show the SubID has been created and the following line shows it has allocated to the BSD FTA Preparation worklist.

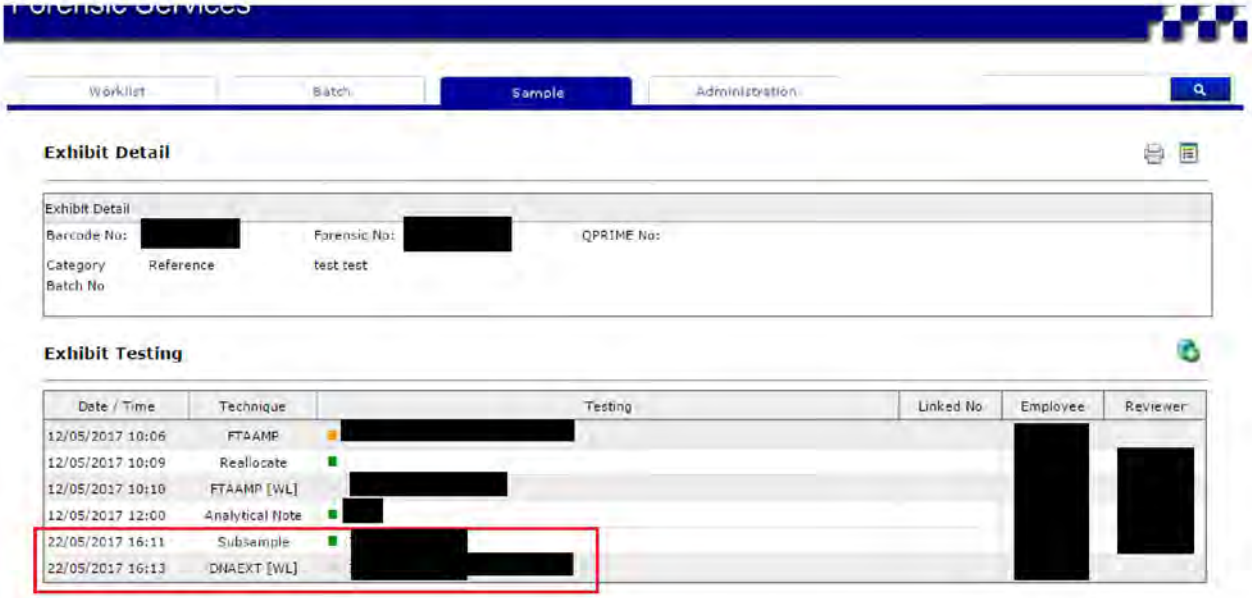


Figure 50 Exhibit testing table

Note: SubID samples may appear on the BSD FTA Preparation storage location PDF sheet.
These samples will not have a storage location or previous batch ID and are ready to be processed.

The envelope will need to be labelled with the subsample barcode (refer to section 6.6.2).

13.4 Appendix D. Form 6 authorisation for coronial sample destruction

As of 4 January 2018 – all Form 6 emails are being automatically forwarded to the FSS Biology Quality email [redacted].

To determine whether we have any items that require destruction:
Look at the Form 6 for date of autopsy

- If the date is prior to FR going live (15 June 2017), search in AUSLAB by the name of the person under Patient enquiry – add the surname to the "Name" field, hit enter then F12. This will return a list of all people with that surname in AUSLAB – scroll down till you find the correct person. Enter into the sample and see if any relevant items were provided to DNA Analysis.

- If the date is after FR going live, search in the FR by the name of the person under case file search using the surname as the "Complainant" – scroll through the list until you find the correct person. Enter into the sample and go to the exhibit register to see if any relevant items had been provided to DNA Analysis.

If no relevant items have been provided to DNA Analysis, no further action is required. Move the email into the Form 6 Outlook folder.

If relevant items have been provided to DNA Analysis, follow steps outlined in QIS 17152 – Destruction of reference samples. Once complete, move the email into the Form 6 Outlook folder.

CA-72

Queensland Health

Forensic and Scientific Services

Examination of post mortem and associated samples from deceased persons

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1 Purpose

The purpose of this procedure is to describe the procedures for the examination of evidentiary items from deceased persons by Scientists in Forensic DNA Analysis using the Forensic Register.

2 Scope

This procedure applies to all Forensic DNA Analysis staff that examine or interpret examinations of items from deceased persons, including post mortem (PM) samples, tissue samples and bone/teeth samples for coronial casework and Disaster Victim Identification. This standard operating procedure is an adjunct to individual methods for particular screening tests.

The nature of post mortem and associated samples from deceased persons is sensitive and may be confronting to some staff. Care and caution should be taken by all staff when examining samples of this nature and briefing and debriefing conducted where necessary.

If attendance in the mortuary is required (approval by a team leader only), staff should first attend mortuary awareness training.

3 Definitions

- Refer to QIS 23849 (Common Forensic DNA Analysis Terms and Acronyms) for a comprehensive list of abbreviations.
- Periosteum - The connective tissue layer that separates the bone from the muscle.
- Compact Bone - Hard, compact bone found in bones including long bones and the cranium.
- Cancellous Bone - 'Spongy' bone found in bones including short bones, the ends of long bones, and vertebrae.
- Chisel Blocks - Thick, hard plastic blocks that provide a chiselling surface for the bones.
- Dremel® Tool - A handheld electrical tool with multiple attachment bits. [Not necessarily Dremel® brand]
- Bone Saw - A handheld manual surgical saw, used for cutting through compact bone.
- Dewar - The small 10 L liquid nitrogen storage flask used for transferring liquid nitrogen to the Freezer Mill®.
- Main Liquid Nitrogen Vessel - Located inside the secure fencing, outside and to the right of Block 6.
- Liquid Nitrogen - A colourless, odourless liquid (N_2), with a temperature of -146.9ºC used to freeze bone fragments prior to crushing. Inhalation of the gas can cause asphyxiation, and direct contact with the liquid can cause severe frostbite.
- Cylinder Extractor - An instrument used to extract the cylinder from the Freezer Mill® and remove one of the bungs from the cylinder.
- SPEX 6775 Freezer Mill® - The piece of equipment used to crush bone fragments into bone powder.
- Freezer Mill Cylinder - A hard plastic cylinder containing the bone sample, which is inserted into the Freezer Mill®.
- Bungs - The two metal stoppers fitted to the ends of a Freezer Mill® cylinder.
- Impactor - A small metal cylinder that facilitates bone crushing inside the Freezer Mill® cylinder.
- Cylinder Extractor - An instrument used to extract the cylinder from the Freezer Mill® and remove one of the bungs from the cylinder.

4 Coronial post mortem samples for DNA testing

4.1 Sample collection

Post mortem samples for DNA testing are collected by Forensic Pathologists during coronial autopsies at the Forensic and Scientific Services Mortuary and other regional mortuaries across Queensland. Samples can only be collected once directed by the Coroner. Different samples may be collected during each autopsy dependent on the case type and any advice received from QPS. Some samples that may be collected for DNA testing include but are not limited to:

- Whole Nails, nail scrapings or nail clippings
- Swabs (intimate and skin)
- FTA card (refer to QIS 33800)
- Hair (refer to QIS 33800)
- Tissue
- Bone or Teeth

4.2 Sample delivery to Forensic Property Point

Mortuary staff from the FSS Mortuary will deliver samples for DNA testing to Forensic Property Point (FPP) daily or as requested. Regional mortuaries will send samples via courier to FPP. FPP staff will register samples and deliver regional mortuary samples directly to Forensic DNA Analysis, samples from the FSS mortuary will be registered and if the testing requirements are not clear the 'No Testing Required' box will be checked and the samples will remain in FPP. Once registered, PM samples will appear on the received worklist.

4.3 Sample testing requirements

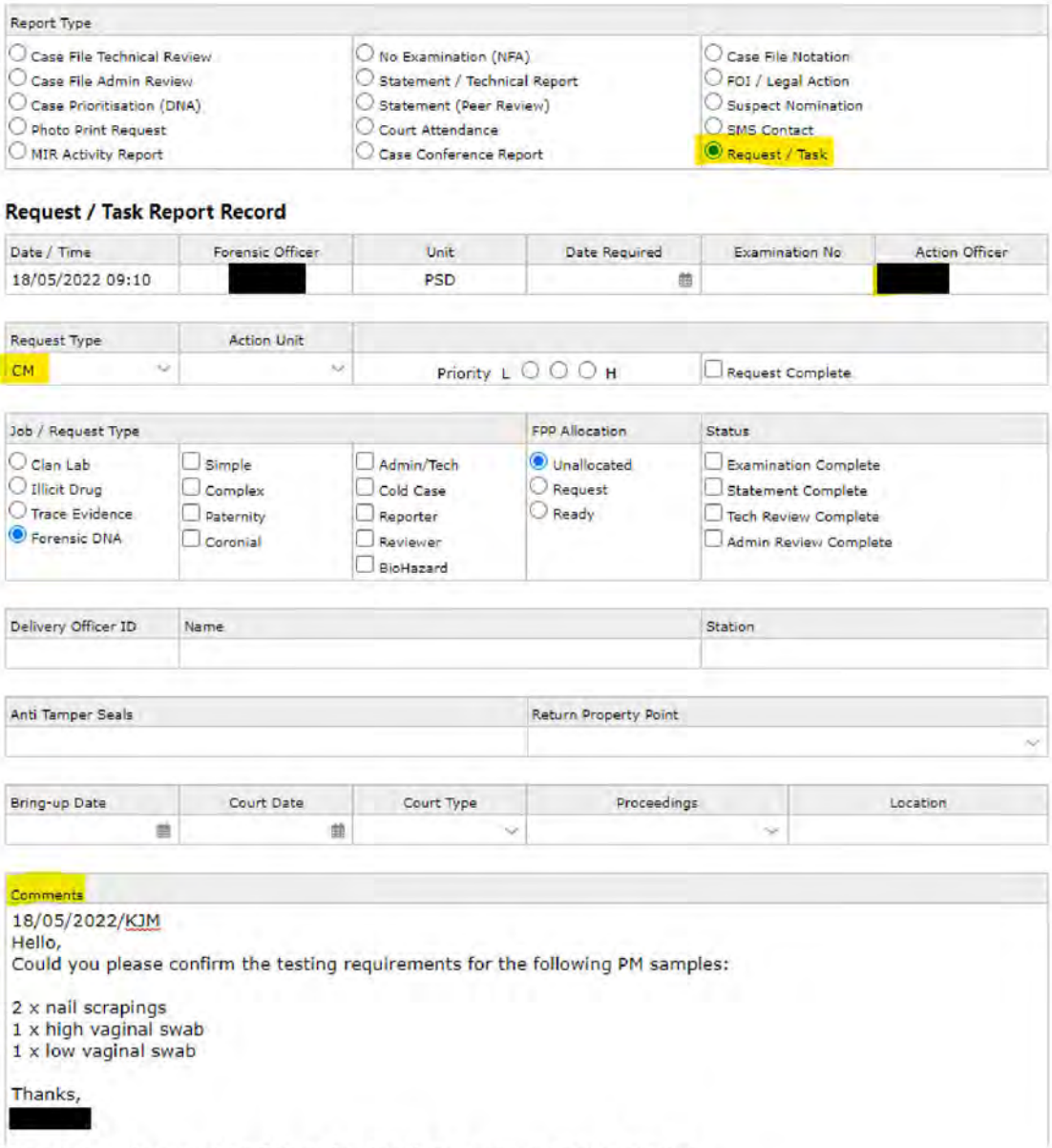
Depending on the case circumstances, including whether identification has been requested by the coroner or a DNA profile is required by QPS or other matters.

Notifications will arrive via one or both of the following methods:

a) E-mails to the following staff: Evidence Recovery Supervising Scientist, Team Leader FRIT, Team Leader ER&Q.
b) An FR task/request to the Evidence Recovery Supervising Scientist as this will also populate the Unit Worklist allowing the Evidence Recovery Team to action samples requiring processing. Once sampling is complete, the request / task can be marked as request complete.

If no notification has been received and the item has populated the received worklist, a request/task is to be sent to SSLU to determine testing requirements (see Figure 1 for request/task requirements). Transfer the item to the on-hold awaiting advice worklist. SSLU will direct the request/task to QPS for advice. If the sample has the 'No Testing Required' box checked, this should be noted in the request/task.

If notification is received that the item/s do not require testing, add a notation stating that no testing is required as per case management reports. This notation will remove the item from the on-hold worklist, if the storage location is within Forensic DNA Analysis it will need to be returned to FPP returns via exhibit movement.



Report Type

○ Case File Technical Review	○ No Examination (NFA)	○ Case File Notation
○ Case File Admin Review	○ Statement / Technical Report	○ FOI / Legal Action
○ Case Prioritisation (DNA)	○ Statement (Peer Review)	○ Suspect Nomination
○ Photo Print Request	○ Court Attendance	○ SMS Contact
○ MIR Activity Report	○ Case Conference Report	◉ Request / Task

Request / Task Report Record

Date / Time	Forensic Officer	Unit	Date Required	Examination No	Action Officer
18/05/2022 09:10	[redacted]	PSD			[redacted]

Request Type	Action Unit		
CM		Priority L ○ ○ ○ H	☐ Request Complete

Job / Request Type			FPP Allocation	Status
○ Clan Lab	☐ Simple	☐ Admin/Tech	◉ Unallocated	☐ Examination Complete
○ Illicit Drug	☐ Complex	☐ Cold Case	○ Request	☐ Statement Complete
○ Trace Evidence	☐ Paternity	☐ Reporter	○ Ready	☐ Tech Review Complete
◉ Forensic DNA	☐ Coronial	☐ Reviewer		☐ Admin Review Complete
		☐ BioHazard		

Delivery Officer ID	Name	Station

Anti Tamper Seals	Return Property Point

Bring-up Date	Court Date	Court Type	Proceedings	Location

Comments

18/05/2022/KJM
Hello,
Could you please confirm the testing requirements for the following PM samples:

2 x nail scrapings
1 x high vaginal swab
1 x low vaginal swab

Thanks,
[redacted]

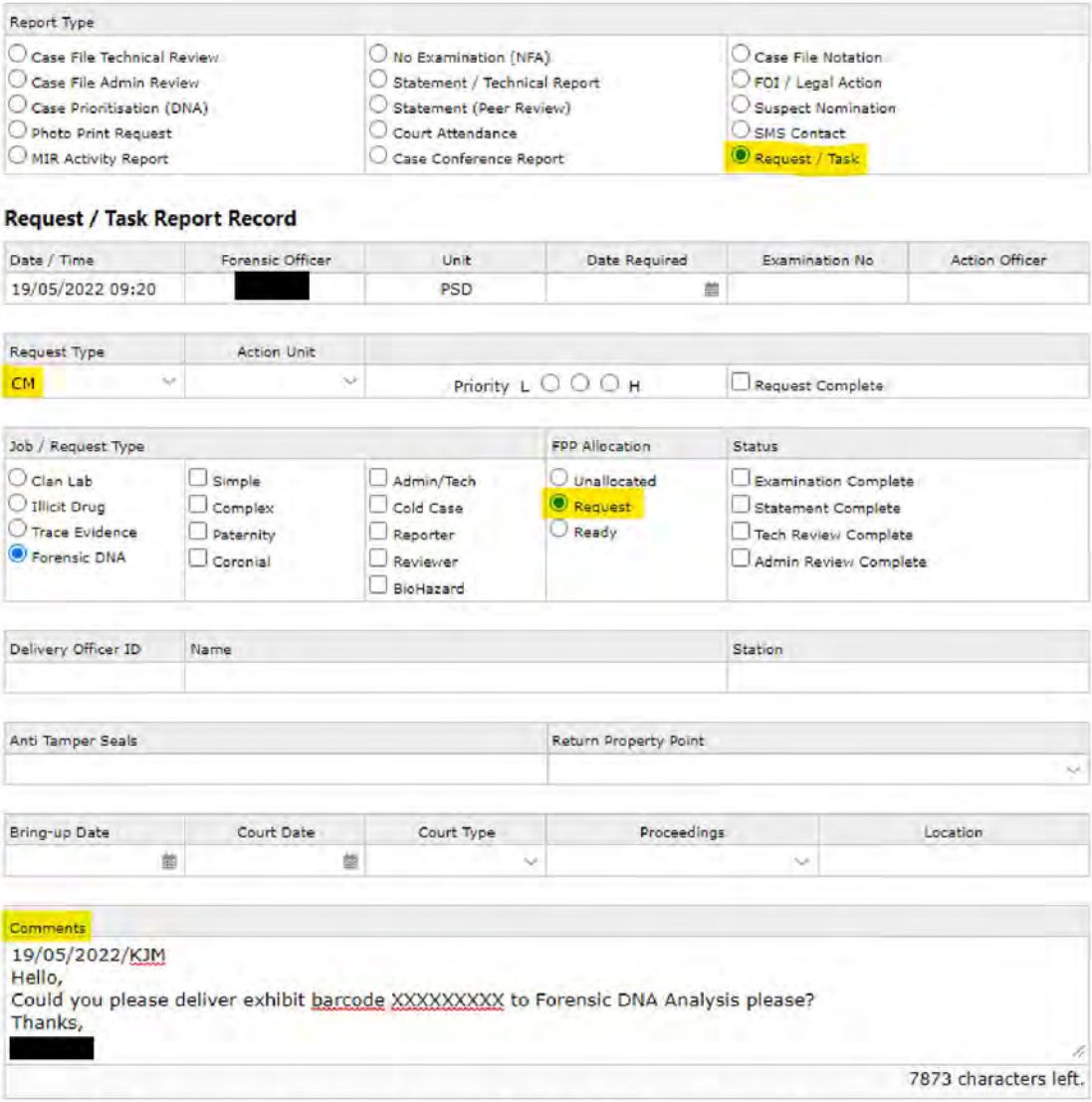
Figure 1 – Request to SSLU for testing requirements advice

4.4 Requesting sample delivery from Forensic Property point

If advice is received from QPS or SSLU that samples do require testing and their storage location is still within FPP, a request/task is to be sent to FPP to have the samples delivered to Forensic DNA Analysis (see Figure 2).

Add a notation to the exhibit to note what the sample requirements are and whether all samples require testing.

If testing is required, add the sample/s to the examination worklist.



Report Type

○ Case File Technical Review	○ No Examination (NFA)	○ Case File Notation
○ Case File Admin Review	○ Statement / Technical Report	○ FOI / Legal Action
○ Case Prioritisation (DNA)	○ Statement (Peer Review)	○ Suspect Nomination
○ Photo Print Request	○ Court Attendance	○ SMS Contact
○ MIR Activity Report	○ Case Conference Report	◉ Request / Task

Request / Task Report Record

Date / Time	Forensic Officer	Unit	Date Required	Examination No	Action Officer
19/05/2022 09:20	[redacted]	PSD			

Request Type	Action Unit		
CM		Priority L ○ ○ ○ H	☐ Request Complete

Job / Request Type			FPP Allocation	Status
○ Clan Lab	☐ Simple	☐ Admin/Tech	○ Unallocated	☐ Examination Complete
○ Illicit Drug	☐ Complex	☐ Cold Case	◉ Request	☐ Statement Complete
○ Trace Evidence	☐ Paternity	☐ Reporter	○ Ready	☐ Tech Review Complete
◉ Forensic DNA	☐ Coronial	☐ Reviewer		☐ Admin Review Complete
		☐ BioHazard		

Delivery Officer ID	Name	Station

Anti Tamper Seals	Return Property Point

Bring-up Date	Court Date	Court Type	Proceedings	Location

Comments

19/05/2022/KJM
Hello,
Could you please deliver exhibit barcode XXXXXXXXX to Forensic DNA Analysis please?
Thanks,
[redacted]

7873 characters left.

Figure 2 – Request to Forensic Property Point for delivery of exhibits

5 Examination

Sections 5.1 to 5.6 are relevant for all types of PM samples excluding reference samples (refer to 33800), refer to section 6 for individual sample examination requirements.

Perform the item exam procedure as detailed in QIS 33800 and refer to QIS 33798 for semen testing where required.

5.1 Description of PM packaging

1. Retrieve the PM samples from the freezer location and transfer to the evidence recovery laboratory.

2. Scan the barcode into the key identifier search icon, press enter or click search. Scroll to the exhibit movement table, track the samples to an examination bench.

3. Photograph the packaging ensuring the barcode is visible in all images (an additional close up image of the PM label may be necessary). Open the outer packaging and photograph the contents (containers, swabs or CSPBs etc.) and upload images to I:\FR Images (refer to QIS 33771 Appendix 1).

   Note: All contents are to be photographed regardless of whether they are being examined or not.

4. Scroll down to the exhibit analytical/testing table, click the create exhibit test icon.

5. In the Testing/Analysis table process field select item exam from the dropdown menu.

6. In the packaging and sample assessment notes field tick the "seal and packaging intact" box if this is the case. If the packaging and seals are not intact use the notes field to describe the nature of the packaging and seals. **Note:** The "sample meets requirements" box is specific to in-tubes and not to be used for item exam.

7. Describe any labelling on the packaging, if the photos are clear "labelled as per images taken by examiner" is acceptable. List the contents and for each item state whether it is to be examined or not.

8. Click on the save button.

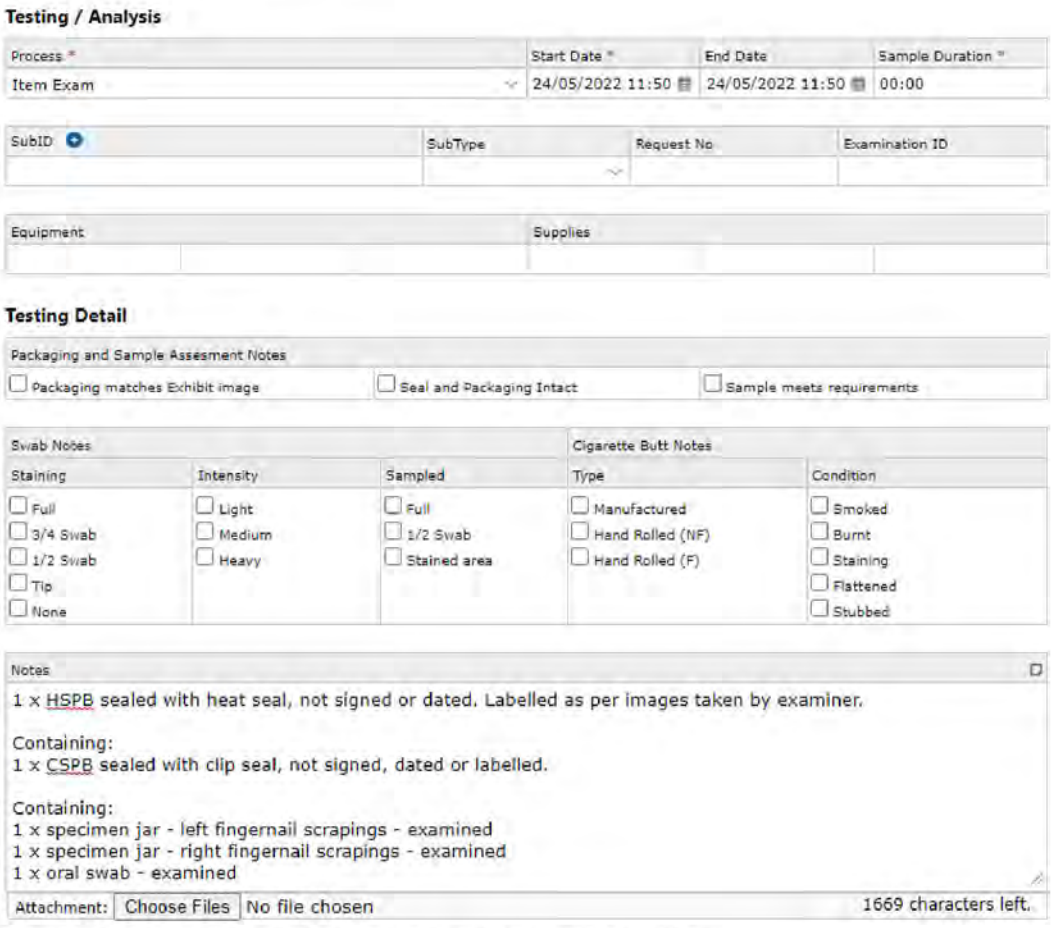
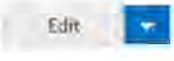


Figure 3 – Item exam packaging and contents description

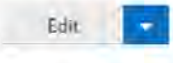
5.2 Creating an examination record and uploading images

1. Click the Examinations tab.
2. Click the add button.
3. Change the start time to a time before the images were taken. In the duration field add an estimate time for the examination.
4. The following check boxes must be ticked as this is required for compliance with software requirements: Examination location – General, Recording Method – Photo General (can tick Photo Explicit if images are of a sensitive nature) and No Case File.
5. In the Examination notes field type a summary of the PM samples packaging and contents including any samples that are not being examined such as unused swabs etc. **Note:** Abbreviations such as HVS or LVS cannot be used. Do not state "examined" or "not examined". The packaging/contents should match what is listed in the item exam.
6. In the exhibits examined field, scan the PM barcode.
7. Click on the save button.
8. Click the arrow 

icon next to the edit button and select upload files/images.
9. Alternatively scroll to the images table and click the upload images plus icon.
10. The examination file upload box will open, click the add files button 

.
11. Navigate to I:\FR Images and find the relevant packaging/contents images. Multiple images can be selected by holding down the Ctrl button. Click open.
12. Click the start upload button.
13. Once the images have uploaded click the save button.

5.3 Registration of PM contents – creating child/related exhibits

1. In the examination record, click the arrow 

icon next to the edit button and select add related exhibit.
2. Click the plus  icon in the forensic exhibit no field to auto assign a new barcode.
3. Choose the forensic category (e.g. fingernail scraping).
4. Type in the description (e.g. left). **Note:** Abbreviations must not be used and the description should not be a repeat of the forensic category.
5. The Located/Owner field will auto fill from the parent item, any information that is not required can be removed. Any additional details in the description field of the parent item must be manually transferred. The located/owner field should indicate ownership, for example "PM samples – name".

6. The parent barcode field will auto fill.
7. Tick the Admission/Intel and Sample has been collected in strict compliance with CSE101 Biological Evidence boxes.
8. Click on the save button.
9. To add more child exhibits, click the back button.
10. Click the plus icon in the forensic exhibit no field to auto assign a new barcode and edit the category and description of the 2nd child exhibit.
11. Click on the save button.
12. Repeat steps 9 – 11 for every component that requires examining.

These steps are not required for samples that do not require examination.

Note: To add an additional child exhibit after completion of the above steps, return to the Exhibit Record page for the exhibit, open the examination from the Examinations table, click the arrow Edit icon next to the edit button and follow the steps above.

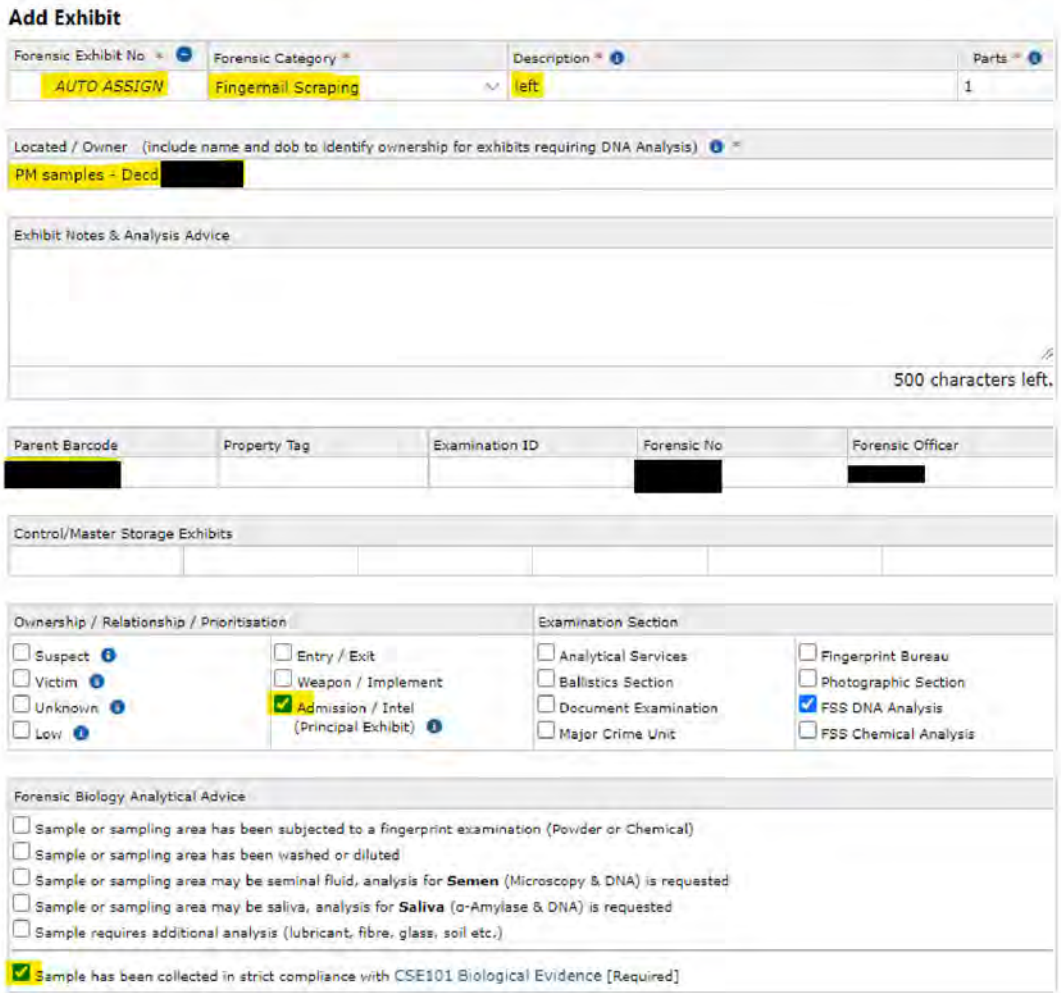


Figure 4 – Creating child exhibits

5.4 Creating sub-samples

1. Click the create exhibit test icon in the exhibit analytical/testing table and select subsample from the dropdown menu in the process field.
2. In the SubID field click the plus icon to auto assign a new barcode.
3. In the SubType dropdown list select MISC.
4. In the Notes field add a description of the subsample.
5. Click on the save button.
6. Repeat steps 1 – 5 for all subsamples as required.

5.5 Converting sub-samples to child exhibits

1. Click on the Exhibits tab and click the add button.
2. Enter barcode of the subsample into the Forensic Exhibit No field.

Note: A warning will display when a barcode has already been used (e.g. when upgrading a subsample to an exhibit).

3. In the Forensic Category field select the relevant subsample type from the dropdown menu.
4. Add a description of the subsample.
5. In the Located/Owner field, copy the relevant description from the parent item. Any additional details in the description field of the parent item must be manually transferred. The located/owner field should indicate ownership, for example "PM samples – name".
6. Add the parent barcode into the Parent Barcode field.
7. Tick the "Admission/Intel (Principal Exhibit)" and the "Sample has been collected in strict compliance with CSE101 Biological Evidence [Required]" boxes.
8. The examiner must enter their FR User ID in the Delivery Officer Rego field, press tab for the Surname field to auto-populate and select Queensland Health Scientific from the dropdown list in the Station field.
9. Click on the save button.
10. Repeat steps 1 – 9 for all subsamples if required.
11. Perform the item exam procedure as detailed in QIS 33800 and perform any necessary presumptive testing.

5.6 Exhibit result lines

Refer to QIS 33800 appendix 10.1 for specific result lines and add to child exhibits where necessary following the below process:

1. Click the create exhibit test icon in the exhibit analytical/testing table and select Result from the dropdown menu in the process field.
2. In the Police Report field select the appropriate result(s) from the dropdown menu (up to three results can be added at any one time).
3. Click on the save button.

Note: No result lines are required for bone/teeth samples.

5.6.1 Printing sample tube labels

1. On the exhibit record page click the arrow icon next to the edit button and select "3 Part Tube Barcode".

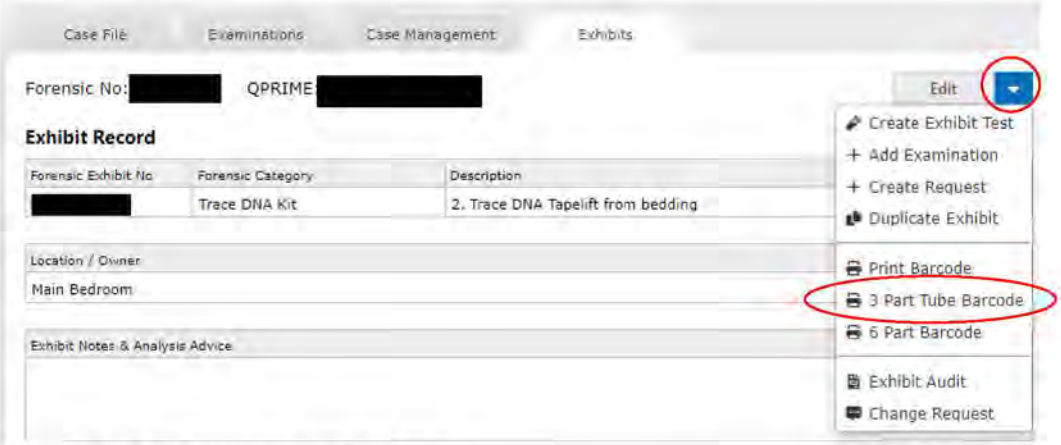


Figure 5 – Printing sample tube labels

2. A new window will open displaying the 3 part label, click the printer icon and select print.
3. To print a subsample barcode, click on the subsample hyperlink from the exhibit record page and follow the above steps.

6 Examination of samples for submission for DNA profiling

6.1 Swabs

Intimate swabs (i.e. those taken for a sexual offence including vaginal, anal and oral) are examined according to standard SAIK examination procedures including analytical note requirements (refer to QIS 33798).

6.2 Nails

Nails, nail clippings or nail scrapings will be collected from either the fingers, toes or both.

Nail scrapings are collected by using a wooden stick to scrape under each nail separately on the right side and the left side. All nails/clippings/scrapings from the left side are submitted to DNA together and all nails/clippings/scrapings from the right side are submitted to DNA together. Toe and fingernails/clippings/scrapings will be submitted separately.

1. Register the packaging (container or CSPB) as a related exhibit under the parent barcode as per section 5.3.
2. Photos of the packaging are to be taken and uploaded to the parent examination record. Images are not required to be taken of nails/clippings/scrapings unless there is something unusual present.
3. In the child item exam, describe the packaging and contents as well as a description of the contents including the number and size.
4. Note any staining to the nails/clippings/scrapings and perform representative TMB testing of red/brown staining if visible on more than one nail/clipping/scraping.
    a. If the same staining is visible on all nails/clippings/scrapings for the left or right side all nails/clippings/scrapings are to be submitted together.
    b. If TMB positive staining is present on two nails/clippings/scrapings but no staining is visible on the remaining nails/clippings/scrapings then two subsamples will need to be created and upgraded to exhibits for submission of "unstained" and "stained" nails/clippings/scrapings separately.

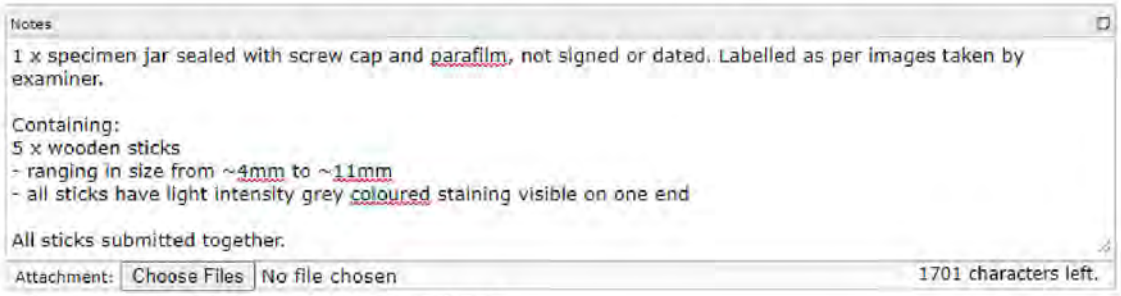


Figure 6 – Description of nail scrapings

If a portion of tissue is attached to a nail, a moistened swab can be used to sample potential foreign DNA from the underside of the nail, taking care not to sample the deceased person's tissue (i.e. targeting the distal end of the nail).

6.3 Examination of Tissue Samples

Tissue samples may include such things as flesh, muscle, organ, paraffin tissue blocks, products of conception or partial/intact foetuses.

If tissue samples are received within a bag of multiple samples follow all standard examination procedures as described above and in QIS 33800. Presumptive testing is not required on tissue samples.

Products of conception (POC) are to be examined only when directed by the Evidence Recovery Senior Scientist. A Forensic Pathologist should be made aware that they may be required to assist in the examination depending if any anatomical structures are visible. The preferred sample for submission is a ~5mm x ~5mm section of tissue and/or thigh bone avoiding any external tissue. Once the sample has been selected, it must be moved to fresh petri dishes and washed three times with nanopure water. The sample is to be registered and submitted as 'flesh'. Depending on the condition of the POC and any advice from a Forensic Pathologist, alternate samples may be required.

Note: For all tissue samples (with the exception of paraffin tissue), the validator is to select the extraction method "QIAsymphony Pre-Lysis" unless otherwise notified by the Analytical team. Paraffin tissue must have "Nucleopsin Tissue" selected in the method field.

To obtain the best possible DNA profile, the following needs to be assessed:

1. The smell of the tissue can determine decomposition (no odour is preferable, mild to strong odour indicates decomposition and is not recommended).
2. Colour of tissue (red to pink is preferable, brown to green indicates decomposition and is not recommended).
3. Tissue type (good quality muscle, organ tissue and flesh is preferable, cartilage and connective tissue is less preferable, fatty tissue should be avoided). Good success has been obtained from fingernails previously.
4. Assistance from a Forensic Pathologist can be sought if there is any uncertainty regarding products of conception. Liaise with the Evidence Recovery Senior Scientist to organise Forensic Pathologist attendance.

Note: This is a guide only, many environmental factors, possible tissue diseases and anatomical features can affect obtaining a DNA profile from tissue. If the tissue is poor quality and good quality bone is available from the same set of remains, bone should be submitted for DNA profiling in addition to the tissue.

6.4 Examination of Bone/Teeth Samples

To obtain the best possible DNA profile, the order of sample preference is as follows:

1. Adhering muscle tissue that is good quality and not decomposed.
2. Good quality compact bone.
3. Good quality, intact teeth with no fillings or caries (molar teeth preferable).
4. Good quality cancellous bone.

Note: This is a guide only, and many environmental factors and anatomical features can affect obtaining a DNA profile bone. If good quality tissue is available from the same set of remains, the tissue should be submitted for DNA profiling in preference to bone.

6.4.1 Sampling

1. Retrieve the sample, photograph the packaging and contents and add an item exam as per section 5.1. Describe the exhibit and details of sampling, including the number of bones, a description of the quality and level of decomposition, colour, size and remarkable features.

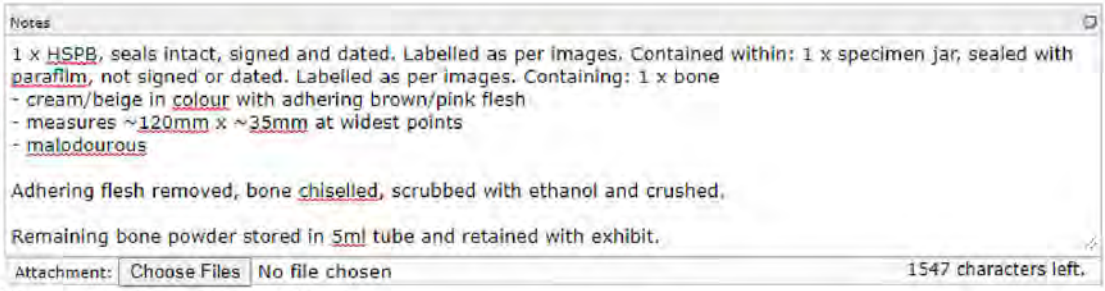


Figure 7 – Description of bone

2. Upload all images to the item exam.

3. Enter the freezer mill equipment number into the equipment number field in the item exam.

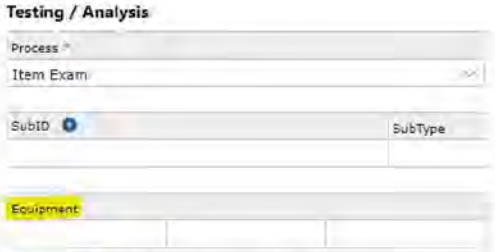


Figure 8 – Equipment field

Note: An examination record is not required.

If good quality muscle tissue is present this should be removed from the bone sample and submitted for DNA profiling.

Before crushing any good quality compact or cancellous bone, it must be thoroughly cleaned. This procedure is essential for obtaining a DNA profile.

De-fleshing is performed when any tissue not viable for DNA analysis, is adhered to the bone. Use a sterile scalpel to thoroughly remove all tissue down to the bone, including the periosteum, and bone marrow. Great caution should be taken to avoid injury, including always use the scalpel in a direction away from the hand. Sterile tweezers can be used to hold the bone firmly in some instances.

Ethanol scrubbing of the bone is performed on dry bones or de-fleshed bones to remove all fatty residue and potential contaminants prior to crushing. Place the bone in a petri dish with some ethanol (100%). Use a new toothbrush to thoroughly scrub all surfaces of the bone. Repeat this process, discarding the old petri dishes in a bio-hazard bin, until all fatty residue or visible contaminants are removed.

Bone cleaning using the Dremel® occurs after de-fleshing and ethanol scrubbing and is used to clean the bone of any potential inhibitors. This method should only be used if standard cleaning is not possible (bone sample is too small to safely handle) due to the heat produced by the Dremel®.

Place paper and the bone in the fume hood and plug in the Dremel® tool with the appropriate tool bit attached. Clean the bone in short bursts so as not to overheat the bone while removing the outer layer of all surfaces. Chiselling the bone into a few small pieces

first, may make cleaning easier, and allow access to all surfaces. Eye protection must be worn. A pair of forceps or mini long-nose pliers can be used to hold the bone firmly if required.

Chiselling the bone into small pieces is necessary to safely fit the fragments into the cylinder prior to bone crushing. Use the hammer and chisel to break the bone into pieces sufficient to fit into the crushing cylinder and still allow the impactor to fit. Each end of the bone/pieces must be chiselled off before transferring to the cylinder to minimise contamination. Wrap the bone sample securely in a rediwipe cloth to prevent escape of bone during chiselling. Care must be taken to avoid injury with the hammer and chisel during this process. Always ensure the bone is stable prior to striking it with the hammer and chisel.

Teeth - Prior to removing any good quality teeth from the jaw, or crushing any loose teeth, you must obtain permission from a Forensic Odontologist. Even single teeth can be used as an identification tool for Forensic Odontologists, who will require examination of the teeth prior to DNA sampling. Perform any de-fleshing, ethanol scrubbing, and bone cleaning on at least two teeth as described above. Carefully split the tooth into small pieces with the chisel, in preparation for bone crushing. All teeth can be crushed in the same cylinder, providing there is no indication they could have originated from different individuals.

6.4.2 Equipment control

Use a sterile swab lightly moistened with nanopure water to swab the inner facing surface of both bungs, inside the cylinder, and the impactor. Place the swab head into a labelled 2ml tube. One equipment control must be prepared for each cylinder set used.

6.4.3 Loading fragments into the cylinder

Fasten one bung into the end of the cylinder and place bone/teeth fragments inside. Caution must be taken to not overload the cylinder. The size and quantity of fragments should not prevent the impactor from moving freely to each end of the cylinder.

6.4.4 Operation of the Freezer Mill®

1. Fill the Freezer Mill® with liquid nitrogen (see appendix 9.1).
2. Ensure both bungs are securely fastened into the cylinder and insert the cylinder into the Freezer Mill® with the largest of the two bungs facing outwards.
3. Slowly close and fasten the lid and turn on the Freezer Mill®.
4. Select the Control Panel button and press the green Run button.

   The freezer mill will complete the following:

   - Pre-cool – 10 mins
   - Run – 30 seconds
   - Cool – 3 minutes
   - Run – 30 seconds
5. Upon completion, the display will indicate Run Complete. Switch off the power, slowly open the lid and use the cylinder extractor to remove the cylinder.

If during the Freezer Mill® cycle, unusual or inconsistent sounds occur at the crushing time, stop the program, turn off the Freezer Mill®, and inspect the cylinder. If the impactor has become jammed, remove the fragments from the cylinder. Reload the cylinder taking care with the size and quantity of fragments selected for crushing. If the cylinder has been damaged, it will have to be replaced and the Freezer Mill® will have to be decontaminated.

The lid of the Freezer Mill® can remain open to facilitate evaporation of remaining liquid nitrogen; however other Scientists working in the area must be warned.

6.4.5 Sub-sampling the powder

It is advisable to allow the cylinder to warm up for several minutes to reduce the pressure before attempting to open it. Fasten the cylinder extractor to the large bung and turn the handle clockwise as far as possible until the bung is released from the cylinder. Avoid moving the cylinder extractor side to side, as it will split and warp the cylinder. A thick padded glove must be worn on the hand handling the cylinder as the cylinder will remain cold and may cause injury. Empty the contents of the cylinder into a 5mL stock tube, this may be easier using a filter paper funnel.

Approximately 100mg of bone powder should be weighed into each 2mL tube. At least four sub-samples should be prepared from each crushed bone. Record the exact weight of each sub-sample in the FR.

6.4.6 Creating sub-samples

1. Click the create exhibit test icon in the exhibit analytical/testing table and select subsample from the dropdown menu in the process field.
2. In the SubID field click the plus icon to auto assign a new barcode.
3. In the SubType dropdown list select MISC.
4. In the Notes field add a description of the subsample the weight.
5. Scan the ERT-AS box barcode into the Storage Box ID field.
6. Scan the barcode affixed to the bag of tubes into the Tube Lot No field.
7. In the technique field select DNA Extraction.
8. In the method field select Organic Bone.
9. Click on the save button.
10. Repeat for further sub-samples.

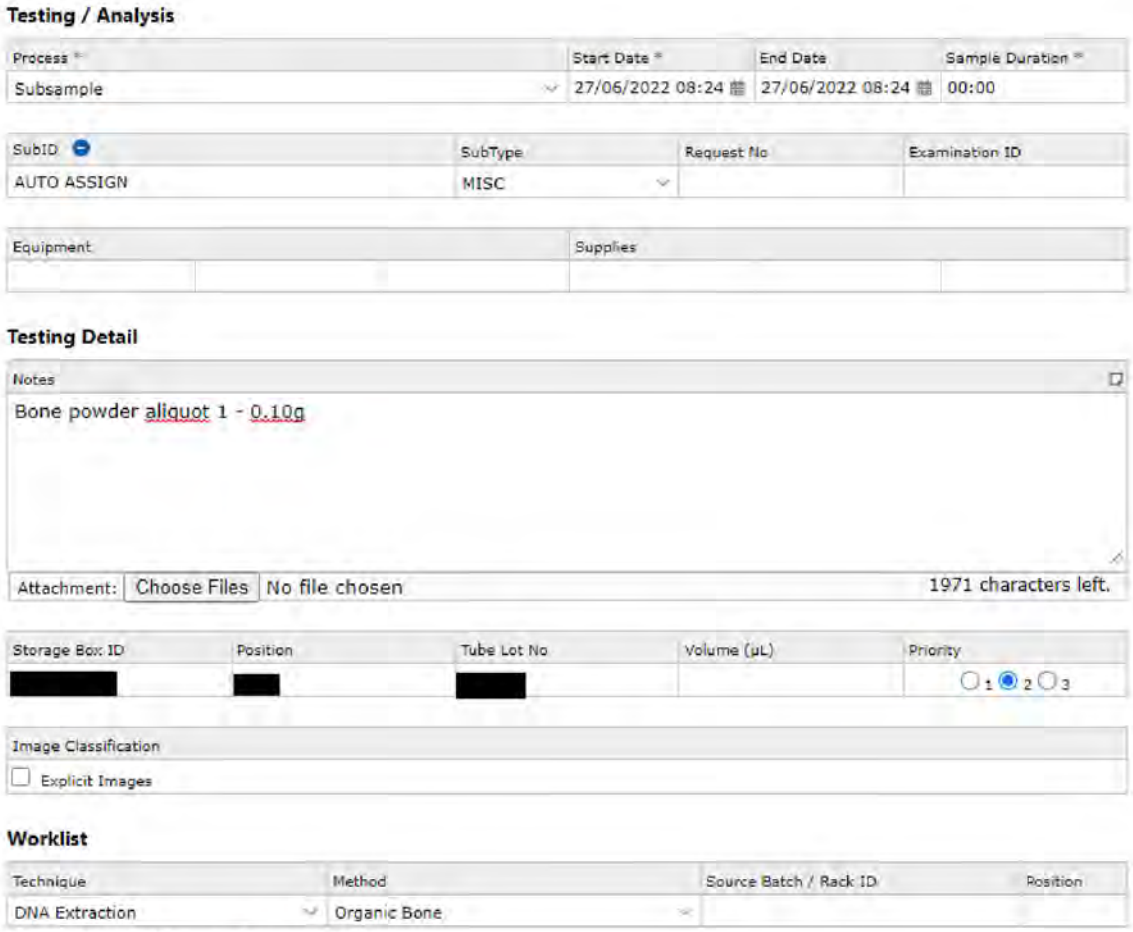


Figure 9 – Subsample creation

6.4.7 Registration of equipment control

1. Click the create exhibit test icon in the exhibit analytical/testing table and select subsample from the dropdown menu in the process field.
2. In the SubID field click the plus icon to auto assign a new barcode.
3. In the SubType dropdown list select MISC.
4. In the notes field add the description "Bone equipment control".
5. Click on the save button.
6. Click on the Exhibits tab and click the add button.
7. Enter barcode of the equipment control swab into the Forensic Exhibit No field.

Note: A warning will display when a barcode has already been used (e.g. when upgrading a subsample to an exhibit).

8. In the Forensic Category field select 'Control Sample' from the dropdown menu.
9. Add "bone equipment control" in the description field.

10. In the Located/Owner field, copy the relevant description from the parent item. Any additional details in the description field of the parent item must be manually transferred. The located/owner field should indicate ownership, for example "PM samples – name".
11. Add the parent barcode (bone) into the Parent Barcode field.
12. Tick the "Admission/Intel (Principal Exhibit)" and the "Sample has been collected in strict compliance with CSE101 Biological Evidence [Required]" boxes.
13. The examiner must enter their FR User ID in the Delivery Officer Rego field, press tab for the Surname field to auto-populate and select Queensland Health Scientific from the dropdown list in the Station field.
14. Click on the save button.
15. Scroll down to exhibit analytical/testing table, Click the create exhibit test icon.
16. In the process field select Analytical Note and in the notes field add "Equipment Control".
17. Scan the ERT-AS box barcode into the Storage Box ID field.
18. Scan the barcode affixed to the bag of tubes into the Tube Lot No field.
19. In the technique field select DNA Extraction.
20. In the method field select Organic Bone.
21. Click on the save button.

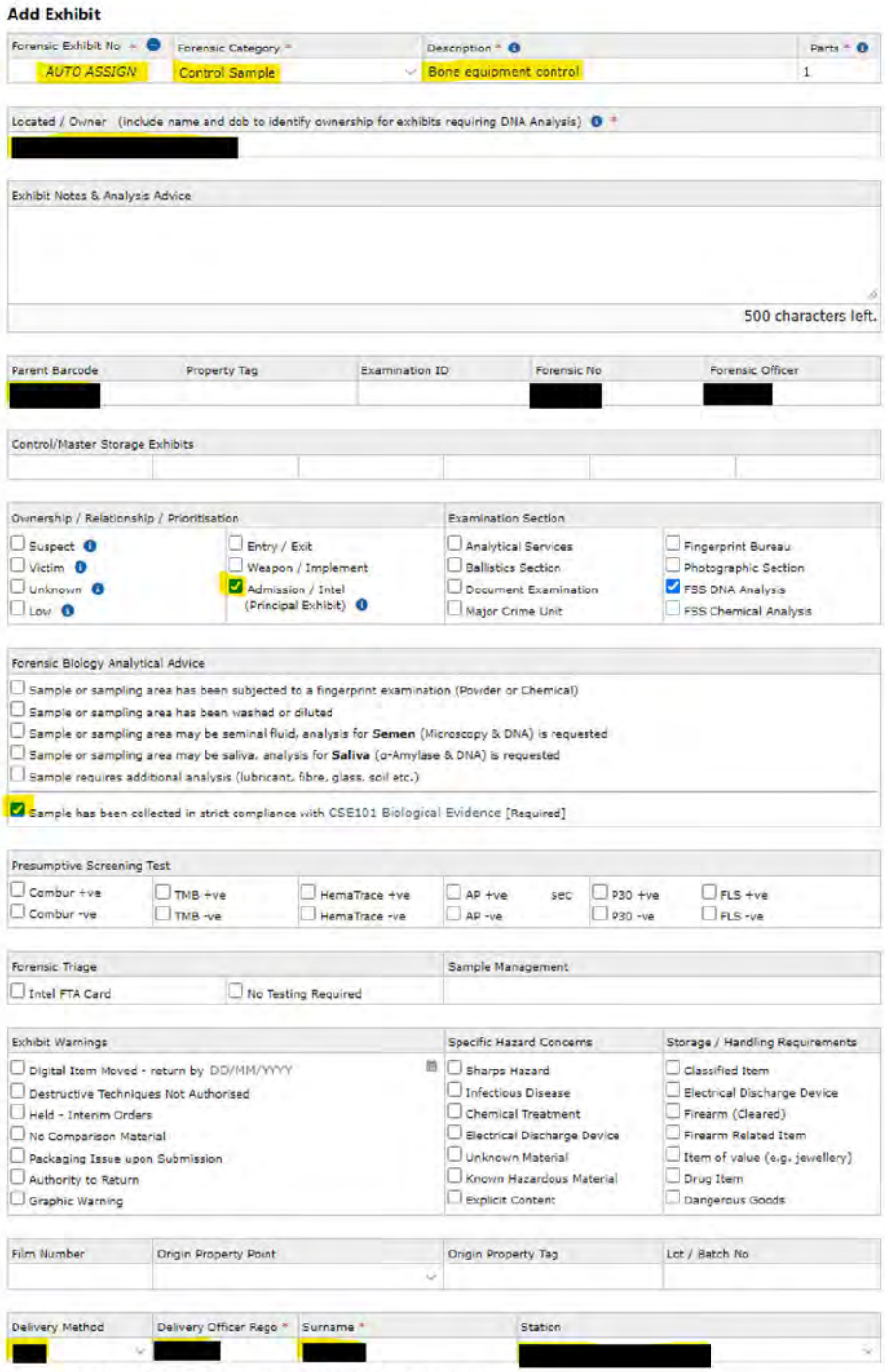


Figure 10 – Equipment control registration

6.4.8 Finalisation

1. Refer to section 5.6.1 to print labels.
2. Scroll down to the exhibit analytical/testing table and click on the date/time hyperlink of the item exam.
3. Click the edit button.

4. In the notes field add details of any bone stock powder remaining, or if the crushed bone powder has been exhausted (see Figure 10).
5. Click on the save button.
6. Return the sample to the original packaging and return to freezer returns via exhibit movement.
7. Transfer the ERT-AS transfer rack to the hatch in extraction sorting.

7 Associated Documentation

QIS: 17185 – Detection of Azoospermic Semen in Casework Samples
QIS: 17186 – The Acid Phosphatase Screening Test for Seminal Stains
QIS: 17189 – Examination For & Of Spermatozoa
QIS: 17190 – Tetramethylbenzidine Screening Test for Blood
QIS: 22857 – Anti-contamination Procedure
QIS: 23849 – Common Forensic DNA Analysis Terms and Acronyms
QIS: 23945 – Workplace Health and Safety in DNA Analysis
QIS: 23959 – Storage Guidelines for Forensic DNA Analysis
QIS: 29696 – Taking DNA Samples at Coronial Autopsy: Guidelines for Pathologists & Mortuary Staff
QIS: 30355 – Operation of ELSA
QIS: 33771 – Examination of In-tube samples
QIS: 33798 – Examination of Sexual Cases
QIS: 33800 – Examination of Items

8 Amendment History

QIS² Edition			
Version	**Date**	**Updated By**	**Amendments**
1	18/07/2017	A Ryan & A McNevin	First issue.
2	30/01/2019	C Savage	Added step 3 in section 5.1.4. Amended screen shots. Amendments to reflect changes in processes. Added 5.1.9 Analytical notes.
3	12/10/2020	A Ryan & A McNevin	Amendments to reflect change in cleaning procedures. Unnecessary screenshots removed. Updated freezer mill model number and operating instructions.
4	27/06/2022	K Morton	New template, general content updating and formatting. Addition of general coronial information, requesting testing requirements including addition to on-hold worklist, request to deliver samples from FPP. Added basic examination notes for nails/scrapings/clippings. Removal of examination record for bone examinations, added teeth and POC sampling.

9 Appendices

Appendix 1: Procedure for safe handling of Liquid Nitrogen
Appendix 2: Decontamination and maintenance of bone/teeth sampling instruments

9.1 Appendix 1: Procedure for safe handling of Liquid Nitrogen

Handling of liquid nitrogen must only be performed by trained staff who have completed the relevant training and are deemed competent.

Any injuries or near misses that occur when handling liquid nitrogen must be adequately recorded and reported as per standard procedures (QIS 23945).

9.1.1 PPE required

The following protective equipment must be worn (some items are found in the "Liquid Nitrogen" box in the bone sampling room) and all bare skin covered:

1. A lab coat fastened at the front, with sleeves rolled down for dispensing from the main vessel. A standard PPE gown is sufficient when handling occurs within the lab.
2. Thick, padded safety gloves.
3. Fully closed in shoes.
4. Protective face shield.

9.1.2 Refilling dewars from the main Liquid Nitrogen vessel

Two staff members (one to refill, one to observe) must always be present during dewar refilling for workplace health and safety. Both staff must have completed the safe liquid nitrogen handling training.

A key for the gate padlock to access the main liquid nitrogen vessel is located with Security. Staff members are required to sign for access to this key (Key 78). **Note:** The gate should always be locked, except when refilling the dewar. The area should not be left unlocked and unattended at any time during refilling of the dewar. The dewar is transported to and from the main liquid nitrogen vessel using a trolley.

Place the main vessel liquid nitrogen nozzle inside the dewar and turn on the main valve. The flow of liquid nitrogen into the dewar should be steady enough to allow an adequate quantity of liquid nitrogen into the dewar without significant evaporation. If the flow is too hard, liquid nitrogen will spurt from the top of the dewar, in which case the flow should be reduced.

To reduce evaporation during refilling, keep the main liquid nitrogen nozzle below the liquid nitrogen level in the dewar. To determine the level of the liquid nitrogen in the dewar, move the main vessel liquid nitrogen nozzle above the liquid nitrogen level in the dewar. This can be ascertained by a change in the filling noise made by the main liquid nitrogen nozzle. Fill the dewar to approximately 4/5 of its capacity. If the dewar is over-filled, the lid of the dewar will not fit on securely (the lid allows for the dissipation of air. The nozzle hose should always be held during this process.

Note: During the filling process, the observing staff member must stand clear of the area to avoid potential contact with the liquid nitrogen, and inhalation of nitrogen gases. The person refilling the dewar must avoid inhalation of vapours by positioning themselves upwind. The main valve must be turned off immediately if either person is being overcome by the nitrogen gas.

Once the dewar is filled to the appropriate level, turn the main valve off tightly and return the main vessel liquid nitrogen nozzle from the dewar to the nozzle holder. Replace the dewar lid and lock the gate to the main liquid nitrogen vessel area. The staff member transporting the dewar back to the laboratory must continue to be escorted by the observing staff member.

9.1.3 Filling the Freezer Mill® with Liquid Nitrogen from the Dewar

The Freezer Mill® should always be filled on the floor or on the bench. The Freezer Mill® should never be filled on a chair, or any unstable surface.

Other Scientists in the vicinity must be warned to stand clear during pouring of the liquid nitrogen. Fill the Freezer Mill® to the level indicated, insert the cylinder and slowly secure the Freezer Mill® lid (close the lid slowly to avoid spurting of liquid nitrogen onto the floor/bench). Return the lid to the dewar and store the dewar in an appropriate location free from any traffic. Return the closed Freezer Mill® to the dedicated bench if required.

Warning: Never lift the Freezer Mill® from the floor to the bench with the lid open or unsecured. Always be careful when lifting the Freezer Mill® that liquid nitrogen does not leak out the rear vent – the Freezer Mill® is not a closed vessel.

The bone preparation laboratory is fitted with a low oxygen alarm that will sound if oxygen levels drop below safe levels. If this alarm sounds, exit the laboratory immediately and do not return until the alarm stops sounding, and oxygen levels return to safe levels. Under exceptional circumstances, it may be necessary to enter a low oxygen environment. In which case, the ELSA located outside of the bone preparation laboratory should be used (refer to QIS 30355 – Operation of ELSA).

9.2 Appendix 2: Decontamination and maintenance of bone/teeth sampling instruments

Standard laboratory personal protective equipment (PPE) including enclosed shoes, gloves, hair net, mask, gown and goggles must be worn during cleaning procedures.

The "Prior to Use" procedures must be done on the day that the bone is to be sampled. This reduces the risk of contamination of the instruments with environmental DNA.

Any injuries or near misses that occur when using bone sampling equipment must be adequately recorded and reported as per standard procedures (QIS 23945).

9.2.1 Chisels, hammers and chisel blocks

Prior to and after use: Chisels, hammers and chisel blocks need to be thoroughly cleaned with viraclean, bleach and ethanol.

Maintenance: If the chisel requires sharpening after use, wet the sharpening stone with mineral oil and sharpen tip, rinse with water, and dry. The chisels should be replaced with new ones if the metal surface becomes rusty or eroded, or if the tip can no longer be sharpened sufficiently. **Note:** To avoid injury, be very careful when handling sharp chisels.

9.2.2 Bungs, Impactors and Freezer Mill Cylinders

Prior to use: Bungs, impactors and cylinders are to be cleaned using the Miele dishwasher.

Check the dishwasher is available for use and access the tub labelled BONE in kit room.

Load the bungs and cylinders into a (shallow) rack. Load a pair of forceps, and the rods into the wire basket.

Set the dishwasher to SPECIAL 93C-10' cycle and select the drying button (middle button). Press the green button to start the clean. Refer to figure 2 Dishwasher display.

Affix the "BONE EQUIPMENT " tag onto the front of the dishwasher using the Velcro dot.

Once the cycle is complete place a set (two bungs, cylinder and rod) into an individual CSPB using the forceps. Transfer into the bone room and place in the "Clean Bone Equipment " container ready for next use.



Figure 11 – Dishwasher display

After use: Rinse thoroughly using tap water and a toothbrush to remove all visible bone powder and place in "Bone equipment for cleaning" container. When several sets are collected perform a dishwasher run.

9.2.3 Hand Saw and Bosch® Electric Saw and Blade

Prior to and after use: Clean the hand saw components with viraclean, bleach and ethanol. Take caution when dismantling bone saw. The outer casing of the Bosch® electric saw needs to be thoroughly wiped down with ethanol. Take caution not to wet the inside components. Use the allen key to remove the Bosch® electric saw blade. Clean the blade with viraclean, bleach and ethanol. The blades should be stored immersed in mineral oil (e.g. in a large petri dish) to prevent corrosion.

Maintenance: When the blade of the saw requires sharpening, alert Forensic Pathology staff who will organise a contractor to sharpen all surgical saws.

9.2.4 Dremel® Tool and Bits

Prior to and after use: The outer casing of the Dremel® tool needs to be thoroughly cleaned with alcohol. Take caution not to wet the inside components of the Dremel®. In addition, wipe down the collet and fastener after use when the tool bit is removed.

Use the Dremel® wrench to remove the Dremel® tool bit. Thoroughly scrub the Dremel® tool bit (especially the grooved portion) with a toothbrush, rinse thoroughly with tap water and dry.

The bits should be stored immersed in mineral oil (e.g. in a large petri dish) to prevent corrosion.

Maintenance: The Dremel® tool bits should be replaced with new tool bits when the metal surface becomes rusted or eroded.

CA-73

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Examination of Items

1 PURPOSE

To describe the procedure for the examination of evidentiary items by case examiners in Forensic Biology.

2 SCOPE

This standard operating procedure is an adjunct to individual methods for particular screening tests. Interpretations and limitations of reporting are to be found in each method.

3 ASSOCIATED DOCUMENTS

[redacted]

Anti Contamination Procedure
Procedure for Case Record Documentation and Evidence Management
Tetramethylbenzidine Screening Test for Blood
The acid Phosphatase Screening Test For Seminal Stains
Examination For & Of Spermatozoa
Detection of Azoospermic Semen in Casework Samples
Phadebas Test For Saliva
Procedure for Basic Hair Screening
Handling and Analysis of Syringes and Needles
Digital Imaging in Forensic Biology
Procedure for the Retention and Storage of Items
AUSLAB Users Manual – Forensic Biology

4 REFERENCES

Monahan, DL and Harding, HWJ (1990) Damage to Clothing – Cuts and Tears. *J For Sci* **35**:901-912

5 CASE FILE DOCUMENTATION

- Refer to [redacted] (Procedure for Case Management) for details on case file components and item identification.
- All items must be uniquely identified.
- All notes must be legible and in ink. Diagrams and sketches must also be in pen. Areas of interest may be highlighted with colour pencils.

Not Current

- Use standard abbreviations such as:

  - BPB brown paper bag
  - HSPB heat sealed plastic bag
  - CSPB clip seal plastic bag
  - CSSE crime scene sample envelope
  - watb what appears to be

  Refer to 23849 (Common Forensic Biology Terms and Acronyms) for a comprehensive list of abbreviations.

- Where possible a scale should be included in any photographs to provide a size estimate of the exhibit.

- Errors must be crossed out, initialled and dated.

6 CONTINUITY OF EVIDENCE

- Refer to 17167 (Procedure for the Retention and Storage of Items) for further information.

- Use the transfer function in AUSLAB to record the removal of items from storage and their subsequent storage location, for example, team trolley, returns box.

- Record details of the packaging in the case file including labelling and nature of seals.

- Where possible, open packages in such a way that original seals are maintained. Sign and date where you have opened the package.

- Items are not to be left on benches unattended for extended periods of time. Each case analyst has access to a secure area in the exhibit room where items undergoing examination can be stored.

7 ANTI CONTAMINATION PROCEDURES

- Health and Safety protocols must be followed. Full personal protective equipment (PPE), including gown, gloves, cap and mask, must be worn when entering an examination area (that is an area delineated by a yellow line).

- Benches and large examination tables must be cleaned prior to examination with sodium hypochlorite solution (bleach) and ethanol. Benches can be covered with brown paper as long as this is changed between items.

- Examine only one item at a time ensuring the bench is cleaned with bleach and ethanol before each examination or for small items place brown paper on bench and change after each item.

- Scissors, forceps and scalpel holders must be cleaned thoroughly by flaming with alcohol before coming into contact with items of evidence and between excising stains from the same item. Disposable scalpel blades should be used wherever possible as flaming of scissors can affect the cutting edge.

- Plastic formers used for stretching items of clothing and for separating front and back surfaces must be cleaned with bleach and ethanol before and after use.

No Current

- Cap sample tubes immediately after placing each sample inside.
- Equipment not required or in use should be cleaned and put away and the work surface kept clutter-free.
- Heavily stained items should be handled carefully to minimise the spread of aerosolised particles.
- **Items attributed to the complainant and those attributed to the suspect must be examined on different benches to avoid the possibility of contamination.**
- Record the bench location and examination trolley/box of the examination in your notes and in AUSLAB.
- Items should be repackaged as soon as possible after examination.

8 CHARACTERISATION OF BIOLOGICAL MATERIAL

Biological material should be characterised where possible prior to DNA analysis. Where a case examiner elects not to perform a screening test on an item it must be because the screening test will consume the evidence. The case notes must indicate why characterisation was not performed.

9 GENERAL EXAMINATION PROCEDURE

- Read the associated case details, such as the [redacted] medical notes, documented communications with FSLU, IO, QPS Scientific or Scenes of Crime case conferences etc. before starting to be certain of the circumstances of the case and the types of examination required and the focus of the examination. The forensic relationship for each item and the EXR results case status, Police priority field and UR notes should be checked to see if testing is still required. Prioritise the order of examination of items accordingly. Where required the case scientist may provide specific guidance to the examining scientist. This is generally contained within the minutes of the case file or in the UR notes. Contact the investigating officer or the QPS DNA Unit for further information or have your FSLU representative gather further information if necessary.
- The aim of a volume crime examination is to get maximum result from as little sampling as possible i.e. sample blood in preference to cells and in general only one swab from all blood cases. Refer to **Appendix 2**:Volume Crime Sampling Flowchart.
- Examination notes must be made on standard examination forms found in QIS. Examination notes must be completed at the time of examination whilst still in the examination area. Registration of samples should be completed as soon as possible after examination is complete to minimise the chance of errors.
- Describe the outer packaging noting any labelling and the nature of the seals on form 22870 Outer Packaging Record or 17033/4 General Examination Record.

  Example: **1 x HSPB with exhibit tag '[redacted], Det [redacted], [redacted] Rec'd 11:00 1/1/05", heat seals intact.**
- List the details of the packages contained within the outer packaging.

  Example: **3 x crime scene sample envelopes**

2 x BPBs
1 x yellow OHMS envelope (A5 size)
1 x yellow OHMS envelope (A4 size)
1 x property tag (A12345)

- With the exception of SAIKS, all items should be barcoded. An FBFB should be requested for improperly labelled or packaged items. (Refer to 16004 AUSLAB Users Manual for requesting an FBFB). Refer to **Appendix 4**:Registration of SAIKs or Multiple Items.

- Photocopy the packages contained within, showing the labelling and barcode if possible.

- Describe the packaging of the item to be examined, noting any labelling and the nature of the seals.

Example: **1 x BPB, labelled in part "[redacted], 1 x red shirt, item 24", evidence tape seal intact, signed and dated.**

- All QPS packaging should be photographed. Refer t[redacted] (Photography of Exhibits in Forensic Biology).

- Open the package in such a way that original seals are maintained. Sign and date where you have opened the package.

- Give a detailed description of the item contained within, examining both the inside and outside surfaces. Note measurements where necessary.

Example: **1 x red tartan shirt**
"XYZ" brand, size 12
long sleeved, button up shirt
brand logo on left chest area

- If there is some indication that the item is to be fingerprinted, keep all handling to a minimum. Avoid touching the item where fingerprints are likely to be found.

- Describe the condition of the item, noting areas of damage. An attempt may be made to assess if the damage is due to wear and tear or the application of force. An attempt may also be made to assess if the damage is old or new, e.g. fraying indicates the damage is not recent. A study by Monahan and Harding classifies damage based on two criteria:
  - The appearance of matted and tangled fibres at the ends of cut yarns indicated that the garment had been washed since the damage occurred.
  - If the fibres at the end of cut yarns are still completely "in line", perhaps slightly frayed, then "recent" could mean that the garment has not been worn to any great extent since being damaged.

- If appropriate, take an overall photograph of the item including the identifying barcode and a scale.

- Extraneous surface material such as hairs, glass fragments, fibres and vegetation may be easily lost from an item. Such material should be collected into separate labelled CSPBs or Petri dishes using sterile forceps. The location of these must be recorded on the examination sheet. Following examination repackage the CSPB containing the material with the item.

- Make note of any items or staining found within pockets.

- Record all areas of staining on the item and include diagrams or photographs.
- Describe stains as accurately as possible with relation to:
  - Shape (smear, circular etc)
  - Size
  - Colour
  - Intensity
  - Distribution
  - Which side the staining appears to have originated on and whether it has soaked through to the other side.
- Perform presumptive tests and confirmatory tests (if applicable). Circle those areas giving a positive reaction using a chinagraph pencil or felt tip marker.
- The examiner must not positively identify substances, objects or stains that are outside their area of expertise. If a confirmatory test is not available to positively identify a substance such as mould the examiner must state in the examination notes "what appears to be (or WATB) mould".
- Those areas that will be sub-sampled and submitted for DNA analysis are assigned unique barcodes.
- Take a close up photograph of those areas to be submitted for DNA analysis. Include a scale and the sub-sample's unique barcode. If the scale is reusable make sure to clean before and after use.
- A swab moistened with 70% EtOH or distilled water can be used to sample stains on solid substrates such as weapons and items of footwear. Write in your examination notes whether EtOH or water was used. (Note: 70% ethanol swabs are best used when the item is on a solid substrate, water is best used when transfer of the stain could be difficult e.g. suede shoes, absorbent substrates)
- The size of the sample that is submitted for DNA testing is dependent on the intensity and type of the stain. If at all possible, attempt to leave part of the staining on the item in case re-examination is required. (Only 1-2cm^2 stained fabric, or ¼ - ½ a swab should contain enough DNA when the item is heavily stained. It is recommended that all of the outer part of the swab be submitted for cells when sampling handy DNA)
- Excise the area using sterile forceps and a disposable scalpel blade. Place the sub-sample into a sterile 1.5mL tube which is then placed into a labelled 5mL tube. The tube must be labelled with the barcode, a short description of the sample, the extraction type to be performed, and the scientist's initials and the date. It is also an option to submit subsamples in 2 tubes – one half of the stain cut and placed into a 1.5mL tube inside a 5mL tube and the other half of the stain in a 5mL tube which will be archived. In the 9Plex page in AUSLAB enter "2x" in the processing comment.
- If the item appears to be expensive or it has been requested that the item be returned to the complainant, stains may need to be removed in such a way as to minimize damage to the item. If this is the case it may be more practical to swab the item or perform a superficial scraping on the area.
- Repackage the item in its original packaging and seal the opening. Ensure that potentially dangerous items, eg. a knife, are repackaged safely with appropriate warnings.

- Continue the examination of other items, cleaning the bench and utensils with bleach and ethanol between each item.

- When examination of all items is complete, repackage all items together in a clean BPB. Label with the relevant exhibit tag label and seal with evidence tape, signing and dating across the seal.

- If not all items are examined, make note of the barcodes and comment that they were not examined at this time and why.

10 SPECIFIC EXAMINATION PROCEDURES

10.1 Examination for epithelial cells

- Generally only a small number of epithelial cells are deposited by touching or wearing items. It is best to try to concentrate those cells into as small amount of substrate as possible. It is best to use one side of a swab or a piece of tape no more than 2cm long to collect for submission. Generally armpit areas, collars, waist bands, hat bands and other parts of clothing that are in constant contact with the wearer are good areas to sample.

- Suspected epithelial cells on items can be collected for DNA analysis by scraping the area with a scalpel blade (best used on loose weave clothing fibres such as cotton or wool) or by tapelifting using small pieces of adhesive tape. If using the adhesive tape method, ensure to use a newly exposed part of adhesive, press the tape to the item until the tape's adhesive properties are lost. Alternatively, the area may be excised and submitted.

- Submit these items for DNA analysis in a sterile 1.5mL tube within an appropriately labelled sterile 5mL tube. The tape should be curled and placed in the tube sticky side inwards. Do not cut the tape into small pieces.

- Saliva stains are detected and characterised using the Phadebas Test (See [redacted] for further details).

10.2 Examination of Swabs

- Blood, Cells & Semen are often submitted on a Swab. Refer to the Examination For and Of Spermatozoa ([redacted]) for further details of Examination of a Semen or Sexual Assault Swab.

- Record the amount of the swab that is stained, the colour, the stain intensity and the amount of the swab that is submitted for DNA analysis.

- A specific Form is available for recording the examination of swabs ([redacted])

10.3 Examination of Gloves

- When a glove or pair of gloves is received it should be described as to which side is the outside and which side is the inside. If not known, assign a side based on how the glove was received.

- A swab (for latex or vinyl gloves) or tapelift/scraping (leather, fabric) should be prepared from the inside of each glove (a separate swab for each hand). Where the inside is not known both the inside and the outside should be sampled (a total of 4 separate samples for a pair would be submitted).

- The fingertip area and the palm area are good areas to sample.

10.4 Examination of Clothing/Shoes/Footwear (For Examination of Clothing refer to 9 General Examination Procedure)

- Describe the item as per clothing examination. The straps of thongs or sandals, the heel and toe area of socks and shoes are generally good areas to sample.

10.5 Examination of Bottles/Straws/Ice cream Sticks

- Ice-cream sticks should be sampled at both ends
- Bottles/Drink containers should be sampled around the neck or opening of the bottle/container and also in the thread under the cap.
- Straws should be sampled at both ends unless it is clear which end has been in the mouth (eg lipstick present).

10.6 Examination of Food

- Examine the food item for possible bite marks.
- Describe the food item and the amount of the food item remaining
- Sample the area around the region that appears to have been consumed with a swab moistened with water. Alternatively, scrapings or excision can be used. Generally this area has the greatest contact with the mouth. Gum and lollies can be put directly in a tube and extracted using a nucleospin extraction method (NUCC).

10.7 Examination of Hats/Balaclavas

- Describe the item as per clothing examination
- Hats – Tapelift (fabric) or Swab (leather) the sweat band, look for any hairs and examine under microscopy for their suitability for further analysis.
- Balaclavas (including stockings used as balaclavas) – If there is an identifiable mouth area tapelift or perform a scraping (cells). If there is no identifiable mouth area Phadebas testing of the whole item (inside and out) may be required to locate the area to sample.

10.8 Examination of Cigarette Butts and other small items for saliva

- Cigarette butts, envelope seals or stamps, swabs from drink containers and swabs from spitting cases are submitted for DNA analysis without screening for saliva. The supernatant for these samples may be retained at the extraction stage for future Phadebas testing if required. The request for retention of the sample supernatant for Phadebas testing must be entered into the Processing Comment on the relevant 9PLEX page. The 5ml tube should also have a red dot sticker placed on the lid, and the sample needs to be inserted onto the SALIVA worklist.
- When examining cigarette butts, indicate whether or not the cigarette appears to have been smoked, whether it has been stubbed/flattened and any brand names visible on the butt. Excise the filter paper from the butt using a scalpel blade. A specific form is available for recording the examination of cigarette butts [redacted]

Not Current

10.9 Examination of fingernails

- Fingernails or fingernail scrapings are examined to find blood or cells on or under the nails. Clippings, loose scrapings, scrapings on swab sticks or complete nails may be submitted.
- Fingernails or fingernail scrapings can be examined under the low power microscope if required.
- Describe the fingernails in terms of number, size and any visible staining.
- Submit these items for DNA analysis (noting if all or some submitted). Try to avoid submitting the swab stick as the chemically treated pine may inhibit PCR.
- Pool all samples for each hand, ie. all samples from the left hand together and all samples from the right hand together. Unless the cases requires to see which finger was used in digital penetration.

10.10 Examination of weapons/tools

- Handle any weapons with extreme care.
- Describe the weapon in detail including such things as the nature of the cutting edge, e.g. serrated, and the positioning of the blade within the handle, e.g. the blade may be bent from its normal position. Include measurements of the length and width of the weapon, and maximum width of blade.
- Examine the weapon for hair, blood and other biological material. The handle of the implement should be sampled for cells in an attempt to identify the person holding/using the weapon.
- Mark the position of bloodstains with a felt tip marker, particularly where the stain is likely to be swabbed off completely during testing.

10.11 Examination of condoms

- When a condom is received it should be described in terms of which side is the outside and which side is the inside upon receipt.
- Describe any fluid that may be present on or within the condom.
- Perform presumptive and confirmatory tests as necessary.
- Swab both the inside and outside with **separate** sterile swabs and submit for differential lysis extraction. Refer to appendix 6 on how to register samples for differential lysis extraction.

10.12 Examination of Syringes

- Specific Syringe Handling Kits are available to make this process as safe as possible. Refer to [redacted] Handling and Sampling of Syringes and Needles.

10.13 Examination of Urine

- Urine identification is not performed in this laboratory however the presence of urine can be inferred based on the visualisation of pale yellow staining in visible light, the fluorescence of urinary pigments under ultraviolet light, and by its characteristic smell.
- Samples may be submitted for epithelial cells. Urine samples are not generally tested by this laboratory.

Not Current

10.14 Examination of Faeces

- Faecal identification is not performed in this laboratory however the presence of faeces can be inferred based on the visualisation of brownish staining in visible light and by its characteristic smell.

- Faecal samples are not generally tested by this laboratory. Success has been achieved through mitochondrial DNA profiling, a technique not performed within this laboratory.

10.15 Examination of Vomitus

- Vomitus identification is not performed in this laboratory however the presence of vomitus can be inferred based on the visualization of staining in visible light and by its characteristic smell.

- Vomitus it is not generally tested by this laboratory.

11 FURTHER INFORMATION REGARDING EXHIBITS FOR EXAMINATION STRATEGY

11.1 Forensic Relationship

The Forensic Relationship field is given by QPS to indicate the relationship between the exhibit and the case, and where the exhibit appears to have originated from.

The Forensic Relationship of an exhibit can be viewed in two ways:

i. In the SF9 Summary Page of a case, listed in the "Relation" column.
ii. On the EXR page of the exhibit, listed in the "For Relationship" field.

Definitions:

S: Item/sample is believed to have originated from the **suspect**
V: Item/sample is believed to have originated from the **victim**
E: Item/sample is from a known source, to be used as an **elimination** sample
X: Item/sample is has been found/originated from the point of **entry/exit**
W: Item/sample is believed to have come from/been used as a **weapon**
A: This item sample has been identified as a key sample of interest and is preferred to be sampled due to **admission/ intelligence** value

The Forensic Relationship field can be used to help prioritise the examination of exhibits for a case based on where QPS believe they have originated from, or who they believe is the source of any DNA on the exhibit.

11.2 Additional Sample Information

Information given by QPS regarding the exhibit is transferred into the sample information field of the exhibit in AUSLAB. However, if there is too much information to fit into the sample information field then this information is also transferred into the clinical notes of the exhibit.

11.3 Screening Tests

Results of any screening tests conducted by QPS will be transferred into AUSLAB into the sample information field of the exhibit, and the clinical notes if required.

<u>TMB screening:</u>

Not Current

In cases where the sample information field for an exhibit indicates a positive TMB screening test result conducted by QPS but does not visually have the appearance of blood, the scientist will not perform additional screening tests. The scientist will submit the sample directly for DNA profiling without performing a presumptive screening test for blood.

Acid Phosphatase screening:

On items where QPS have performed a screening test for the presence of seminal fluid QPS are to provide accurate details of positive AP reaction times and mark the precise areas that gave a positive reaction. The scientist will only perform further presumptive screening tests if the case information changes or if the initial testing fails to confirm the presence of spermatozoa and further testing is therefore required.

12 ITEM NUMBERING

1 Each evidence item must be assigned a unique number (referred to as the sample ID).

The standard numbering system used in Forensic Biology is to use a unique barcode. Any sub samples of this item will also be given a unique barcode however a reference numbering system is also used to relate a particular item or subsample back to the receipt barcode it was received under.

Eg. If 3 items are received under Receipt Barcode [redacted] the following numbering system applies:

1st item [redacted]
2nd item
3rd item

A further sub-sample from Item 3 would be numbered

[redacted]

The barcode must be attached to each item. Any sub samples must also be bar-coded. It is essential that all evidence items and sub samples be easily identified.

13 SUBMISSION OF SAMPLES TO THE ANALYTICAL SECTION

1 Sub samples of examined items are submitted to the analytical section for DNA analysis. All samples for DNA analysis must be clearly labelled with the barcode ID. All samples for DNA analysis are registered in AUSLAB and must be stored to the rack in the freezer in AUSLAB at delivery. Refer to **Appendix 1**: AUSLAB Registration.
2 Samples should not be placed into the freezer in the Analytical section until they are registered and all tests are ordered in AUSLAB.
3 Urgent – 1 Priority cases – The 'Urgent' priority is reserved for samples of the upmost urgency. It is advised to discuss the case with a supervisor before using the Urgent Priority.
4 High – 2 Priority cases - Major Crime & Volume BVAA cases should be assigned a High priority. These will be processed with priority.
5 Medium – 3 Priority Cases – This priority is given to general Volume Crime cases.
6 Low Priority – 4 Priority Cases - This priority is given to low priority Volume Crime cases. Note: a 9PLEX is ordered on these cases now.
7 Requests can be made to perform a 9PLEX (Profiler) or COFIL (Cofiler).
8 If a sample is particularly dirty or known inhibitors are present a nucleospin may be requested. NUCB – Nucleospin Blood, NUCC – Nucleospin Cells & NUCT –

Not Current

Nucleospin Tissue can be requested on the sample registration page. Specimen = NUCC or NUCB or NUCT.

9 Microcon Concentration is generally not requested at the time of sample registration. This is generally used as a rework technique for samples important to the case.

10 Samples can also be pooled refer to Appendix 5: Requesting samples to be pooled.

14 RECORDS

[redacted]

General Examination Record (Unruled)
General Examination Record (Ruled)
General Swab Exam Record
Outer Packaging Record
Cigarette Butt General Examination Record
Clothing General Examination Record
General Examination Record (Volume)

15 AMENDMENT HISTORY

Revision	Date	Author/s	Amendments
0	17 Feb 1999		
1	26 Jun 2001	V Ientile	
2	18 Sep 2002	V Ientile	Amendments to references, (8) Characterisation of Biological material and (22) Reference Samples
3	26 May 2005	K Lee	Entire document revised and rewritten
4	21 Oct 2005	M Gardam	Added when to use "what appears to be" for when a confirmatory test is not available.
5	22 June 2006	M Gardam	Added Techniques for various exhibits, added AUSLAB Flowcharts.
6	14 Feb 2007	L Weston	Update with new processes for AUSLAB-LIMS

16 APPENDICES

1 AUSLAB registration
2 Volume crime sampling flowchart
3 Volume AUSLAB Registration Requirements
4 Registration of SAIKs or multiple items
5 Requesting samples to be Pooled
6 Requesting samples for differential lysis

Not Current

16.1 Appendix 1: AUSLAB Registration

Exhibits eg: Cig. Butts, individually received swabs and sub-samples

After examination is complete:

Return/transfer exhibit in AUSLAB and physically (if required)

EXR Page (info. For police)

- In AUSLAB > **Patient Enquiry**, scan case/exhibit barcode, press **SHIFT F9** > summary page
- **ENTER** on exhibit in question, checking barcode
- On EXR page, **SHIFT F2** to edit entire page
- Fill in *'Overall Status'* (F1 drop-down menu), *'Team'* name (and in box) *'Lab #'* with barcode and *'Results/Status'* (F1 for drop-down menu)
- Press F8 to get out of edit mode

FBEXAM / Sample Registration (on EXR page for exhibit of interest)

- **SHIFT F10** > exhibit registration page
- **F7, F4, SHIFT F5** to copy page
- Fill in *Specimen:* (EXT type) eg: CELLS, DLYS
  Primary Site: (specimen type) eg: fabric, swab
  Client Ref. #: (= receipt # - 00x)
  ***DNA priority*:** fill in according to priority of sample
  Sample Info 1: (description) eg: Swab of Bottle
- Enter '**FBX**' in box, press **ENTER** and follow prompts at bottom of page
- Enter '**9PLEX**' in box, press **ENTER**
- Prompt appears: enter in any necessary processing comments, eg. retain supernatant
- **F7, F4, F4,** (automatically returns to EXR page)
- **SHIFT F9** to view summary page
- Repeat procedure for other exhibits/ samples if required

Sub-sample Registration (on EXR page for exhibit of interest)

- **SHIFT F10** > exhibit registration page
- **F7, F4, SHIFT F5** to copy page
- Scan in new barcode for sub-sample
- Fill in *Specimen:* (EXT type) eg: CELLS, DLYS
  Primary Site: (specimen type) eg: fabric, swab, paper
  Client Ref. #: (= receipt # - 00x-y)
  ***DNA priority*:** fill in according to priority of sample
  Sample Info 1: (description) eg: HVS, Stain 1
- Enter '**9PLEX**' in box, press **ENTER**
- Prompt appears: enter in any necessary processing comments, eg. retain supernatant
- **F7, F4, F4,** (automatically returns to EXR page)
- **SHIFT F9** to view sub-samples on summary page
- Enter on sub-sample and add *'Team'* name
- Repeat for other sub-samples if necessary

Not Current

Printing Labels:

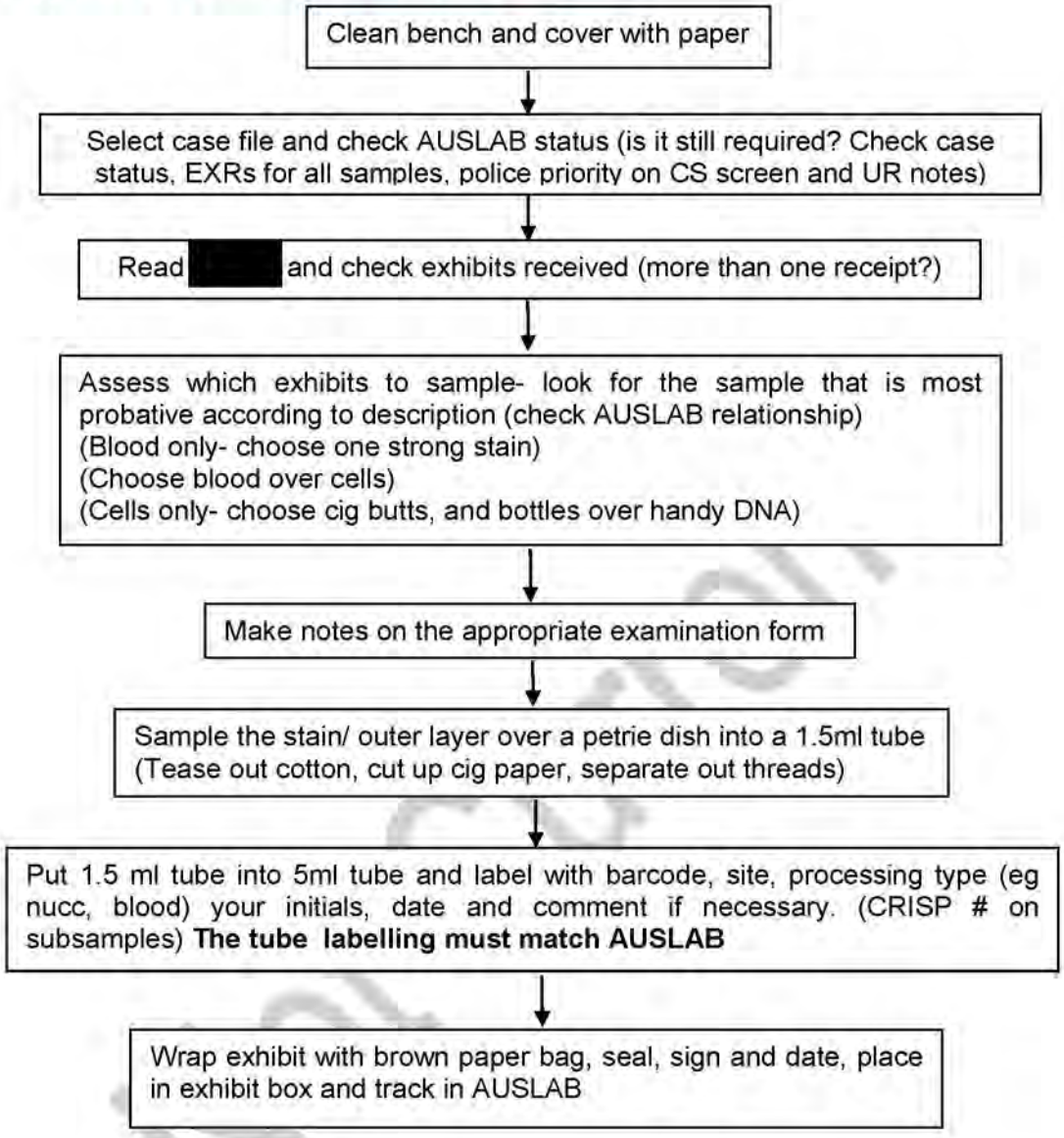
- From AUSLAB main menu, press **7, 3, 3**
- Type in label type wanted (either FBLAB6 or PROP)
- Change *'Printer Name'* as required
- Follow prompts at bottom of page (**F6, F5** scan barcode/s required, **ESC** from edit mode, **F7** to print)

Transferring Exhibits: (before or after physically moving items):

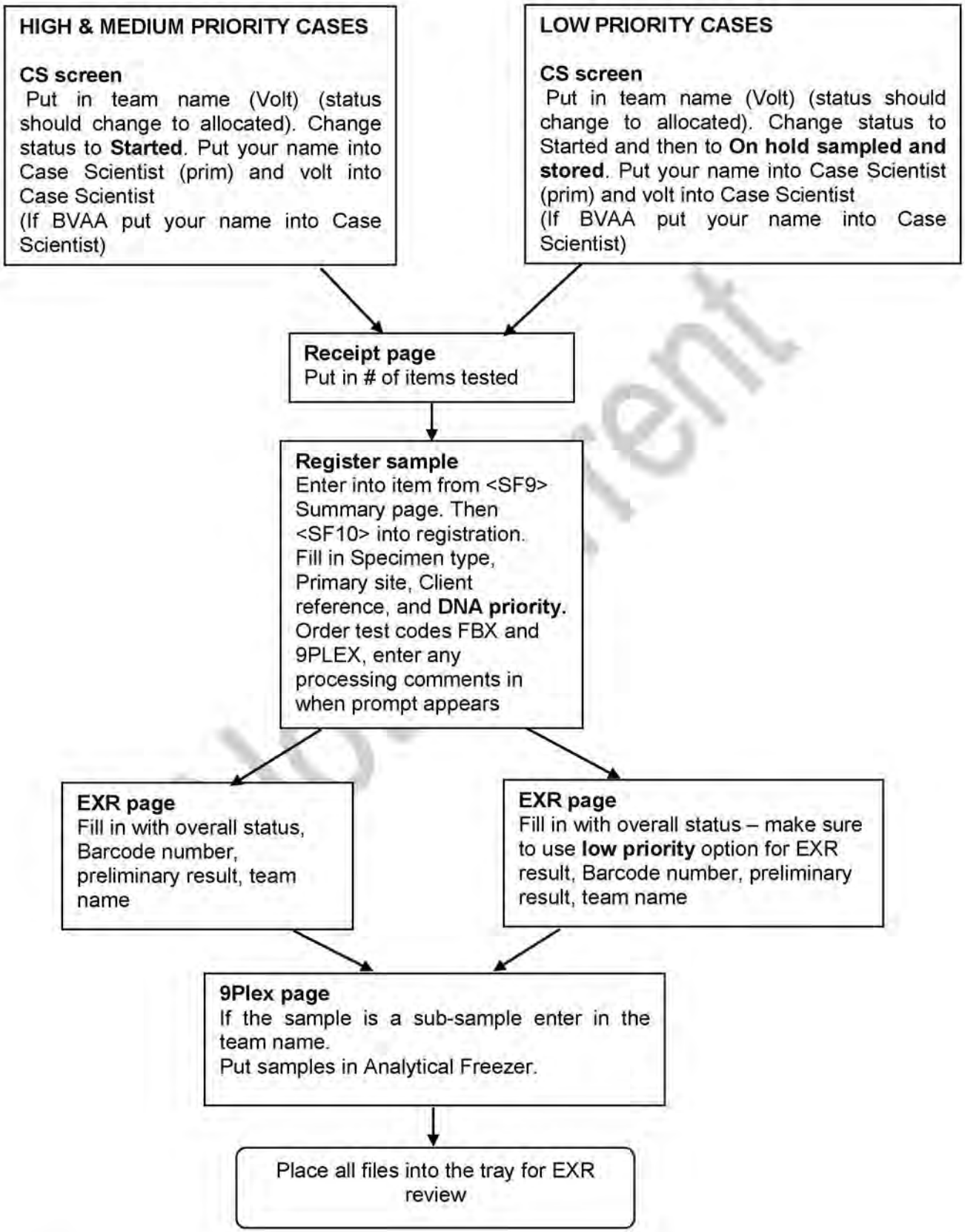
- In AUSLAB > **Patient Enquiry**, scan case/exhibit barcode, press **SHIFT F9** > summary page
- Press **SHIFT F5** on a receipt barcode line to show were exhibit is stored
- Highlight line for receipt barcode of interest (should be stored to a shelf)
- Press **SHIFT F7** > to transfer item, **F1** for drop down list and select desired storage location (see codes below) Press **ENTER,** and you will be prompted to confirm transfer (at bottom of AUSLAB page)
- Check item of interest has been transferred to desired location.

Not Current

16.2 Appendix 2: Volume Crime Sampling Flowchart



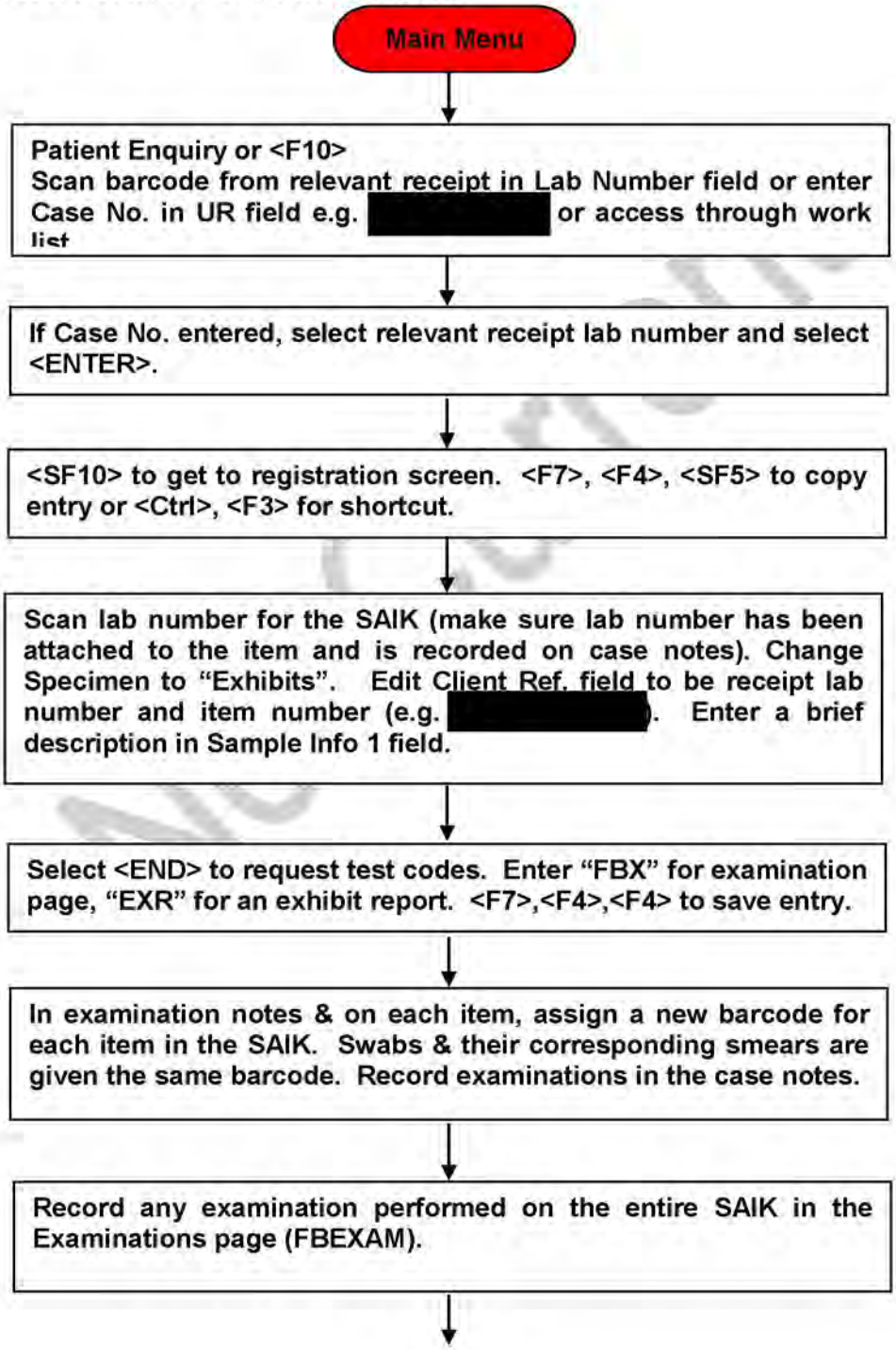
16.3 Appendix 3: Volume AUSLAB Registration Requirements



16.4 Appendix 4: Registration of SAIKs or multiple items

Purpose: Sexual Assault Investigation Kits (SAIKs) are registered in the QPS Forensic Register under a single exhibit barcode. Therefore results for the entire sex kit must be reported back to the QPS Forensic Register on that exhibit barcode. Sometimes more than one item are packaged together in the same bag and given only one exhibit barcode. These should be treated the same as SAIKs.

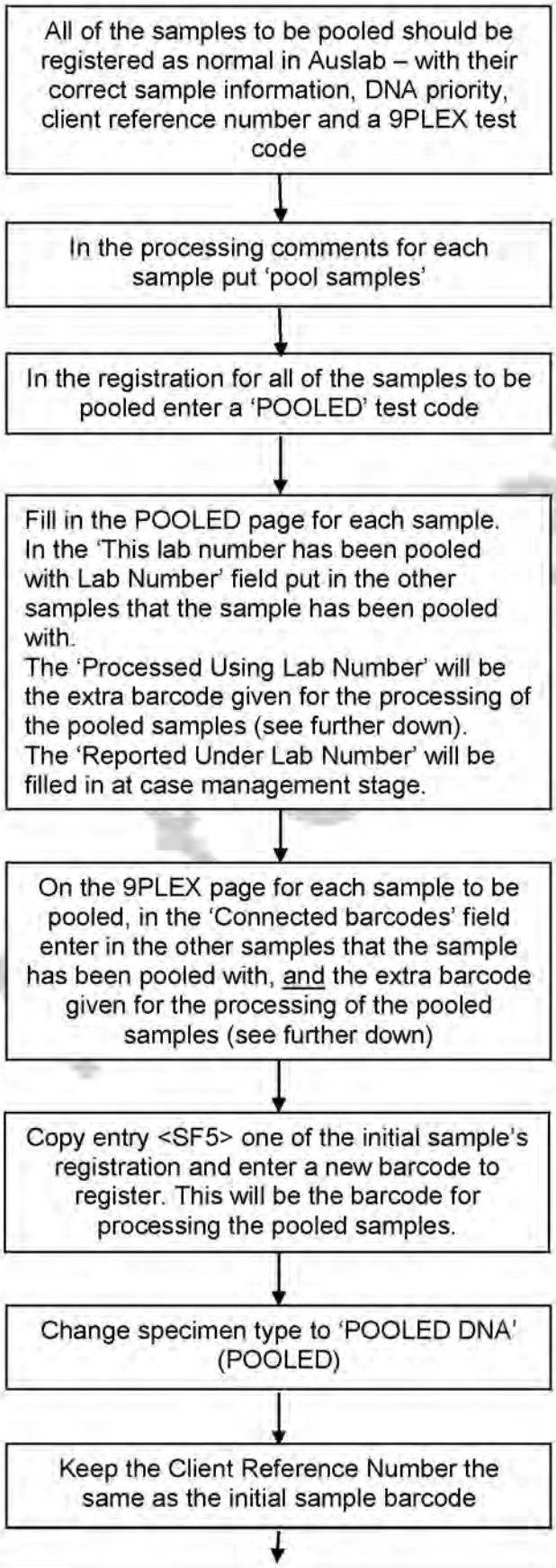
To record details of SAIK examinations:

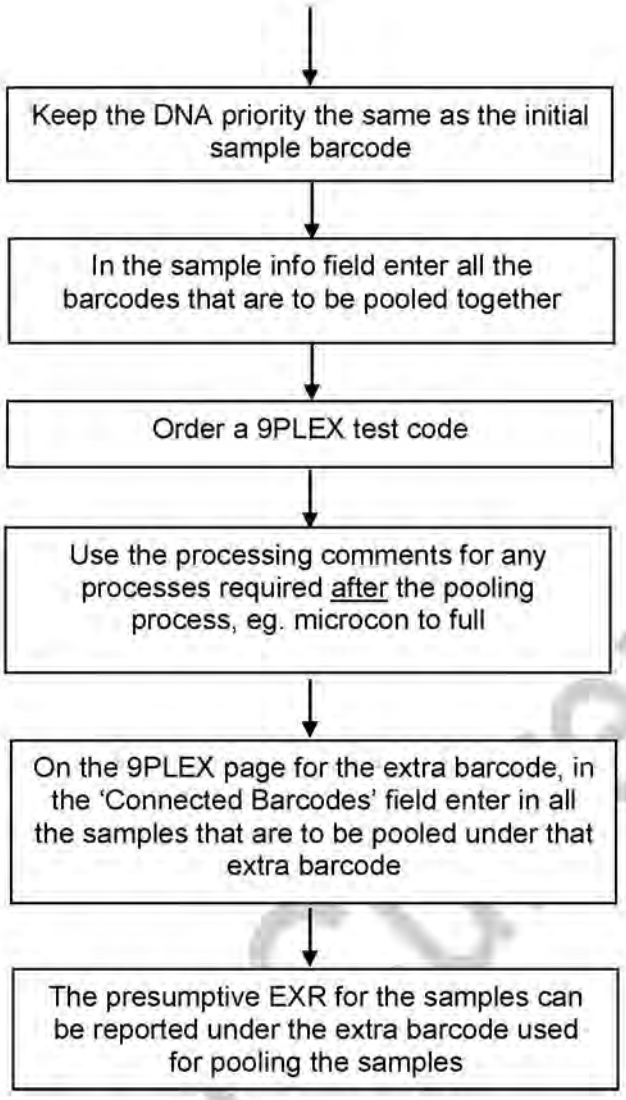


Only register the samples that are being submitted for DNA analysis with 9PLEX as the test code. Refer to Requesting DNA Analysis section for details. In the Client Reference field, record the receipt, item and sub sample number, (e.g. [redacted].

Not Current

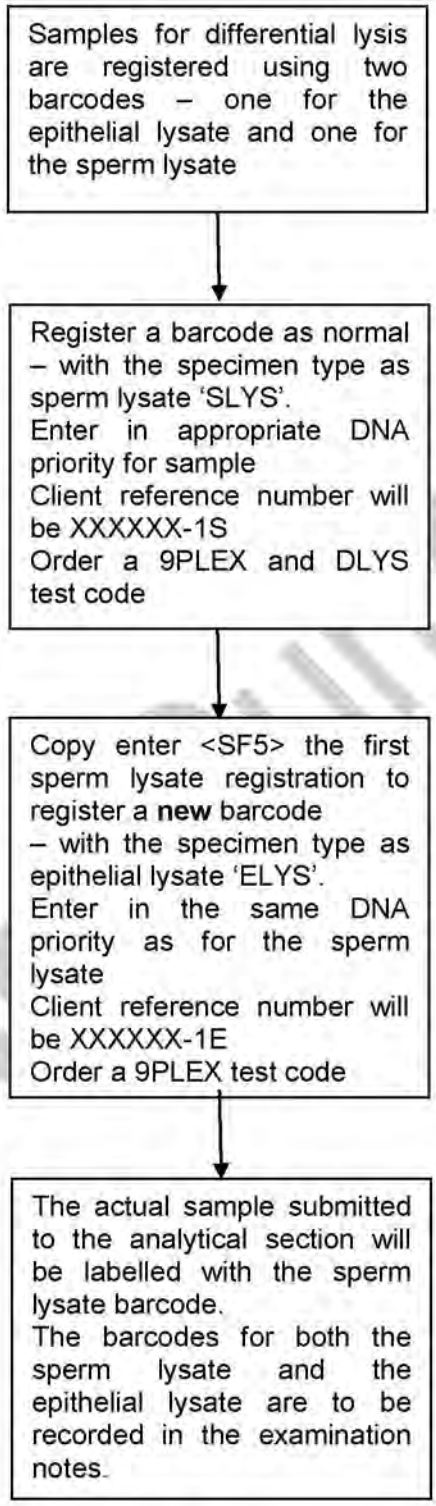
16.5 Appendix 5: Requesting samples to be Pooled




Keep the DNA priority the same as the initial sample barcode
In the sample info field enter all the barcodes that are to be pooled together
Order a 9PLEX test code
Use the processing comments for any processes required after the pooling process, eg. microcon to full
On the 9PLEX page for the extra barcode, in the 'Connected Barcodes' field enter in all the samples that are to be pooled under that extra barcode
The presumptive EXR for the samples can be reported under the extra barcode used for pooling the samples

Not Current

16.6 Appendix 6: Requesting samples for differential lysis



Non-current

CA-74

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Procedure for the Receipt of Biology Exhibits

1. PURPOSE

This procedure covers the steps involved in receiving Major Crime and Volume Crime cases, exhibits and post mortem samples in AUSLAB and storage of received items whilst in the Forensic Sciences Property Point. It involves the case management details.

2. SCOPE

This procedure shall apply to all Property Officers, Administration staff and Case Scientists who receive exhibits.

3. DEFINITIONS

UR/Case No: is the CRISP number provided by the police. It may also be a SSF number (for missing persons) or COR number (for coronial cases).

Lab number: refers to the barcode number for the Case, Exhibit, OR sub-sample taken from the Exhibit.

Test code box: The set of four boxes at the bottom of the screen on a Forensic Registration page. If needed you may press <F3> to obtain a further four (4) boxes for test code entry.

Volume crime samples are high instance, low status crime scene samples collected for inclusion on the National DNA database, in CRIMTRAC. These samples are often received in bulk and may be allocated differently to major crime case work in that they are allocated in bulk a considerable time after receipt.

A ***case record*** includes the case folder and its contents (case file) workbooks, work sheets, the absence record, court appearance records and AUSLAB records.

The ***case folder*** is used to record information relating to the case, e.g., case number, names and minutes of conversations.

The case file consists of the case folder and its contents.

4. ASSOCIATED DOCUMENTS

[redacted]

5. PRINCIPLE

5.1 Exhibit receival shall be the responsibility of a Property Officer. Scientists and Technical Officers may fulfil this function in the absence of a Property Officer.

5.2 Exhibits are received at the Central Property Point from a member of the Queensland Police Service.

Not Current

5.3 Work from private individuals, companies or other government departments will only be accepted if approved by the Chief Scientist of Forensic Biology.

5.4 When items are delivered to the front counter of the Property Point, the procedure outlined below should be followed. If any part of the procedure cannot be followed, all relevant information should be noted in the case file and the UR notes and brought to the attention of the Supervisor or delegate. It may be necessary to raise an OQI.

5.5 To reduce the risk of contamination, items from different cases should not be received at the same time. Alcohol solution is stored at the front counter to clean the bench.

5.6 Gloves, Safety glasses and personal protective equipment (PPE) should be used if necessary when handling items; use appropriate spill kit items located at the front counter if necessary.

5.7 Take necessary precautions when opening packages containing sharp objects. There are cut resistant gloves available at the front counter if necessary. If knives or other weapons are received, ensure they are safely packaged and labelled with appropriate stickers to warn others. A biohazard cabinet is available for use in the Property Point if necessary.

5.8 When a sharp exhibit is submitted to FSS and is not packaged properly (lab mailers/specimen containers/cardboard), the item will be refused.

5.9 Reference blood tubes should be checked to ensure there is no damage or leakages.

5.10 Damaged and leaking blood tubes shall not normally be accepted.

6. PROCEDURE

6.1 Define Exhibit

a) Determine which area of Forensic Biology the exhibit will be allocated to from the available paperwork or by asking the delivering officer.

b) Major Crime cases are determined as being crimes against a person

c) Volume Crime case are determined as being crimes against property

6.2 Preparation

a) All submissions for Forensic Biology must be accompanied by a [redacted] Submission of Articles Form.

b) The [redacted] Submission of Articles form must have the required fields completed as outlined:

i. Crisp number/Occurrence No.: is mandatory for all cases with the exception of Coronial cases without a COR number and QPS or CMC Internal Investigations. These cases can be received with an SSF.
ii. Forensic Register Number
iii. Property Tag Number

c) The top of the form must also be signed by a police forensic 'Scenes of Crime' officer to indicate that the exhibits have been checked for correct packaging,

Not Current

labelling and appropriate case information. An exception to this is when the only item is a sealed Sexual Assault Investigation Kit (SAIK) which can be received without being checked by a forensic officer as these are packaged and sealed by doctors. SAIK's sealed by Government Medical Officers are not required to be signed off by a forensic officer but MUST be barcoded.

d) Ensure the Delivering Officer has signed and dated the [redacted] in the appropriate field.

e) It is a requirement for the transfer of results to the Forensic Register that all items have been clearly labelled with exhibit barcodes by the SOCO.

f) Ensure there is a Property Tag or legible copy of a Property tag attached to the exhibits.

g) If exhibits are questionable as to relevance to the case scenario, consultation with a case scientist is necessary. If items are rejected, the reasons must be communicated to the delivery officer and recorded in UR notes in AUSLAB as a record if a case already exists.

h) Any packages where the primary packaging (i.e. the packaging containing the actual exhibit) is sealed upon receipt and are opened at the front counter are to be signed "opened by ....,, time & date".

i) Check all items are dry. If items are received wet after consultation with a Scientist, they are to be wrapped in plastic and placed immediately into the Forensic Biology Exhibit Freezer. A note must be added into the UR notes outlining the state of the exhibits and emphasizing that they have been placed in the freezer wet.

j) If these requirements have not been met then we do not receive the items.

6.3 Receipting in AUSLAB

a) Having established the nature of the exhibit. It is registered using AUSLAB in accordance with procedures as outlined in Appendix 1.

b) Post mortem samples received from Pathology are registered under the same COR number as the Pathology registration. If no COR number exists search under the deceased person's name for Pathology SSF number and register items with a new barcode under the original SSF. Currently reference samples from post mortems are received directly from the police in the Coronial Support Unit or Pathology staff. Samples will come accompanied by an email from Mortuary staff originating from Forensic Sciences Liaison Staff detailing the crisp number and person particulars. Any additional information required can be gathered from this paperwork.

c) Post mortem samples are to be registered using AUSLAB in accordance with procedures as outlined in Appendix 2.

d) If the electronic system of receival and registration AUSLAB is not functioning, a manual hand written receipting system is employed in accordance with [redacted]

e) If changes are made to the registration/receipt fields, a UR note detailing the change is required and amended receipt is to be issued in accordance with Appendix 3. An amended receipt is only required if the information on the initial

receipt issued has been changed. If the incorrect information has been made by the Property Officers then they are responsible for preparing the amended receipt. If a scientist has found an inconsistency that couldn't have been identified by the Property Officers then it is the scientist's responsibility to prepare an amended receipt.

f) If there is an issue with the items a feedback code can be sent to QPS Forensic Standards unit or DNA Unit for correction.

g) To request an FERRO code the following steps are to be undertaken:
   i. In the case in AUSLAB, press Shift F10 to return to the registration page
   ii. Enter the FERRO code in the test code box
   iii. Resave the registration (F7, F4, F4)
   iv. Page down to the relevant page and enter the name of the Collecting Officer
   v. Enter the QPS exhibit barcodes for the items which are incorrectly packaged
   vi. Press Shift F11 to send to fax, F7 to direct to , type FAX then enter
   vii. Enter the fax number as [redacted] and enter, type 's' to send single page and enter
   viii. If the information is to be sent to the DNA Unit enter the fax number [redacted] and enter, type 's' to send single page and enter.

7. STORAGE OF EXHIBITS AFTER RECEIVAL

7.1 Once received, the items are packaged according to the type of exhibit. Items that can be kept at room temperature are packaged in paper and items requiring freezing are packaged in plastic. Items that require freezing are the following
   a) Sexual Assualt Investigation Kits (SAIK's)
   b) Food stuffs of any kind
   c) Post Mortem samples
   d) Tissue samples including flesh
   e) Used condoms, sanitary pads or tampons
   f) Wet items

7.2 If any of the above items that require freezing at receive at room temperature from QPS then the Property Officers will repackage the item for storage in the freezer. They will record this in the UR notes and request a Feedback Code (FERRO) to send this information to the police.

7.4 All Exhibits are to be labeled with the correct Exhibit Tag (printed from AUSLAB) and the seals signed and dated by a Property Officer. The items are to be stored in the appropriate Property Point storage location. Packaging and storage for each type of exhibit is detailed below:

(b) **Small Volume Crime not requiring freezing-** Exhibit, paperwork, leftover barcodes and white exhibit tag are stapled together and then tracked to a barcoded *Volume Crime Box (white labels)*.

(c) **Large Volume Crime not requiring freezing-** Exhibit is wrapped in paper, labeled with a white Exhibit Tag sticker and stored the *Property Point Exhibit Transfer Trolley* ([redacted]). Paperwork and spare barcodes are stapled together and placed in a tray for transfer to Forensic Biology.

(d) **Small Major Crime not requiring freezing-** Exhibit is wrapped in paper, labeled with a yellow Exhibit Tag sticker and then stored in a barcoded *Property Point Exhibit Transfer Trolley* ([redacted]). Casefile is then made up and stored in *Forensic Biology Property Point Tray* ([redacted]).

(e) **Large Major Crime not requiring freezing**- Exhibits are wrapped in paper, labeled with a yellow Exhibit Tag sticker and then stored in the *Property Point Exhibit Transfer Trolley* ([redacted]). Casefile is then made up and stored in *Forensic Biology Property Point Tray* ([redacted]).

(f) **Major Crime Exhibits requiring freezing**- Exhibits are wrapped in plastic, heat sealed, labeled with a yellow Exhibit Tag sticker then stored in the *Property Point Exhibit Freezer Transfer Trolley* ([redacted]). Casefile is then made up and stored in *Forensic Biology Property Point Tray* ([redacted]).

(g) **Volume Crime Exhibits requiring freezing**- Exhibits are wrapped in plastic, heat sealed, labeled with a white Exhibit Tag sticker then stored in the *Property Point Exhibit Freezer Transfer Trolley* ([redacted]). Paperwork and spare barcodes are stapled together and placed in a tray for transfer to Forensic Biology.

7.5 All items must by stored through AUSLAB.

7.6 Exhibits requiring storage in the freezer are transferred to the freezer in the undercroft of block 8 using a trolley and stored on shelves in the freezer.

7.7 Exhibits requiring storage in the exhibit room are transferred in a secure trolley by two Property Officers. Exhibit Runs can only be done before 10am or after 2pm. Exhibits are stored onto designated shelves or cage in the Exhibit Room.

8. APPENDICIES

Appendix 1 – Biology Exhibit Receival for Volume Crime, Major Crime Cases
Appendix 2 – Biology Exhibit Receival for Coronial Cases
Appendix 3 - Amended Receipts
Appendix 4 – Crime Classification Codes and Case Type

Not Current

9. AMENDMENT HISTORY

Revision	Date	Author/s	Amendments
3	28 Mar 2001	V Ientile	
4	16 Sep 2002	V Ientile	Changes to reflect change in police policy, QP127 forms. List item not received on receipts.
5	11 Jun 2003	V Ientile	Changes to reflect use of AUSLAB
6	13 Oct 2003	V Ientile	Added flowchart appendix, updated with changes to AUSLAB procedure.
7	23 Jun 2004	N Benson V Ientile	Amended procedures, removed flowchart, added appendix.
8	8 Aug 2005	S Hammond	Updated changes to Auslab procedure, receival at Central Property Point, referred to Appendices, changed PM receival procedure
9	17 Oct 2005	S Hammond	Added packaging processes and storage post-receival in PP.
10	Sep 2006	Janine King	Added procedure for amended receipts and blood clothing code. Refusal of sharps if not packaged correctly. Use of FBFB code and packaging of items
11	Nov 2007	Janine King	
11	April 2008	QIS2 Migration Project	Headers and Footers changed to new CaSS format. Amended Business references from QHSS to FSS, QHPSS to CaSS and QHPS to Pathology Queensland

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APPENDIX 1

BIOLOGY EXHIBIT RECEIVALS (Volume Crime, Major Crime Cases)

(1) AUSLAB ENTRY

Log into AUSLAB, ensuring you are working within the 'BIOLOGY' or 'ALL DEPARTMENTS' registration field, and follow the appropriate table:

DATA FIELD	VOLUME CRIME	MAJOR CRIME
Search AUSLAB	N/A	N/A
Lab Number	Scan the barcode sticker	Scan the barcode sticker
UR/Case Number	Enter 'QPS' then CRISP number/Occurrence number (no slashes) (eg. [redacted] or [redacted])	Enter 'QPS' then CRISP number/Occurrence number (no slashes) (eg [redacted] or [redacted])
Surname	Enter 'CASE' then CRISP number (with slashes) (eg. CASE [redacted]	Enter 'CASE' then CRISP number (with slashes) (eg. CASE [redacted]
Location/Client	Enter 'P' + F1 to select station name (eg. City Station)	Enter 'P' + F1 to select station name (eg. City Station)
Collected	Enter '?' and seized date (eg. ? [redacted]	Enter '?' and seized date (eg. ? [redacted]
Received	Enter current time and press <enter> (today's date is automatically entered)	Enter current time and press <enter> (today's date is automatically entered)
Specimen	Enter 'CASE'	Enter 'CASE'
Client Ref	Scan the barcode sticker	Scan the barcode sticker
Court Date	If provided enter in court date (eg. [redacted]	If provided enter in court date (eg. [redacted]
If no previous exhibit received, enter 'CS' in test code field and enter through I/O prompt then enter 'FORREC' in the test code field to initiate following prompts **If previous submission only enter 'FORREC' in the test code field to initiate following prompts**		
Receiving Officer	Enter your own name or mnemonic	Enter your own name or mnemonic

Non-current

Investigating Officer	Enter I/O's name from [redacted] (eg. Sgt Joe BLOGGS)	Enter I/O's name from [redacted] (eg. Sgt Joe BLOGGS)
Delivery Officer	Enter the delivery officer's name (eg. Const. Jack BLACK) If the same as Investigating officer you can enter past this prompt.	Enter the delivery officer's name (eg. Const. Jack BLACK) If the same as Investigating officer you can enter past this prompt.
Delivery Station/Location	Enter the Delivery Officer's station (eg. City Station) If the same a Location/Client you can enter past this prompt.	Enter the Delivery Officer's station (eg. City Station) If the same a Location/Client you can enter past this prompt.
Work Area	Enter 'FBI'	Enter 'FBL'
Press <F7> to enter client billing information section		
Billing Code	Enter 'NFO' for notional billing	Enter 'NFO' for notional billing
Requested Date	Enter the collected date	Enter the collected date
Press <F4> twice to save and <F10> to enter Patient Enquiry section Scan the barcode to bring up the case management screen. Press <Shift F2> to edit screen		
Person(s) Involved	Enter 'SURNAME, First Name' (eg. SMITH, John) of each person involved	Enter 'SURNAME, First Name' (eg. SMITH, John) of each person involved
Date of Birth	Enter each person(s) date of birth (eg. [redacted]	Enter each person(s) date of birth (eg. [redacted]
Class	Enter class type for each of the person(s) involved (eg. 'compla' for complainant, 'ssct' for suspect or 'dec' for deceased). 'F1' for list of class types.	Enter class type for each of the person(s) involved (eg. 'compla' for complainant, 'ssct' for suspect or 'dec' for deceased). 'F1' for list of class types.
Items Received	Enter items received followed by the property tag number, using a new line for each item eg. 1 x Swab [redacted] 'F4' to save	Enter items received followed by the property tag number, using a new line for each item eg. 1 x Swab [redacted] 'F4' to save

If receiving a Sexual Assault Investigation Kit (SAIK) unused items received in a SAIK are to be kept together with the used items in the SAIK ***NOTE**: All items received must match the itemized list on the* [redacted] *Any items missing from the form should not be received unless it is confirmed by the Investigating Officer that they do require testing by Forensic Biology. If confirmation is received the items must be added to the* [redacted] *and initialed and dated by the delivering officer. If any items listed on the* [redacted] *are not being received they must be removed from the* [redacted] *and the change initialed and dated by the delivering officer*
Press <F8> to finish editing and <F6> to validate entry. If you do not validate this page the information on the page will not be searchable **Press <F11> to print receipt, Select <s> for single page** **Detail in UR notes any items that were not received and reasons why not received.**

Not Current

Once the registration information has been entered within AUSLAB, and a receipt issued you must undertake the following actions:

(2) FORENSIC REGISTER RECEIVAL

Enter the received details into the forensic register 'registration page' (if a hot key has been created, press <Control F7>):

DATA FIELD	
	From Main Menu go to <3> Patient Enquiry Scan the forensic register exhibit barcode (if a hot key has been created, press appropriate hot key to complete all below steps) <Shift F10> to go to the registration screen
Received Date	Enter in the time and date the exhibit was received (eg. [redacted] for 8.30am 15 May 2005)
	Press <F7> for billing <F4> twice to save
NOTE: If after scanning in barcode it comes up with "no data available" you need to contact the DNA Unit and establish why it has not transferred. The exhibit can not be transferred to Forensic Biology until it has been received off the Forensic Register.	

(3) AUSLAB EXHIBIT TAG

Generate an AUSLAB sticker property tag (if a hot key has been created, press <Control F1> or <Control F2> as a shortcut), if no hot key has been created then complete the following:

DATA FIELD	
	From Main Menu got to <7> Utilities, <3> User Utilities, <3> Label Printing
Label Type	Type 'PROP'
	Press <F6> for label list entry <F5> to insert new label number Scan the barcode sticker Press <Esc> Press <F7> to print label and affix same to the exhibit.

(4) SCAN [redacted] INTO AUSLAB

The [redacted] must be scanned in Auslab and assigned to the appropriate lab number:

- Main Menu
- <1> Request Registration
- <3> Request Form Images
- Select the appropriate scanner (eg. [redacted] + Enter
- Place document face down with the top of the document to enter scanner first and ensure the document feeds into the scanner.
- Press <F7> to scan
- Highlight the appropriate barcode number and press <F6> to attach the image to the case
- Check the barcode and Crisp number to ensure they match what is on the [redacted] Left click on the mouse to zoom in and right click on the mouse to zoom out. If the two barcodes do not match scan in the correct barcode. This will overwrite the wrong information with the correct information.
- Press <F5> to confirm
- Press the spacebar and <Esc> to exit and return to main menu of AUSLAB.

(5) STORE CASEFILE AND EXHIBITS

DATA FIELD	
From Main Menu go to <2> Sample Processing, <6> Sample Storage	
Rack Name	Enter Rack name [redacted] for Major Crime Case files [redacted] or one of the barcoded Volume Crime or Small Major Crime boxes (eg. [redacted] for exhibits.
Press <Shift F5> then scan Lab Number to store Press <Esc> to close.	

APPENDIX 2

BIOLOGY EXHIBIT RECEIVALS (Coronial Cases)

(1) AUSLAB ENTRY

Log into AUSLAB, ensuring you are working within the 'BIOLOGY' or 'ALL DEPARTMENTS' registration field, and follow the steps below:

DATA FIELD	CORONIAL CASES
	Go into Pathology registration **Page down to "Inter Departmental" page. The column detailing items *Sent* should already be completed.** **Press <Shift F2> to edit screen**
Transferred From	Enter details of delivering officer
Department From	Enter Department/Station delivering officer from
Transferred To	Enter your name as receiving officer
Department To	Enter Forensic Sciences Property Point
Transferred Date	Enter Time of delivery (eg 1315) and enter will automatically fill with date
Search AUSLAB	Under patient enquiry (may require extended enquiries therefore refer to QIS doc [redacted] search existing records using name of deceased or COR no. provided.
	Press <Shift F10> to go back to the original Registration screen **Press <F7> for Billing, <F4> to save** **Press <Shift F5> to copy entry**
Lab Number	Scan the new barcode sticker
Received Date	Change time and date received to the same time and date you entered on the "Items for Special Examination – Forensic Biology" page (eg. [redacted]

Specimen	Enter 'CASE'
Enter 'FORREC' in the test code field to initiate following prompts.	
Receiving Officer	Enter your own name or mnemonic
Investigating Officer	Enter I/O's name from [redacted] (eg. Sgt Joe BLOGGS)
Delivery Officer	Enter the delivery officer's name (eg. Const. Jack BLACK)
Delivery Station/Location	Enter the Delivery Officer's station (eg. City Station)
Work Area	Enter 'FBL'
Press <F7> to enter Client Billing information section	
Billing Code	Enter 'NFO' for notional billing
Requested Date	Enter the collected date
Press <F4> twice to save and <F10> to enter Patient Enquiry section Scan the barcode to bring up the Case Management screen. Press <Shift F2> to edit screen	
Items Received	Enter items received, using a new line for each item eg. 1 x blood sample 2 x fingernail scrapings *NOTE: What is entered here on the receipts will appear on statements.*
Press <F8> to finish editing and <F6> to validate entry. If you do not validate this page the information on the page will not be searchable. Press <F11> to print receipt, Select <S> for single page	

If the samples received contain either a blood sample or FTA blood card from the deceased you need to perform the following steps. If no blood sample or FTA Card has been received skip down to step (3)

NOTE: Post mortem bloods are not received through the DNA unit and therefore are not registered as normal reference samples. If a post mortem blood sample is received then an extra registration step must be performed to ensure the blood sample has a unique laboratory number and the appropriate test codes are requested.

Press <Shift F10> to go back to the Registration screen Press <F7> for Billing, <F4> to save Press <Shift F5> to copy entry		
	FTA Card	**Blood Sample**
Lab Number	Scan the new barcode sticker	Scan the new barcode sticker
Specimen	Enter 'FTARB' for FTA – Reference Blood	Enter 'FTARB' for FTA – Reference Blood
Sample Info 1	N/A	If the sample is an actual blood sample in a tube enter 'BLOOD' in this field. If not, leave this field blank.
Test Code Field	Enter '9FTAR' test codes	Enter '9FTAR' and 'BBCLO' test codes
BCPM Post Mortem	N/A	Enter 'Y' or 'N"
Receiving Officer	N/A	Enter your receiving details
Received the Following	N/A	Enter what you have received i.e. '1 x envelope said to contain 1 x blood sample'
Press <F7> for billing		
Billing Code	Enter 'NFO' for notional billing	Enter 'NFO' for notional billing
Requested Date	Enter the collected date	Enter the collected date
Press <F4> twice to save		
Link UR/Case to CRISP	If results of extended or patient enquiries identifies a relevant CRISP no./occurrence, link via AUSLAB corrections [redacted] the COR no. issued to the associated CRISP/Occurrence number.	

Once the registration information has been entered within AUSLAB, you must undertake the following actions:

(2) LABEL BLOOD SAMPLE TUBE OR FTA BLOOD CARD

If Post Mortem blood samples or FTA blood cards are received for coronial cases:

- Stick barcode used to register blood sample or FTA blood card onto original receipt (next to line where it is written)
- Stick new barcode onto blood tube or FTA blood card envelope and attach remaining barcodes to tube or envelope.

(3) AUSLAB EXHIBIT TAG

If there are post mortem samples other then the blood sample or FTA blood card they need to be labeled and stored like all Major Crime exhibits. Generate an AUSLAB sticker property tag (if a hot key has been created, press <Control F1> as a shortcut, if no hot key has been created then complete the following:

DATA FIELD	
From Main Menu got to <7> Utilities, <3> User Utilities, <3> Label Printing	
Label Type	Type 'PROP'
Press <F6> for label list entry **<F5> to insert new label number** **Scan the barcode sticker** **Press <Esc>** **Press <F7> to print label and affix same to the exhibit.**	

(4) SCAN [redacted] INTO AUSLAB

If you have received a Form 1 with your exhibits it needs to be scanned in Auslab and assigned to the appropriate lab number:

- Main Menu
- <1> Request Registration
- <3> Request Form Images
- Select the appropriate scanner (eg [redacted] + Enter
- Place document face down with the top of the document to enter scanner first and ensure the document feeds into the scanner.
- Press <F7> to scan
- Highlight the appropriate barcode number and press <F6> to attach the image to the case
- Check the barcode and Crisp number to ensure they match what is on the [redacted] Left click on the mouse to zoom in and right click on the mouse to zoom out. If the two barcodes do not match scan in the correct barcode. This will overwrite the wrong information with the correct information.
- Press <F5> to confirm

- Press the spacebar and <Esc> to exit and return to main menu of AUSLAB.

(4) STORE CASEFILE AND EXHIBITS

DATA FIELD	
	• **From Main Menu got to <2> Sample Processing, <6> Sample Storage**
Rack Name	Enter Rack name. [redacted] for Major Crime Case files, [redacted] or one of the barcoded Volume Crime or Major Crime boxes (eg. [redacted] for exhibits. Note: The FTA cards and Blood samples get stored to the trolley [redacted])
Main Press <Shift F5> then scan Lab Number to store **Press <Esc> to close.**	

Not Current

APPENDIX 3
AMENDED RECEIPTS

Should an amended receipt be required you are to undertake the following steps:

1. Log into AUSLAB
2. Type or wand in the lab number for the case
3. Press Shift F10 to go to the registration screen
4. Press end
5. Request code "FORREA"
6. Press F7, then F4 twice to resave the registration
7. Page down to the blank receipt page
8. Fill in the following details
    i. Receiving Officer
    ii. Delivering Officer
    iii. Delivering Station
    iv. Person amending receipt
    v. Date of Amendment
    vi. Enter the correct description to print onto the amended receipt
    vii. Enter the reason for the correction
9. Press F11 to print amended receipt
10. Sign receipt and send one to the delivering officer and one to Forensic Biology to be filed with the case file.

Not Current

11. APPENDIX 4

CRIME CLASSIFICATION CODES AND CRIME TYPES

MAJOR CRIME				
Work Area = FBL, Receipt page request = FRECL				
Case Type	HOMICIDE	ASSAULT (N/S)	ASSAULT (S)	LIBERTY
Crime Class Codes	[redacted]	[redacted]	[redacted]	[redacted]
Case Type	PERSON	EXTORTION	CORONIAL / DVI	PROSTITUTION
Crime Class Codes	[redacted]	[redacted]	N/A	[redacted]
Case Type	DRUGS	DRINK DRIVING	DRIVING	
Crime Class Codes	[redacted]	[redacted]	[redacted]	

VOLUME CRIME				
Work Area = FBI, Receipt page request = FREC				
Case Type	ROBBERY	U/ENTRY	FRAUD	STOLEN
Crime Class Codes	[redacted]	[redacted]	[redacted]	[redacted]
Case Type	THEFT (V)	THEFT (O)	PROPERTY	ENVIRONMENT
Crime Class Codes	[redacted]	[redacted]	[redacted]	[redacted]
Case Type	GOVTSEC	JUSTICE	WEAPONS	LIQUOR
Crime Class Codes	[redacted]	[redacted]	[redacted]	[redacted]
Case Type	GAMING	TRESPASSING	FORCE	STOCK
Crime Class Codes	[redacted]	[redacted]	[redacted]	[redacted]
Case Type	GOOD ORDER	OTHERS	UNKNOWN	
Crime Class Codes	[redacted]	[redacted]	[redacted]	

CA-75

From: Vanessa Ientile
To: Adrian Pippia; Biology Management; Deborah Nicoletti; Shannon Merrick
CC: Greg Smith; Jennifer Rossiter
Date: 20/05/2008 5:41 pm
Subject: Changes to QPS sampling - swabs in tubes/trace DNA kits

Hi guys

I have heard through unofficial channels that QPS will introduce these changes to sampling on te 1/7/08.

The changes as far as I know at this stage are as follows and will have a significant impact on our workload and work practices.

Putting aside the obvious lack of consultation and communication, we need to engage actively in this process at an operational level to ensure our needs are met and any potential issues are identified and resolved collaboratively.

The changes apparently approved by Michael Keller (Superintendent) as I understand them are:

From 1/7/08

All volume crime samples will be received as either swabs in tubes or tape lifts in the Trace DNA Kits.
These sampling procedures will also be in place for major crime samples, although we will still receive actual items for examination (I have no knowledge on number, type etc)

Clearly there are significant changes and issues to resolve required and to this point this has not occurred. It was however, our suggestion initially to move towards this model as a mechanism to increase productivity and streamline processes. Some of our team have been involved in some planning and preparation discussions.

Bottom line is this will happen and we need to manage it from our perspective.

A couple of issue headings that pop into my mind are - interface, reporting and biological material interpretation issues, DPP consultation, changes to reports/statements, sampling teams, roles, analytical workload, case files, monitoring sampling techniques, feedback to QPS, success rates, process evaluation, storage requirements, property point issues.

My approach - immediately set up an operational working party to manage this change chaired by myself with FSS representatives from each area affected and QPS staff (Troy, Inspector, Sgt from Forensic Standards Unit, Scientific and one or two regions).

Please think about this and we can discuss in more detail tomorrow afternoon and on Friday at the management meeting.

Regards

Vanessa

Vanessa Ientile
Managing Scientist
DNA Analysis
Queensland Health
Forensic and Scientific Services
[redacted]

Telephone: [redacted]
Fax: [redacted]
Email: [redacted]

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QPS and FSS Meeting Minutes

PRESENT AND APOLOGIES			
Chairperson:	Greg Smith	Date and Time:	8.30 am to 10 am, 6 June 2008
Venue:	Conference Room 111, Forensic and Scientific Services, Coopers Plains	Secretariat :	Glynis Tucker
Attendees:	Michael Keller, Tony Carstensen, Troy O'Malley, Greg Shaw, Greg Smith, Jennifer Rossiter, Vanessa Ientile, Cathie Allen, Justin Howes, Andrea Norton		
Apologies:	Justin Howes		

1.0 PREVIOUS MINUTES ENDORSED

Nil.

2.0 BUSINESS ARISING FROM MEETING

Item	Topic	Discussion	Action required (inc: Officer, Due date)	Communications to go out
2.1	*NEW QPS Plans re DNA Sampling and Testing, and Implications for FSS*	• Michael explained QPS have prepared a flow chart to show how they anticipate their reviewed processes to work after 1 July 2008. Hopefully, this will result in a backlog of samples waiting testing not building up with QPS Scientific Officers (SO) processing some exhibits themselves. Investigating Officers (IO) will still send exhibits (whole items) to FSS for testing. • A wide consultation occurred within QPS in the preparation of the new process / flow chart and State wide training is being rolled out at present including regional areas. The proposal was presented to QPS Senior Executive Conference (SEC) where it was well received as long as QH will not be overburdened and results are received faster. Also consulted was Acting Director, DPP, Paul Rutledge, who was happy with the proposal and was writing a letter to the Commissioner expressing his support. • Troy explained the aim was for QPS to maximise the use of robotics using NATA accredited facilities across the State with the ability to do work in a sterile laboratory environment. Some		

2.1	***NEW QPS Plans re DNA Sampling and Testing, and Implications for FS***	of the differences in the new processes from 1 July will include: ○ QPS will do tape lifts and/or swabs at the crime scene and do the sub sampling later in the laboratory in certain circumstances. ○ In regard to volume crime, Scenes of Crime Officers (SOCO) will conduct presumptive tests in the field, making notes, taking photographs, swabbing the stains and barcoding, etc. ○ Trace DNA Kits are being made up in the Scientific Section, QPS laboratory following advice from Justin Howes, FSS using correct PPE under strict controls. SOCO are receiving appropriate training. ○ QPS are trying where possible not to take possession of physical items including clothing but will forensically examine at the scene. ○ For major crime, items will be collected, barcoded and registered. In future QPS SO will determine if items are suitable for sub sampling. Sexual crimes will have SAIKs and samples submitted to FSS for testing. As with volume crime, other items will be sub sampled from swabs in the QPS laboratory. ○ Only principal items will be sent to FSS for DNA analysis and, if necessary, other items will be sent for testing. SOCO and SO will determine what will and will not be sent to FSS for testing. ○ Three (3) types of exhibits will be submitted in tubes: hand picked trace evidence, swabs and tape lifts. ○ Numbers of samples submitted to FSS for testing will be monitored constantly as follows: ▪ If more than five (5) items are received for a volume crime this will be flagged to DNA and FSS. ▪ For major crime, average of 30 biological exhibits per case has been agreed; however, in some instances the number may be higher. ○ Eventually, hopeful allocation process will no longer be required. ○ FSLU will be utilised to determine what needs to be tested for major crime. Volume crimes will be triaged by the SOCO. ○ Exhibit storage requirements will be less as the majority of exhibits submitted will be in tubes. ○ Statement writing process – for trace evidence [redacted] will not be used as information will		

QPS and FSS Meeting Minutes

		be sent electronically through the interface. SOCO and SO will enter information regarding profile matches. Changes to Evidentiary Certificates will be required. • Allocation notification forms will have items marked that do not require testing. SO will use SAIK as primary source of evidence and will await results from FSS before sub sampling is undertaken. • Exhibit records will have categories added for test types and batch numbers which will be monitored. Will add information/ tick boxes to replace [redacted] • Results from FSS – will include a template for pasting into Statements for use by SOCO and SO providing details on profiles found and who undertook the DNA analysis. • Vanessa raised a question regarding partial and mixed profiles. Partial profiles will be referred to FSS for further testing and results. Glossaries will be included in statements which will include meanings for full profile, partial profile and mixed profile. FSS will be called in Court for partial or mixed profiles. The current format of the Evidence Certificate (under Evidence Act) does not allow for statistics or opinions to be provided. Guidelines for when Statements are required may be needed. Tony mentioned that Paul Rutledge is happy to meet to discuss. • Vanessa requested time to consider the following: o changes to procedures that will be required to meet QPS requirements under their new process o changes to the team structure of DNA Analysis o changes to current reporting • FSS and QPS need to work through the current format of statements and evidence certificates to determine the changes to be made. • SO will be expected to look for results and know when court trial dates are due.	Tony will speak with Paul to determine a suitable date to meet. Attendees from FSS to include: Vanessa Ientile Cathie Allen Justin Howes Meeting will take place at QPS venue.	

WIT.0019.0012.1998

QPS and FSS Meeting Minutes

		• As of 1 July, SO will only sub sample on items they collect and there will be no triaging process on those sub samples. Exhibits collected by IO will be tested by FSS. • In future, Michael may consider hiring biological samplers if necessary. When the next step is determined FSS will be informed. • With regard to quality control procedures and environmental monitoring, Troy advised Rochelle is creating written procedures which will be rolled out to the QPS laboratories across the State. • With regard to elimination databases for detecting contamination events, this is still in briefing form determining whether this will be a National initiative. It was suggested profiles for QPS forensic personnel could be added to the FSS staff database. Vanessa pointed out consideration also needs to be given to people other than QPS officers present at the scene needing to be included for the purposes of elimination. • For regional areas, exhibits are being sent via Australia Post daily. To ensure chain of custody is maintained, QPS may need to supplement the Air Wing with their own liaison staff as it is difficult to find someone prepared to accompany the exhibits to Brisbane. QPS is looking to resolve this issue. • Trace DNA Kits need validation as contamination free – a kit from each batch will be submitted to FSS for testing prior to kits being sent out for use. Rochelle will include this aspect in the written procedures. • Engagement of AUSLAB will be required for building the interface with appropriate information to replace the [redacted] This needs to be undertaken as soon as the required changes to AUSLAB are known. • Vanessa suggested a staged approach may need to be taken with the discontinued use of the [redacted] until the functionality can be built in AUSLAB and with other changes needing to occur such as wording of statements, the quality aspects, the interpretation aspect re certificates,		

QPS and FSS Meeting Minutes

		etc. • Vanessa requested the details of appropriate contact people so they can be engaged in a more formal manner as this is seen as a major change process within DNA Analysis. Troy is the main point of contact, Rochelle is the contact for written procedures and Andrew is contact for training. • Troy stated Andrew Stanley is mainly responsible for training, including trace DNA component involving cleaning, PPE, etc, by providing demonstrations, training guides and refresher courses across the State to an accredited level. Troy has been explaining the new process end to end and Andrew has been doing the practical training. Processes that currently exist in FSS procedures are being explained in training sessions. • Michael stated the aim is to make DNA evidence work as much like fingerprints as possible so that offenders are identified quickly and do not have the opportunity to re-offend. • Vanessa requested the flow chart from Troy. • Greg Shaw thanked Michael, Tony and Troy for attending.	Troy to send flowchart to Glynis to circulate with meeting minutes.	

5.0 NEXT MEETING

The next meeting is scheduled for: TBA

Minute Authorisation: **Name:** Greg Smith **Date:** 12 June 2008

CA-77

DNA Analysis Staff Update

18 June 2008

Background

- MOU between FSS and QPS developed over last 12 months
- Covers high level statements about how we interact, documents responsibilities
- Major component is TAT
- Current TAT – average of 50 days between receipt and first EXR result
- Current case completion TAT is approx 6 months
- QPS have requested desired TAT of 48 hours from receipt to DNA result

Issues

- We have an existing workload
  - Approx 3000 unstarted items (1300 V/C, 1700 M/C)
  - "Work in Progress" backlog - analytical, results, reviews
  - Have advised that will we work towards reduction of TAT with end goal being as close to 48 hours as we can manage with current capacity

QPS Changes – to commence 1 July

- QPS have confirmed the priority is major crime work
- All major crime is HIGH, volume crime is LOW
- QPS forensic officers (SOCOs and Scientific officers) will perform that majority of the examination and sampling
- Majority of samples received will be subsamples, not actual items

QPS workflow

- For volume crime – SOCOS will attend scene and sample in situ using presumptive tests and appropriate method such as swabbing, tapelifts, scraping, excise stain.
- These samples will be submitted directly to us in tubes for extraction.

QPS Workflow

- For major crime, forensic officers will attend scenes and collect items.
- In scientific labs, items will be examined, screening tests performed and stains sub sampled into tubes similar to approach for volume crime.
- Scientific will hold the item, awaiting our results.
- Items that cannot be sub sampled will be delivered to us for examination

What will be delivered to us for examination

- SAIKs
- Cig butts
- Chewing gum
- Syringes
- Condoms
- Sanitary pads/tampons
- Items requiring phadebas testing
- Items collected by I/Os
- Last 2 will be incorporated into QPS over time

QPS workflow

- Forensic officers will determine which samples are submitted based on case history.
- Major crime cases with >30 items and Volume crime cases with >5 items will be further prioritized and triaged by DNA Liaison Unit after receipt.

QPS Workflow

- All other cases will be reviewed and critical items determined once case status has been changed to "Allocated"
- Major Crime cases by DNA Liaison Unit, Volume Crime by SOCOs.

QPS Workflow

- DNA results sent back to QPS via EXRS.
- Forensic officers will report DNA results in "cradle to grave" statements covering scene attendance, collection, presumptive screening and sampling and results with wording similar to:
- *Computer records show a DNA profile was obtained from sample 123434643 and matched evidence sample 23354543*

What won't be reported by QPS

- Statistics
- Partial profile statistics
- Mixture interpretation
- Interpretation of DNA involving questions of quality and quantity

Exhibit management

- We will photograph then discard any packaging for sub sampled items
- We will store any unused portions of samples
- Same process as current for volume crime swabs
- Only entire items submitted will be returned to QPS property points

Reworking strategies

- Focus is major crime
- We will determine rework strategy of submitted sample (re –extraction & pooling if too large initially, concentration or clean up)
- If re-sampling required, a negative EXR results and request from us will trigger QPS to re-examine (using case EXR)
- Majority of re-sampling will be performed by QPS but dialogue between case scientist and scientific officer may determine item should be delivered to us.
- QPS will provide parent child information for each sample to assist in determining which samples can be pooled

Reworking strategies

- Volume crime – reworking should be minimized
- Develop guidelines for reworking strategies for uploadable profiles
- Volume crime can be prioritised as HIGH if linked to major crime, reworking then more important

Sexual Assault workflow

- SAIK submitted and examined by us
- Negative results through EXRs will trigger prioritisation, examination and sub sampling of additional items to be submitted to us
- Can also recommend additional examinations commence through case EXRs

Quality procedures

- We will batch test blank trace DNA kits
- QPS will submit environmental monitoring samples from each site based on our procedures
- QPS scientific labs will perform monthly deep clean based on our procedures
- Elimination database – QPS looking at implementing

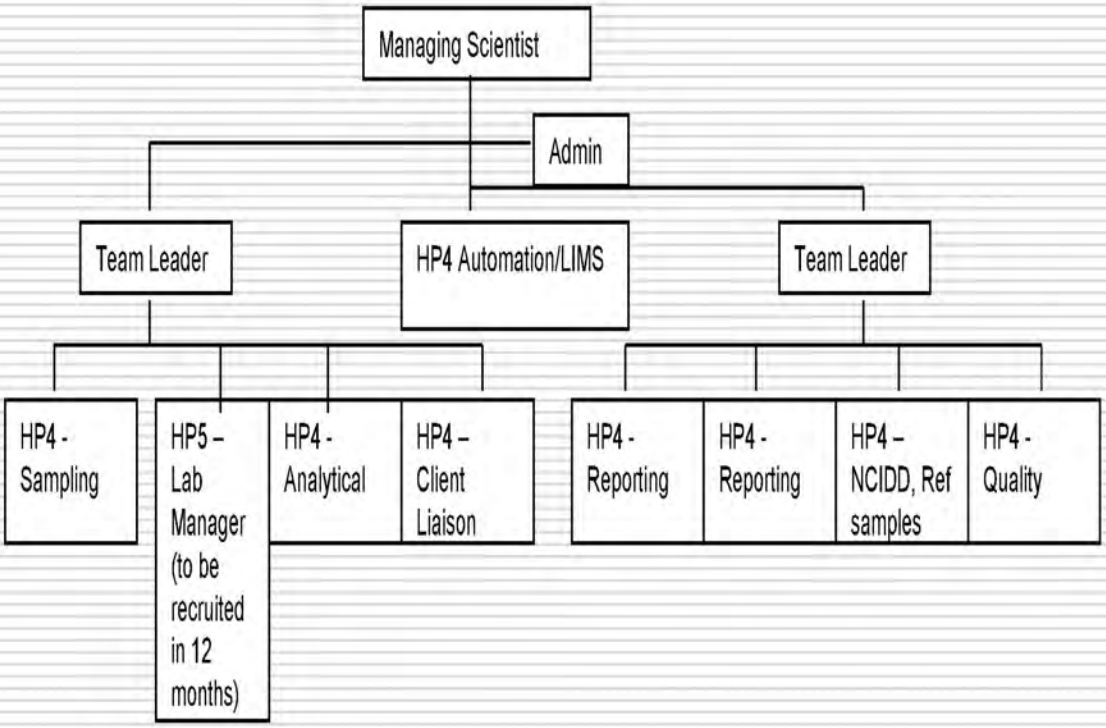
Issues for DNA Analysis

- How to reduce TATs
- How to manage completion of existing work in progress
- Cross over period where cases may be sampled by both us and QPS.
- Review team structures, identify bottle necks
- Separation of new and old processes

Impacts on all areas

- Receipt and storage of items at property point
- Photographing packaging of all items
- Sampling assessment – suitable for off deck lysis or futher sub sampling required
- Managing prioritisation of samples through analytical, keeping new vs old separately

Proposed team restructure



Where to from here?

CA-78

Minutes of meeting with QPS on 16th July 2008

Attendees: Emma Caunt, Justin Howes, Troy O'Malley, Lindon Smallwood, David Keatinge, Lysa McMenz

1. Strategies

I explained the strategies we have put in place to meet the requirements of the QPS under the new system. This included the new team structure, how the samples will be processed, i.e. as items and not cases. Also that we will be collating data to enable us to provide TATs in the future.

2. Primary site information

If a sample of fabric is submitted in a tube the primary site will state "Fabric Blood" if it is TMB +ve and "Fabric Cells" if it is TMB neg.
For a swab the primary site will state "Swab Blood" if it is TMB +ve and "Swab Cells" if it is TMB neg.
A batch number infers that the sample is being submitted in a tube.

3. Content of QPS statements

Discussion around content of QPS statements. Preliminary EXR results will not be reported as these are defined and accepted. The information that will be going into QPS statements will be limited to 9L profiles. The information in the statement will state that a record exists and that that record has come from QHFSS. They will be commenting on the fact that a record exists and not 'the fact of the matter of the record'. A definition of a full profile will be provided by the QPS in their glossary. With respect to any other types of DNA profiles, i.e. partials and mixtures, they will not be making any comment at all and will state simply something along the lines of 'a DNA result has been received but this result will need to be explained by a biologist'. If no profile is obtained then they will report the record of this fact.
The information regarding 9L profiles will consist of three clear elements '...item.....full profile match.....person...'. This information will automatically pull into the Forensic Register and will be copied and pasted into the statements. There will be no ability for this wording to be changed by the person writing the statement.
I have asked that we be provided with an example statement so that we can be aware of the content.

4. Case conferences

For 'old' cases, the arrangement for case conferences will remain as is.

For 'new' cases it has been agreed that case conference will no longer be required since items will already have been examined and prioritised by QPS.
There may be the occasion where the QPS will require our advice and they will call us as and when this is required.
Troy will speak to Patricia Holden about the case conferences that have been arranged for the 'new' cases.

5. SOCO Training

I asked whether this needs to be revised in the light f the changes. Dave Keatinge to speak to Pat O'Reilly and get him to call me about this.

6. Proposed testing of drying ability of new swabs – Water vs. EtOH

I suggested that we test some swabs to see if water takes longer to dry that ethanol once the swab has been put into the new tubes with the hole in the top. This may push the QPS towards using either water or ethanol rather than both. Since the holes in the tubes are rather small, there may be the risk that swabs wet with water will not dry. We may wish to progress this further to test the swabs wet with water and blood and ethanol and blood. Lysa to consider this and contact me.

7. Whole swabs

I stated that we were still receiving whole swabs rather than swabs in tubes and asked what we should be doing about these.
This shouldn't be happening, and if it does we should just put them in tubes and profile them.

8. Moot court training

They will be carrying out moot courts around presumptive testing and have been provided with a list of FAQ by VKI. They would like answers to these questions. Since Scientific and SOCO have experience of going to court, they only need questions relating to the science, combur testing and questions around blood and cells.
They will provide me with a statement and I will provide them with answers to the questions.

9. Assessment of labs / review of sampling techniques

Asked if they needed assistance with this. Difficult since labs are all over state. They will wait 2-3 months for the processes to be bedded in

and for some environmental monitoring results to come back before progressing this.
They may require some consultation for the new masters course that they are setting up.

10. Feedback mechanism and review of FERROs

To be done on an ad hoc basis as required.

11. Sampling issues

I raised some sampling issues and can provide further information if required.
Some key points are:
If any mistakes with regard to semen examinations are made, they should be flagged to QPS Quality Management straight away. They will contact Lindon Smallwood who will liaise with me.
If a swatch is sent in a tube from an AP+ve area, submit as cells. Any mistakes are the fault of the QPS if they haven't been sampled appropriately.
Some tape lifts have had two tubes submitted under one barcode. This is because the kits did contain two of everything. This shouldn't happen any more, but if it does, QPS are happy for the two tapes to be combined. They should be from the same area.

12. Hairs

I understood that SOC were recovering hairs into tubes and submitted for analysis without carrying out any examination for roots or RSM. I explained that many hairs would be submitted that would not be suitable to analysis if microscopic examination was not performed first. Troy explained that in SA they were obtaining profiles from DNA adhered to the outside surface of the hair and this was the DNA that the QPS were targeting. We discussed that placing the hair into the tube may not be the best submission method since longer hairs would not be fully immersed in the extraction buffer. Cutting the hair up into the tube would also not be appropriate as it would be difficult to get it into the tube due to static and that the hair would not stay in the bottom. Suggested that the best way forward would be to either swab the surface of the hair with the corner of a piece of filter paper or to submit the whole hair to us (wrapped in paper) with the advice that the QPS require the hair to be tested for DNA adhering to the hair. Lindon suggested that Scientific were examining some hairs to see if root are present. I offered to provide some training around assessing hairs for roots and RSM, since it is the RSM from which we obtain a profile. Lindon is going to progress this.

I have since discussed this with Cathie Allen who has suggested that it may be better (when looking for DNA on the outside surfaces of the hair) to stick the hair to tape and process as a tape lift.

13. Tricky items

I have had some call asking the best way to sample the more tricky items, this has resulted in the whole item being submitted for us to sample. I asked if they would require me to go into QPS to assist with the more tricky examinations. Not at this stage. They will call me to get advice about how to examine the item. If they decide to send the item in then they request that we let them know how we actually examined the item once we had it in front of us and what result was obtained. This will assist them to decide what to do in the future.
I was asked to provide feedback on [redacted] – knotted fingers of latex glove used to transport drugs.

14. Environmental sampling

These swabs will be submitted as 'swab head in tube' and will be submitted via property point as an ordinary case. Each lab will have its own UR number and will retain this number. Troy to notify me of what these numbers are.
Batch testing of tape lifts will be submitted in the same way.
Dave to send environmental cleaning procedure through to me to have a look at.

15. Analytical issues

Issues raised by AI:

Floppy post-it flag is much better than stiff post-it because the floppy one can be scrunched easier for immersion in 0.5ml of buffer.

Noted

1.5ml tubes for tapes and excised stains are better that 2.0ml tubes due to the increased vertical tolerance for sample size when immersing in 0.5ml of buffer. (1.5ml tubes have a more conical base, and 2.0ml tubes tend to be flat sided with a round or pointy bottom)

Lysa stated that she thought that the 1.5 ml tubes could not be used as they did not fit onto the platform. She is planning on outsourcing the kits so needs to know ASAP which tubes we require. AI to address this.

Please label with smallest barcode vertical so that we can scan it

Noted

DNA IQ as we have validated it and kit is manufactured for is for a sample to be 0.5 x 0.5 cm in size. Anything more than that reduces quality of results.

Noted

If using 4N6 swab, try to break near to swab head please. If not using 4N6 swab, break as close to swab head as possible.

They are trying to do this, but have had an issue where breaking the stick against the side of the tube caused the tube to split. Tory stated that he had been told that it only takes 20-30 secs for analytical to trim the sticks on the swabs and therefore they don't see this as a time issue for us. If we find that it is taking longer than this then we need to let them know.

16. Additional sampling issues

Cig butt recovered from scene on Friday, it was raining and item was wet. It was placed in a CSSE and was delivered on Monday. CSSE was stained – discuss item should have been dried or frozen.

EJC to send case number through to Lysa

Tape lift taken for touch DNA had hairs on it. Remove hairs from item before tape lifting.

SOC and Sci have been told to hand pick any hairs off of items before tape lifting. If any come off onto the tape lift after that – so be it.

If whole swab received post 1st July that it thought to be blood stained and there is no evidence from FR that TMB test has been done – do we TMB test it or just submit?

TMB test please, but also bring this to the attention of the QPS because this shouldn't be happening.

17. Is there anything else we can assist QPS with?

They requested being able to call somebody out of hours, especially at the weekends. Primarily to assist with any lab based issues. We will look into this but is not available at the moment.

QPS requested our support during this time of change. They have lots of people to train and these people are scattered over a large area. It will take time for the processes to become embedded. Please be patient.

18. Discussion with Michael Keller and Tony Carstenson

Michael and Tony expressed their concern over the time frames that we are giving. We explained that these are for the completion of the case. We had discussion around moving to item based timeframes as this is the more critical information. For a sexual assault case, for example, they want to know how long it will be for results to be reported back on the SAIK, not the SAIK, trousers, bedding and any other items.
We are happy to give time frames on items rather than cases, however we do require the QPS to be more specific when requesting such information.

Emma Caunt
24th July 2008

CA-79

Meeting with QPS regarding changes to workflow from 1 July 2008

Location: QPS Headquarters
Date: 17th July 2008
Attendees: VKI, JAH, CJA (FSS, DNA Analysis)
Michael Keller, Troy O'Malley, Dave Keatinge, Andrew Stanley, Lyndon Smallwood, Brad Hall (QPS, FSB)

Discussion Point	Information/Agreed outcome	Action (and by)
Sub sampled item packaging (in CS envelope?)	Samples in tubes will be submitted in crime scene envelopes. QPS looking at reducing size of envelope but window will remain.	
Will envelope details be photographed and envelopes discarded as per current V/C procedures?	Agreed FSS will photograph envelopes and discard packaging as per current volume crime swab procedures for all sub samples submitted (volume and major crime)	FSS to ensure current procedure expanded to include all relevant samples by 1 July 2008.
Will items like cig butts, food, i.e. small items that are not tape lifts or swabs be sub-sampled?	Cig butts will be submitted as whole items to FSS. Food will be sampled by QPS. FSS advised best approaches is swabbing for hard food items, sampling directly for soft food items. Syringes, sanitary pads, tampons, condoms and chewing gum will be delivered to FSS for examination and sampling. Spitting cases – if collected by SOCO, most likely will tape lift or swab, therefore phadebas not an option. If phadebas required, FSS to examine items in short term, QPS to introduce method. Agreed if area can be localised, will excise stain for FSS.	FSS happy to provide advice and assistance regarding sampling strategies. Senior Scientist will be allocated as the main contact person. FSS provide SOPs for phadebas testing. QPS Scientific to introduce phadebas testing.

Confirm sexual assault cases workflow – SAIKs examined by FSS, all other items examined by SCI (collected by SOCOs?)	SAIK submitted to FSS for examination. If negative results returned to QPS, scientific will prioritise, examine and submit sub samples from additional items. Confirmed that examination of SAIK includes all components, this is standard practice within lab. Agreed we would use case EXR to recommend further sub sampling. QPS advised they are hoping that Investigating officers will be informed of the new process at the scene by forensic officers.	FSS can refuse additional items for sexual assault cases, these should be examined by Scientific officers.
Items collected by I/Os examined by SCI not FSS	QPS advised that in the short term, these items will be examined by FSS while they assess capacity. Agreed large numbers are not expected and will be from major crime only. Most likely to be clothing collected by I/Os at secondary scenes and directly from suspects.	FSS will liaise with DNA Unit to prioritise testing of these items as per agreed procedures.
Triage – could QPS just submit the items that need examination? Does this simplify the allocation/triage process?	Forensic Officers will use judgement to identify critical samples for submission. Process in place for DNA Unit to review major crime cases with >30 items and volume crime cases with >5 items.	
Tapelifts – will post it tags be left on the tapelift?	At this stage, the tabs will be left on the tape lift for trace DNA kits used at scenes. Tape lifts from items examined in scientific labs will have tab removed. Agreed that alternative options such as use of double sided tape, or reducing the size of the tab will be explored for future batches.	
Feedback – through Quality management unit	Agreed to use existing feedback mechanism	

to flag inconsistencies in samples	through the Forensic Standards Unit.	
Destruction process for sub-samples – same as current V/C swab process? Sample is either consumed or stored, not returned to QPS property.	Process agreed to. No feedback to QPS required on whether sample has been consumed or any remains. Unused sample will be stored by FSS in line with existing procedures for volume crime swabs.	
Swabs – can they be broken off closer to swab tip?	Not at this stage. Agreed that FSS would manage this process. QPS to discuss changing break point with manufacturer when next batch ordered.	
Who will take responsibility for reworking decisions? Currently us, but have more awareness of sample context, case history etc.	Agreed to following: For major crime, FSS will use current reworking strategies such as concentration or clean up techniques on sub samples submitted. If resampling or pooling is recommended, this decision will be made by scientific officers in consultation with FSS scientist. For sexual assaults, FSS scientists will make decisions for reworking strategies for SAIKs and recommend additional sampling where appropriate. Volume crime – additional work not considered, limited reworking – "one shot, no result, bad luck"	
For samples in tubes, will the High and Low priorities for Major and Volume still be applied?	Yes Occasionally volume crime cases can be prioritised as HIGH if linked to major crime. In these cases, treated same as major crime	

	case with respect to reworking strategies.	
Multiple sub-samples from one item, how many so we profile, needs to be considered as part of the triage process. Also will we be able to see if sub samples have come from the same item?	Each sub sample will have it's own bar code as will each parent item. Parent bar code will be transferred through to AUSLAB via the clinical notes. This in addition to detailed sample description and location information will assist in determining when pooling of samples is appropriate. Discussed fingernail kits – agreed to keep one sample per digit. Can be pooled if required.	
Cold cases – need the DNA Unit to manage the prioritisation and liaison with Investigating Officers	Not discussed	
Do we have access to items if resampling is required? How do we manage this communication? Can we make recommendations?	QPS advised where possible that they will perform any resampling; however this will be assessed on a case by case basis through consultation between scientific officer and case scientist. May occur at FSS. Agreed to use case EXR to request additional sampling as trigger to start discussions.	
Cross over period of old vs new procedures. Unable to establish timeframes immediately for TAT until existing work is managed.	Not discussed.	
Quality – testing of kits prior to use	FSS agreed to test one sample per batch. Will be sent to lab at same time as distribution. FSS will provide feedback on results to QPS Quality management unit.	

Quality – environmental monitoring of QPS lab spaces	Agreed to perform monthly environmental monitoring at all 7 sites for a period of 4 months, then review. Samples to be taken prior to monthly deep clean. Agreed to a maximum of 4 swabs per site. QPS will create a FR number for each site and each sample will have it's own bar code. FSS will report results back through the interface.	Send FSS environmental monitoring SOP to Brad Hall. Send cleaning SOP to Brad Hall
Sampling experience and training – getting the best sample 1st time.	Not discussed	
Interface changes – case and item submission information.	Provided sexual assault and non-sexual assault questionnaires. Troy advised brief is not to include anything in FR enhancements that are not required for us to determine testing methodology. Therefore QPS will be responsible for anything to with interpretation of results such as enquiries about source of profile. Agreed to include the following additional information: Intensity of staining, washed/not washed, substrate (denim, leather, reflective jackets), dry/wet stain, presence of oil/dirt/vegetation/lubricant, fingerprinting.	FSS agreed to provide feedback to Forensic Standards Unit when forensic relationship fields are not used correctly, e.g. when all boxes are ticked. Troy to create additional fields in Forensic Register and provide to FSS to review. Will be transferred initially in clinical notes, to be included in generic interface enhancements.
Reporting framework – what will QPS report?	"Cradle to grave" statements from forensic officers including DNA results.	FSS will review current results and explanatory notes sent across interface and

	Advised they intend to expand this approach to other areas such as fingerprints.	provide suggested phrasing for inclusion in forensic officer statements.
Reporting framework – what will FSS report in statements? When will statements from scientists be required? How will we manage mixtures, results interpretation, statistics	Agreed that statistics, mixture interpretation, paternity results and any questions relating to quality or quantity of DNA will still be reported by FSS scientists.	Meeting with FSS, QPS and DPP scheduled for 27th June at 10am.
What evidence will SOCOs, SCI provide in court?	Will now provide evidence on sampling, sample selection, presumptive screening test results. FSS scientists will still be required if DNA is being questioned.	
Reporting framework – FSS to support moot court training?	Yes FSS provided short list of common questions used for moot court training. Agreed to assist with production of FAQ and standard responses. FSS offered assistance in moot courts.	
Liaison scientist position – role clarification, main contact point	Senior scientist at FSS will be appointed as main contact person for QPS to respond to any queries regarding sampling, reporting, feedback, training etc.	Contact details to be provided to QPS.

CA-80

Queensland Government

Queensland **Health**

Enquiries to: Vanessa Ientile
Telephone: [redacted]
Facsimile:
File Ref: 17072008

Superintendent M Keller
Forensic Services Branch
[redacted]

Dear Michael

I am writing to provide you with an overview of the changes being made within DNA Analysis, FSS to start moving towards meeting the desired service delivery you outlined in the meeting held here at FSS on the 6th June. I am also seeking your support on some initiatives we believe will assist in the delivery of reduced turn around times.

Since the meeting on the 6th June, you would be aware of follow up meetings with both QPS and QHFSS staff to work out the details involved in delivering the changes to sampling and submission of items for DNA analysis. From my perspective these meetings have been very productive and would like to pass on my thanks to you and your staff for their involvement. There will be an adjustment period as the new processes are embedded in both departments and we are committed to working towards solutions for any issues that may arise.

As you might be aware the DNA Analysis unit has commenced implementing major changes to start to meet our client's requirements of faster delivery of DNA results.
The changes include:

- Reorganisation of the team structure to replace Major and Volume crime teams with an Evidence Recovery & Analytical team and a Reporting & Intelligence Team.
- Separation of processes for existing workload and new submissions post 1 July 2008.
- Process analysis to identify bottlenecks and implement changes to streamline processes.
- Investigation into shift work arrangements for DNA analysis staff
- Introduction of a Senior Scientist, Client Liaison position to assist with QPS queries

It is important for me to stress that we <u>are unable to provide a 48 hour turn around time</u> at the moment. As we have discussed previously we have a large body of work in progress that requires completion, and have reduced scientific staff numbers from 76 to 60 as temporary funding for backlog reduction expired at 30 June 2008. Due to the equipment analysis time required to produce a DNA profile, not to mention the human intervention to set up the analysis and interpret and peer review the results, that turn around time cannot be delivered on a routine basis at present. On previous occasions where this has been delivered, these have been exceptional circumstances with severe disruption to normal processing of other samples and overtime for staff.

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We are however working towards being able to provide you with timeframes for DNA results based on your priorities and case types. This will be a staged process as it relies on a number of steps including:

- Complete implementation of separate processes for items delivered before 1 July 2008 and items delivered after 1 July 2008.
- Monitoring of submissions after 1 July 2008 and determination of resources required.
- Data analysis of turn around times for items delivered after 1 July 2008
- Analysis of existing workload to determine timeframes for completion based on current staffing levels
- Allocation of resources to continue working on existing cases submitted prior to July 1 2008.
- Development of target timeframes based on case type and priority.

As I have mentioned, we have implemented separate streams to manage work submitted prior to 1 July 2008 and new work submitted after 1 July 2008. We have allocated our resources to the separate streams.

There are approximately 350 major crime cases received prior to 1 July that are still awaiting analysis to start. The DNA Unit is assisting us to prioritise these cases and items based on investigative requirements and court dates. We are currently able to commence analysis on approximately 4 cases per week and can provide estimated timeframes for completion once the case is actually started.

We are forwarding enquiries from Investigating Officers regarding timeframes to the DNA Unit and it would be appreciated if they are able to manage these enquiries. From our perspective, if a timeframe was requested, we would like the DNA Unit to determine the urgency of the case being enquired after in comparison to the other cases awaiting analysis to decide whether analysis should be commenced urgently or can be placed on the awaiting allocation list. We request the DNA Unit to inform FSS as to whether these urgent cases take precedence over the other cases awaiting allocation. If the case is not deemed urgent, then we request that the case be placed on a priority list as managed by DNA Unit and FSS. If analysis is required urgently, then we can estimate a timeframe based on the work required; however, if a case is not required urgently, then we cannot provide an estimated timeframe until the case is started.

Previously timeframes were always provided to Investigating Officers based on completion of the entire case including a statement as this was often required for the scheduling of court dates. There will still be a need for this, however we are also moving towards providing item based timeframes and would appreciate it if the request could be clarified to ensure we give the most appropriate information.

For submissions received after 1 July 2008, the following process is in place.

- Priority 1 (Major Crime) samples in tubes are started within 24 hours
- Priority 1 Sexual Assault Kits are started within 2 days

Currently we cannot provide timeframes for when the following sample types will be started; however, we endeavour to start these items as soon as possible after receipt.

- Priority 1 (Major Crime) other items

- Priority 3 samples in tubes
- Priority 3 items

We anticipate that as these samples start to move through the process, we will be able to determine accurate timeframes for the provision of DNA results and expect to be in a position to do this by the end of August.

I am aware that it is a large task to roll out these changes across the state and that there will be a period of adjustment where it feels like numerous small operational issues are being fed back from us. We are supportive of this process, but believe that if we do not address these issues immediately, we run the risk of allowing shortcuts and incorrect procedures to become embedded and potentially impacting on the delivery of the overall goal – faster DNA results.

One strategy that would assist greatly would be for the forensic officers to only submit the items that they believe require testing. There have been a few occasions where samples have been submitted and later retracted and I have also received anecdotal feedback that forensic officers are submitting all items at the request of Investigating Officers. I may have misunderstood the intention of the changes, but I thought that the forensic officers were taking on the role of selection of appropriate samples for DNA analysis.

As mentioned, the purpose of this letter was to give you a detailed overview of the changes we have made and reinforce our commitment to working towards the delivery of DNA results much faster.

If you have further questions or require any clarification, I would be more than happy to meet with you to discuss these. I think that it would be timely for us to re-introduce monthly meetings to monitor progress and address any issues that have been escalated and would be happy to arrange these. I would also be happy for you to disseminate this letter to your staff to inform them of the processes we have introduced.

Yours sincerely



Vanessa Ientile
Managing Scientist, DNA Analysis
Forensic and Scientific Services
23 / 07 / 2008

Trial of Copan 4N6 flocked swab

Allan McNevin, Senior Scientist, Chiron Weber, Scientist
DNA Analysis, Queensland Health Forensic and Scientific Services

Introduction

The examination of items for forensic DNA testing is a labour intensive and depending on the item, a time consuming process. For simple items such as swabs, laboratory efficiency could be improved by delivering items to the testing laboratory in a format that is suitable for analytical use. Such a format includes the supply of swab heads packaged in a tube suitable for testing in the analytical environment, i.e. suitable to be used directly in the DNA extraction procedure without the need for examination by a scientist. One such product available is the 4N6 DNA flocked swab (Copan). One format that the product may be purchased in is a kit containing a flocked nylon swab packaged with a 2mL tube (eppendorf) with a vented lid allowing for the drying of the swab head (catalogue number [redacted]). Figures 1 and 2 are reproduced from the 4N6 swab brochure [redacted]
Figure 1 is a representation of the ease with which the flocked swab will elute specimen as compared to a traditional swab in Figure 2.



Figure 1. Flocked swab elutes specimen more efficiently.



Figure 2. Traditional fiber (sic) swab elutes less specimen.

The website also provides a link to forensic studies. However, the information is based around testing for viral and bacterial pathogens rather than forensic testing. There does not appear to be any published papers that directly compare the 4N6 swab with other swabs currently used.

AIMS

The aim of the testing carried out was to compare the 4N6 DNA flocked swab (Copan, product code 3520CF) with two swab types that are currently in use for the collection of material for forensic DNA testing. The swabs would be compared on two criteria:

1. The ability to extract DNA from each swab type and,
2. The ability of each swab type to uptake DNA.

The two swab types chosen to compare against the 4N6 swab were a spun cotton swab with a small swab head and paper shaft (Copan, product code 164C) and a spun rayon swab with a medium sized swab head and plastic shaft (Copan, product code 155C). Initially five 4N6 swabs were received from Interpath for testing, deliveries of five and fifteen 4N6 swabs were received from Queensland Police Services (QPS) for further testing.

MATERIALS AND METHODS

Experiment 1 Release of DNA from blood

30µL of whole blood was spotted directly onto the surface of five swabs of each of the three swab types outlined above. This was done by cutting the head of the swab from the shaft into a sterile DNA-free tube using a pair of scissors sterilised by washing in 10% bleach, followed by 100% ethanol and flaming. 30µL of whole blood from a donor staff member (collected approximately 3 months previous and stored at 4°C) was added to each swab head and allowed to air dry for 1 hour at 56°C on a Thermomixer comfort (eppendorf) with no agitation.

The DNA was then extracted, quantified, amplified and profiles visualised according to standard laboratory procedures. Briefly, this entailed the lysis of cellular material in individual tubes (by incubation of substrate in 500µL of a buffer containing Proteinase K and Sarcosyl). The lysis solution was separated from the substrate by centrifugation and then added to a 96 deep-well plate using the *automate.it* STORstar system (Process Analysis & Automation Ltd. Hampshire. UK). The DNA was extracted from the lysed solutions using the DNA IQ™ kit (Promega Corp.) on a dedicated MultiPROBE® II PLUS HT EX with Gripper™ Integration platform (PerkinElmer). In the final staged of the extraction procedure, the DNA extracts are placed into individual tubes. The DNA extracts were then stored at -20°C between each of the following procedures.

The amount of DNA in each DNA extract was then quantified using the Quantifiler™ Human DNA Quantification kit (Applied Biosytems), prepared on a MultiPROBE® II dedicated to PCR set-up. The real-time PCR is then performed on an ABI Prism® 7500 Sequence Detection System (Applied Biosytems). Once the DNA quantification has been determined, an appropriate amount of DNA template is added to the STR amplification reaction. STR analysis is carried out by amplification with an AMPFℓSTR® Profiler Plus® PCR Amplification kit (Applied Biosytems), prepared on a dedicated MultiPROBE® II and amplified on a GeneAmp® PCR System 9700 thermalcycler (Applied Biosytems). Fragment analysis was performed by capillary electrophoresis on an ABI Prism® 3130*xl* Genetic Analyzer (Applied Biosytems), in combination with GeneScan® (version 3.7.2) and Genotyper® (version 3.7.1) software.

Experiment 2 Release of DNA from blood over dilution series

Dilutions of whole blood were made and spotted onto swab heads of each of the three swab types under test. This was done by firstly diluting whole blood from a donor staff member (collected approximately 3 months previous and stored at 4°C) in nanopure water in the following dilution series; 1 in 5, 1 in 10, 1 in 20, 1 in 50. 30µL of neat blood and one of each dilution series was added to each swab type under test as outlined in Experiment 1. DNA was extracted, quantified and amplified according to procedures outlined in Experiment 1.

Experiment 3 Release of DNA from cellular material

A suspension of buccal cells was made to perform testing. Buccal cells were collected from a female donor (a previously profiled staff member) using the Cytobrush™ method. Briefly, two Cytobrush™ Plus Cell Collector devices (Cooper Surgical, Inc., Trumbull, CT, USA) were used to collect buccal cells from each cheek for 1 minute, then collected into 500µL of 0.9% saline solution (Baxter Healthcare, Old Toongabbie, NSW, Australia) in a sterile 2mL tube. 30µL of buccal cell suspension was spotted directly onto the surface of five swabs of each of the three swab types outlined above. This was done by cutting the head of the swab from the shaft into a sterile DNA-free tube using a pair of scissors sterilised by washing in 10% bleach, followed by 100% ethanol and flaming. 30µL of buccal cell suspension from a donor staff member (collected the same day as testing) was added to each swab head and allowed to air dry for 1 hour at 56°C on a Thermomixer comfort (eppendorf) with no agitation. DNA was extracted, quantified and amplified according to procedures outlined in Experiment 1.

Experiment 4 Release of DNA from cellular material over dilution series

Dilutions of a buccal cell suspension were spotted directly onto the surface of five swabs of each of the three swab types under test. This was done by firstly diluting a buccal cell suspension from a donor staff member (collected approximately 1 week previous and stored at 4°C) in nanopure water in the following dilution series; 1 in 5, 1 in 10, 1 in 20, 1 in 50. 30µL of neat buccal cell suspension and one of each dilution series was added to each swab type under test as outlined in Experiment 3. DNA was extracted, quantified and amplified according to procedures outlined in Experiment 1.

Experiment 5 Uptake and release of DNA from blood and cellular material

30µL of whole blood (collected approximately 3 months previous and stored at 4°C) and 30µL of a buccal cell suspension (collected the same day as testing) was spotted directly onto the surface of new plastic Petri dish and allowed to dry overnight at room temperature in a class II biohazard cabinet. The dried area was marked on the underside of the Petri dish so that the area containing dried sample could later be identified. The dried samples were stored for approximately 15 weeks at approximately -20°C prior to sampling. Five swabs of each type under test were used to sample the dried blood stains using standard laboratory techniques employed within the laboratory for liberating dried blood stains from crime-scene exhibits. Briefly, this entailed wetting of the swab head with nanopure water and rubbing the stained area with the endmost area of the swab head. The procedure was repeated to sample dried cell suspensions. DNA was extracted according to procedures outlined in Experiment 1, with minor modifications to the automated extraction protocol resulting from process improvements incorporated between experiments. Briefly, these modifications included incubation of the substrate in 300µL of buffer during cellular lysis and improved mixing and pipetting steps during the automated protocol. DNA was quantified and amplified according to procedures outlined in Experiment 1. Additionally, capillary electrophoresis data was analysed using GeneMapper-*IDX* (version 1.0) software due to process improvements incorporated into the laboratory between experiments.

RESULTS

Experiment 1 Release of DNA from blood

Table 1 below shows quantitation values for each swab head tested and the average quantitation value for each swab type. The same data is also represented in Figure 1 below.

Table 1. Summary of results from Experiment 1

4N6 Swab		Cotton swab		Rayon Swab	
Sample	**Quantification value (ng/µL)**	**Sample**	**Quantification value (ng/µL)**	**Sample**	**Quantification value (ng/µL)**
1	0.8490	1	0.4290	1	0.6200
2	0.5000	2	0.2650	2	0.6810
3	0.9050	3	0.3690	3	0.5150
4	0.8050	4	0.6040	4	0.4740
5	0.7610	5	0.3810	5	0.4780
mean	*0.7640*	*mean*	*0.4096*	*mean*	*0.5536*

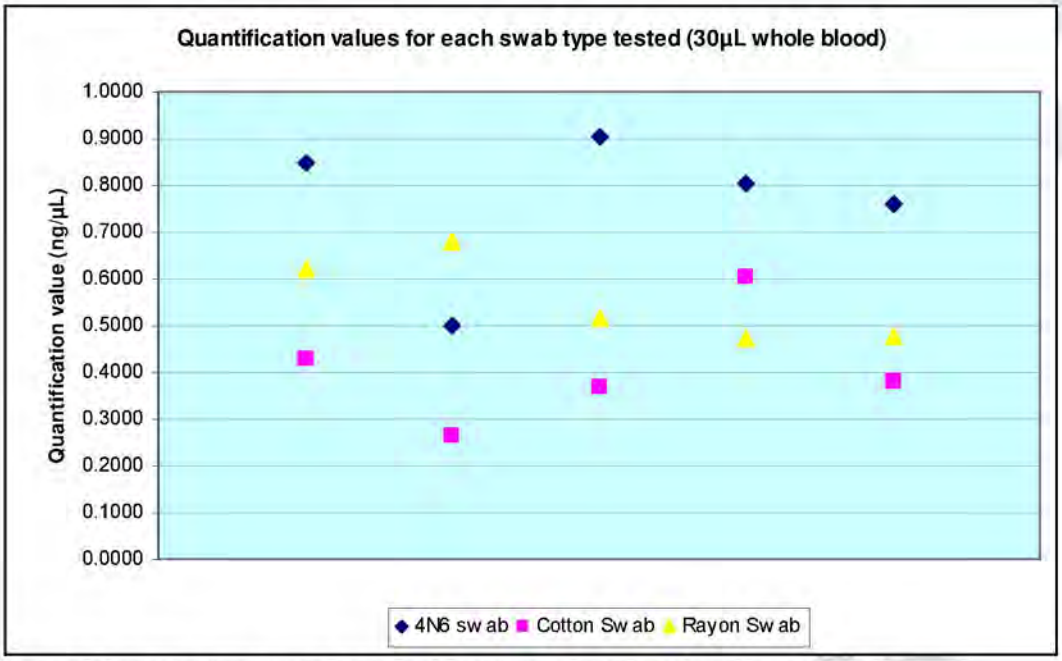

Figure 1. Quantification values for each of 5 replicates for each of 3 swab types tested

For every swab tested, full 9-loci DNA profiles were obtained, consistent with the expected profile.

Experiment 2 Release of DNA from blood over dilution series

Table 2 shows the quantification values obtained or the dilution series for each of the swab types tested. These results are also shown in Figure 2 below.

Table 2. Summary of results from Experiment 2

Dilution series	DNAQuantification (ng/µL)		
	4N6 Swab	Cotton Swab	Rayon Swab
Neat blood	0.517	0.177	0.555
1 in 5	0.0926	0.07	0.0665
1 in 10	0.0982	0.0598	0.107
1 in 20	0.0518	0.0303	0.0499
1 in 50	0.02	0.0177	0.0104

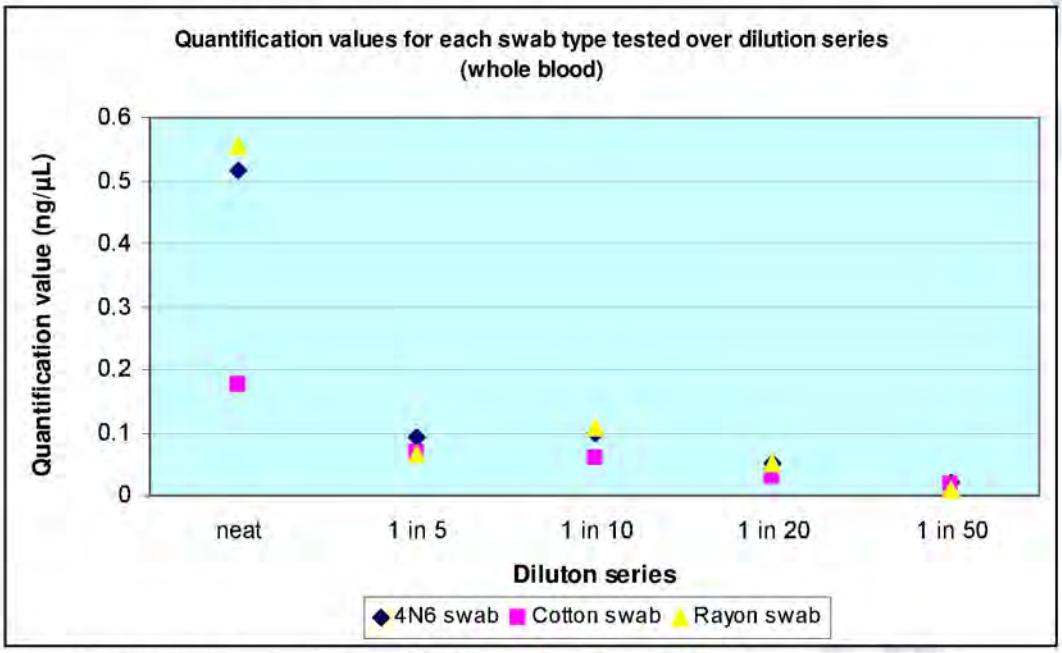

Figure 2. Quantification values from each dilution series for each of the 3 swab types tested

As with Experiment 1, all swabs yielded a full 9-loci DNA profile consistent with the expected profile.

Experiment 3 Release of DNA from cellular material

Table 3 below shows quantitation values for each swab head tested and the average quantitation value for each swab type. The same data is also represented in Figure 3 below.

Table 3. Summary of results from Experiment 3

4N6 Swab		Cotton swab		Rayon Swab	
Sample	**Quantification value (ng/µL)**	**Sample**	**Quantification value (ng/µL)**	**Sample**	**Quantification value (ng/µL)**
1	1.91	1	0.341	1	0.462
2	1.42	2	0.427	2	0.702
3	0.539	3	0.687	3	0.554
4	0.632	4	0.361	4	0.689
5	1.77	5	0.464	5	0.493
mean	1.2542	*mean*	0.4560	*mean*	0.5800

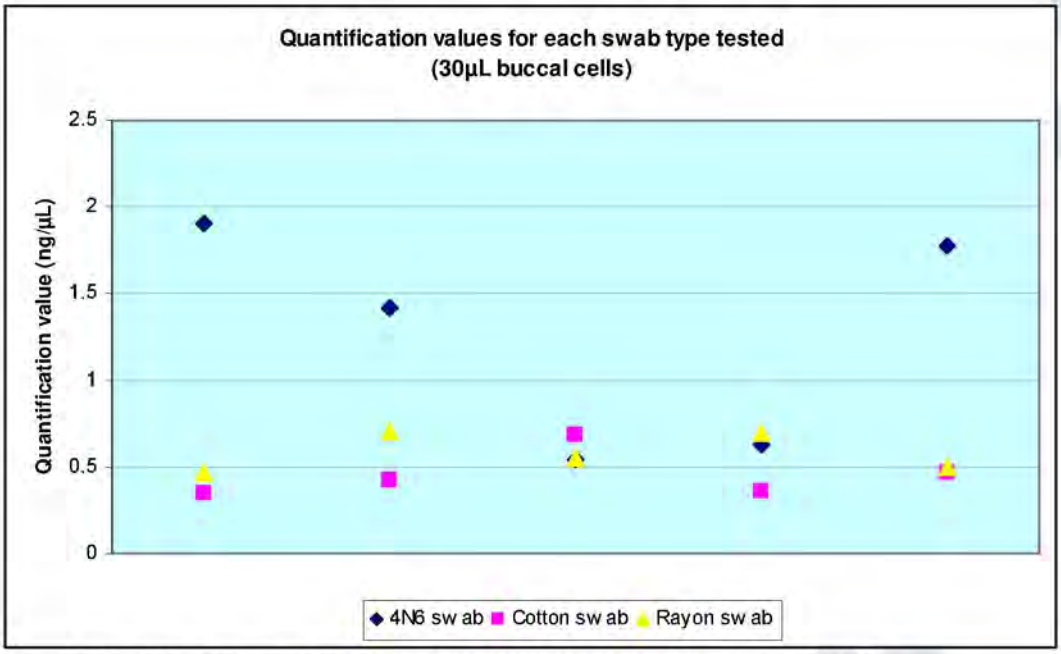

Figure 3. Quantification values for each of 5 replicates for each of 3 swab types tested

As with Experiment 1, all swabs yielded a full 9-loci DNA profile consistent with the expected profile.

Experiment 4 Release of DNA from cellular material over dilution series

Table 4 shows the quantification values obtained or the dilution series for each of the swab types tested. These results are graphically presented in Figure 4 below.

Table 4. Summary of results from Experiment 4

Dilution series	DNAQuantification (ng/µL)		
	4N6 Swab	Cotton Swab	Rayon Swab
Neat cells	1.19	1.06	1.14
1 in 5	0.227	0.257	0.266
1 in 10	0.132	0.101	0.12
1 in 20	0.0652	0.0317	0.0487
1 in 50	0.018	0.0226	0.0401

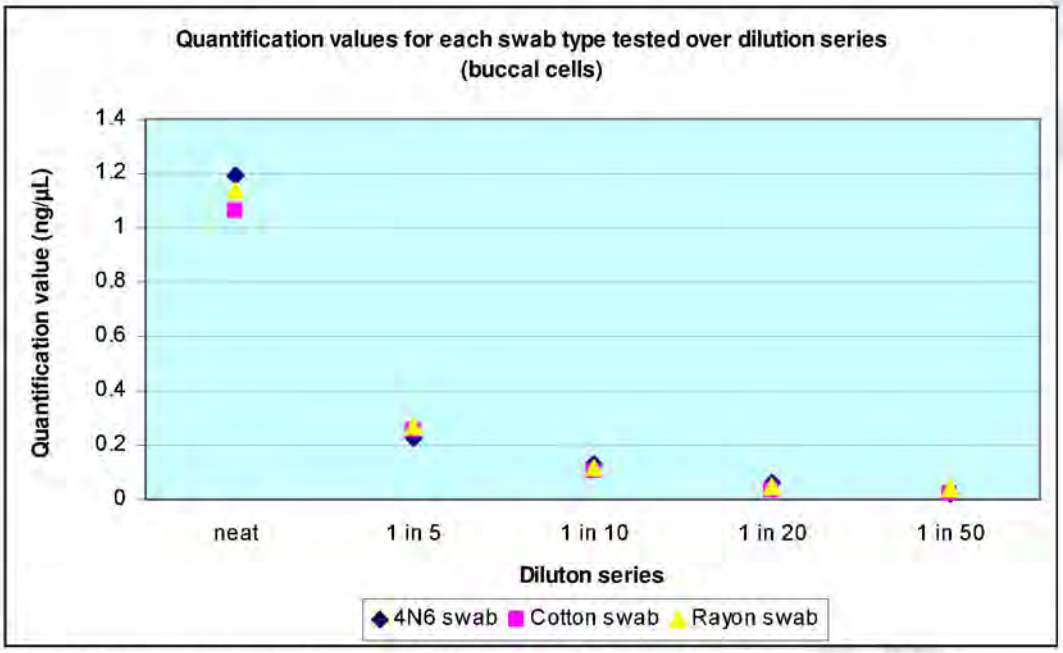

Figure 4. Quantification values from each dilution series for each of the 3 swab types tested

All swabs for samples containing 30µL of buccal cell suspension, as well as all swabs for each of the 1in5, 1in10 and 1in20 dilutions yielded full 9-loci DNA profiles consistent with the expected profile. However, the 1in50 dilution series yielded a full 9-loci DNA profile for the Rayon swab only, with the 4N6 swab and Cotton swab each producing partial DNA profiles (17/18 alleles and 12/18 alleles respectively).

Experiment 5 Uptake and release of DNA from blood and cellular material

Quantification values and profiles obtained for each swab type and sample type are shown in Table 5 below. Quantification values obtained for blood and cell sample types are graphically presented in Figures 5 & 6 respectively.

Table 5. Summary of results from Experiment 5

		4N6 swab		Cotton swab		Rayon swab	
Replicate		Quantification result (ng/µL)	Profile result (alleles)	Quantification result (ng/µL)	Profile result (alleles)	Quantification result (ng/µL)	Profile result (alleles)
Blood	1	0.507	18/18	0.869	18/18	0.785	18/18
	2	0.509	18/18	0.752	18/18	0.536	18/18
	3	0.561	18/18	0.506	18/18	1.12	18/18
	4	0.347	18/18	0.418	18/18	0.421	18/18
	5	0.432	18/18	0.307	18/18	3.39	18/18
	mean	*0.4712*	-	*0.5704*	-	*1.2504*	-
Cell suspension	1	0.298	13/18	0.326	11/18	0.42	10/18
	2	0.252	8/18	0.156	8/18	1.96	3/18
	3	0.26	5/18	0.321	12/18	0.732	4/18
	4	0.367	8/18	0.265	13/18	0.474	13/18
	5	0.456	13/18	0.449	13/18	0.36	13/18
	mean	*0.3266*	-	*0.3034*	-	*0.7892*	-

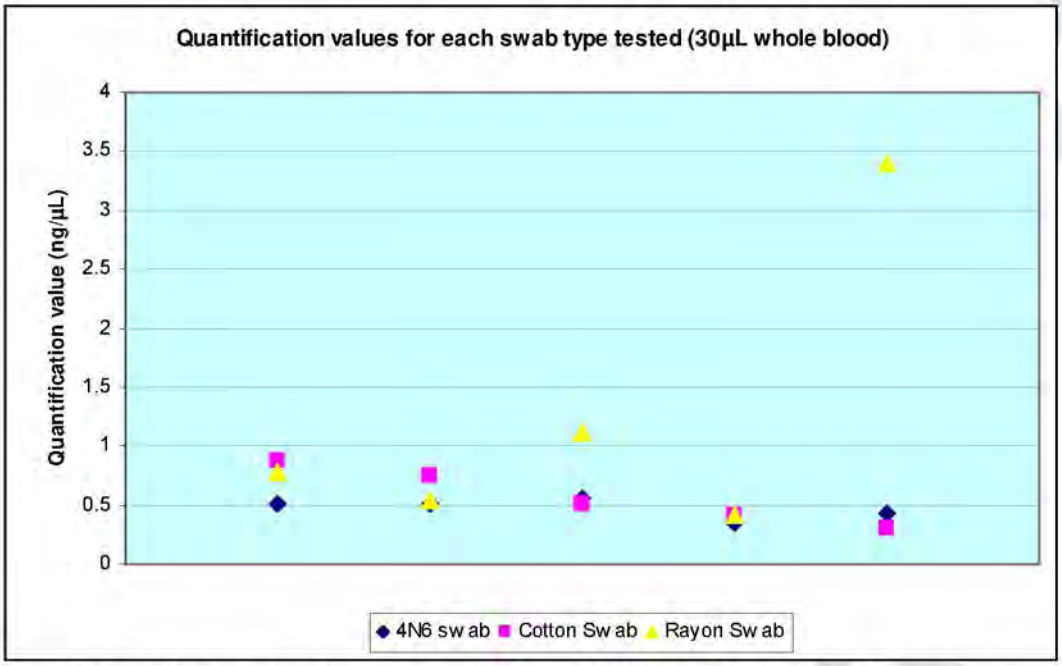

Figure 5. Quantification values from sampling of 30µL of dried blood for each of the 3 swab types tested

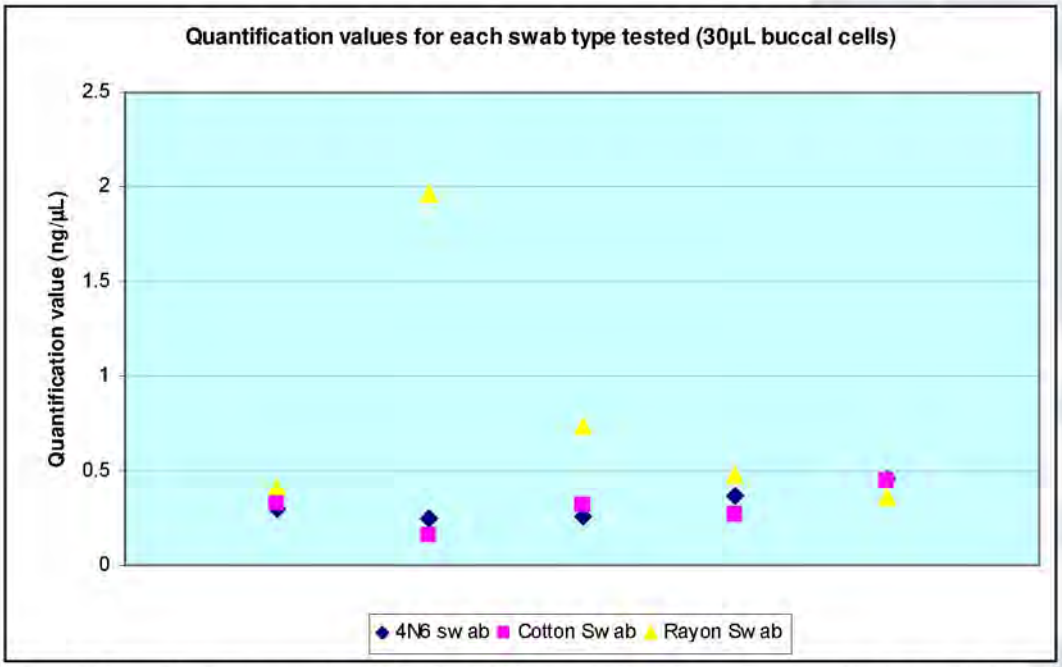

Figure 6. Quantification values from sampling of 30µL of dried buccal cell suspension for each of the 3 swab types tested

Although each swab that was used to sample dried buccal cells yielded partial DNA profiles, each of these samples contained sufficiently high quantification values to suggest that re-amplification with increased DNA template input would yield full 9-loci DNA profiles.

Statistical analysis for significant difference

Quantification values obtained from experiment 1 and from the "neat blood" sample from experiment 2 were compared for various combinations of swab types tested using a two-sided students *t*-test. Additionally, quantification valued obtained from experiment 3 and the "neat cells" sample from experiment 4 were compared using a two-sided students *t*-test. These results are shown in Table 6 below

Table 6. *t*-test results

Comparison**	*p*-value*	
	Blood	Cells
4N6 v Cotton	0.0034	0.0241
4N6 v Rayon	0.0560	0.0486
Cotton v Rayon	0.0234	0.4598

* a *p*-value of <0.05 indicates a significant difference between the two data sets under test when using a 95% confidence interval
**Results generated using Microsoft Excel formulae

Quantification values obtained from experiment 5 were compared for various combinations of swab types tested, using a two-sided students *t*-test. These results are shown in Table 7 below

Table 7. *t*-test results

Comparison**	*p*-value*	
	Blood	Cells
4N6 v Cotton	0.3978	0.7136
4N6 v Rayon	0.1939	0.1640
Cotton v Rayon	0.2577	0.1478

* a *p*-value of <0.05 indicates a significant difference between the two data sets under test when using a 95% confidence interval
**Results generated using Microsoft Excel formulae

DISCUSSION

As can be seen from the two-sided students *t*-test results in Table 6 above, the 4N6 swabs released more DNA (when 30µL of whole blood or 30µL of buccal cell suspension was added directly to the swab head) than cotton swabs. Since the *p*-value that is generated represents a probability of both data sets being not significantly different, and although the *p*-value for the comparison of 4N6 swabs against rayon swabs when 30µL of whole blood was added directly to the swab head falls slightly above the 0.05 threshold (*p*-value = 0.0560), the same can be held true for the comparison of 4N6 swabs and rayon swabs as for the comparison of 4N6 swabs and cotton swabs.

Over a dilution series for each swab type and for each sample type, quantification values and profiling quality obtained were quite similar. As the experiments were not duplicated, no statistical analysis could be performed. These results would support the proposition that, over a dilution series, the 4N6 swabs released DNA at least as well as either cotton or rayon swabs tested.

The two-sided students *t*-test results in Table 7 above show that the 4N6 swabs yielded comparable quantification values when both dried blood and dried cellular material was sampled according to standard laboratory practice. The DNA profile quality (alleles obtained) shown in Table 5 also supports the proposition that comparable DNA profiling was obtained when any of the three swab types were used to sample either dried blood or dried cellular material under controlled conditions. It may be possible that the 4N6 swab actually liberated less material from the dried stain than either of cotton or rayon swabs, but this was balanced by the superior ability of the 4N6 swab to release DNA, therefore resulting in comparable DNA profiling between all three swab types. However this cannot be accurately ascertained as quantification values between experiments 5 and previous experiments cannot be directly

compared as different buccal cell suspensions and slightly different extraction protocols were utilised for each experiment. Additionally, given the small sample size for these experiments (*n*=5), further testing is warranted to draw a clearer conclusion.

Partial profiles obtained for all swab types after sampling of dried buccal suspension may have been due to degradation of DNA from extended storage. It has been the experience within the laboratory that degraded DNA will tend to yield inflated quantification values with the Quantifiler™ Human DNA Quantification kit (Applied Biosytems). These samples were stored for approximately 15 weeks due to delays in testing caused by the demands of routine laboratory testing, and were not part of the testing regime.

There was no evidence of inhibition or other effects on the extraction, quantification or amplification of the DNA extracts obtained from the 4N6 swabs using the methods employed within the laboratory at the time of testing (these included updated methods to be implemented in the short term used in experiment 5).

The shaft of the 4N6 swab contains a breaking point, and with the laboratory procedures currently in place, this breaking point leaves an excessive amount of shaft making it unsuitable for easy processing (i.e. for each swab, it would need to be removed from it's tubing and have the shaft cut at the base of the swab head under sterile conditions, necessitating sterilisation of equipment and work area between each sample).

Recommendations
The testing carried in this trial has been on a small scale and represents some initial evaluation of the 4N6. The testing falls short of a validation or verification. All results should be viewed with caution given the small sample size for each experiment and the limited number of experiments performed, and as such no recommendation is made to either use or not use the 4N6 swab.

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CA-82

[redacted] – excerpt from UR notes re: 4N6 swabs

FULL UR NOTES

Lab : [redacted] UR : [redacted] Name : CASE[redacted] Sex :
Dob : Wd : Dr : Time : 14:00 01-Feb-09

Time/Date	User	Dept	UR Notes
			this info from FIRMU.
12:01 31-Mar-09	ejcl1	L	B - Received call from Cathie exhibits say that 'matches' UKM1 but have other info to say that it's a positive ID to missing person, what does that mean? UKM1 has been loaded to NCIDD. If missing person is also on NCIDD then a match would have been obtained so this other info MAY mean that it has matched on NCIDD. I can't confirm this as I don't have this info. We will only put across a matching EXR line if an evidence sample is obtained. How can they get evidence sample if they have no body? May need to consider surrogate reference sample such as toothbrush.
11:33 31-Mar-09	ejcl1	L	B - Received call from Cathie, some of the swabs were 'soaked' in blood but have still not given profile. All swabs were 4N6 swabs. She will be submitting an additional 3 swabs and some carpet samples for us to look at. Asked her to mark swabs for my attention and we will try a different extraction type.
08:34 31-Mar-09	ejcl1	L	B - Received call from Cathie (Cairns Scientific). Needs to send more samples from the grass mat but wanted to know whether to send in tube or send a section of the mat. Best if she sends section of the mat then we can resample if necessary. Staining is very light but is visible to the naked eye.
07:43 31-Mar-09	dkef1	ALL	B. Ingrid, IO is also sending down another subsample from a mat located outside in household rubbish and may have other unknown contaminants present.

CA-83

Excerpt from QPS_external Communication_Issues log_Current

Date	Question/request	Raised by	Response	Action by	Closed
26/02/2009	Conversation with Lyza McMenz on or about the 23rd or 24th about QPS switching from 4N6 flocked swabs to rayon swabs. Lyza requested some spin baskets (to check the height of the break point of the shaft), and also about the type of tubes that samples could be submitted in.	Lyza McMenz	I sent Lyza some spin baskets in the mail, additionally informed her that screw-cap tubes with o-ring are the best to utilise, received further request from Lyza: Hi Al, I received the spin baskets, thanks. A few suffered in the post. Do I need to take the basket into consideration when sourcing tubes or do you transfer the lysate and sample into a plate / tube after incubation? Also can you tell me the product details of the tube you would prefer to be utilised. I am collecting the swabs tomorrow (5000) and will purchase several types of tubes for trial. If I can get the tubes in next week I will do up a few kits for your evaluation before I send kits to Melbourne for ETO sterilisation. Cheers Lyza my response: Hi Lyza, Discussion around such tubes came up today in a meeting, and I was informed that David (not sure if was David Neville	AM	Ongoing

			or David Keating) already some tubes they had decided on? We currently use SSI brand tubes that we purchase through interpath but have had success with a lot of similar products from other manufacturers and suppliers, lastly - the spin basket does not have to be compatible with the tube you choose, just the swab, cheers Al		

Preliminary Results

40µL of a buccal cell suspension was placed onto 4 each of three different adhesive surfaces as supplied by QPS. A fifth adhesive surface was left as supplied as a blank (negative control) sample. Each of these 15 samples, along with a negative and positive extraction control were extracted using a modified manual Promega DNA IQ DNA extraction procedure. The DNA extracts obtained were submitted for quantification using Applied Biosystems Quantifiler Human DNA Quantification Kit and STR analysis by amplification using Applied Biosystems AMPF*l*STR Profiler Plus PCR Amplification kit and the resultant PCR product analysed through an Applied Biosystems 3130*xl* Genetic Analyzer.

The Quantification results are shown in Table 1 below.

Table 1. Quantification and internal PCR control results

Lab No	Sample Description	Quant (ng/µL)	avg quant	IPCCT
[redacted]	Positive Control	0.453		27.43
	Negative Control	Undetermined		27.4
	White 40uL Blank	Undetermined		27.55
	White 40uL 4	0.0825	0.126375	27.49
	White 40uL 3	0.154		27.43
	White 40uL 2	0.131		27.56
	White 40uL 1	0.138		27.54
	Double-sided Blank	Undetermined		27.68
	Double-sided 40uL 4	0.085	0.15975	27.63
	Double-sided 40uL 3	0.258		27.46
	Double-sided 40uL 2	0.154		27.66
	Double-sided 40uL 1	0.142		27.47
	Post-It Blank	Undetermined		27.53
	Post-It 40uL 4	0.0616	0.02886	27.52
	Post-It 40uL 3	0.0277		27.47
	Post-It 40uL 2	0.00524		27.54
	Post-It 40uL 1	0.0209		27.69

Results obtained from DNA quantification ***indicate*** the following:

- DNA was not detected in the 'blanks' – this means there is evidence to suggest there was no DNA on the tape surfaces prior to testing.
- No samples showed evidence of PCR inhibition (IPCCT >30 indicates inhibition of the PCR)
- "White" and "Double-sided" adhesive surfaces showed superior DNA yields compared to "Post-It" (shown in Figure 1 below) tape.

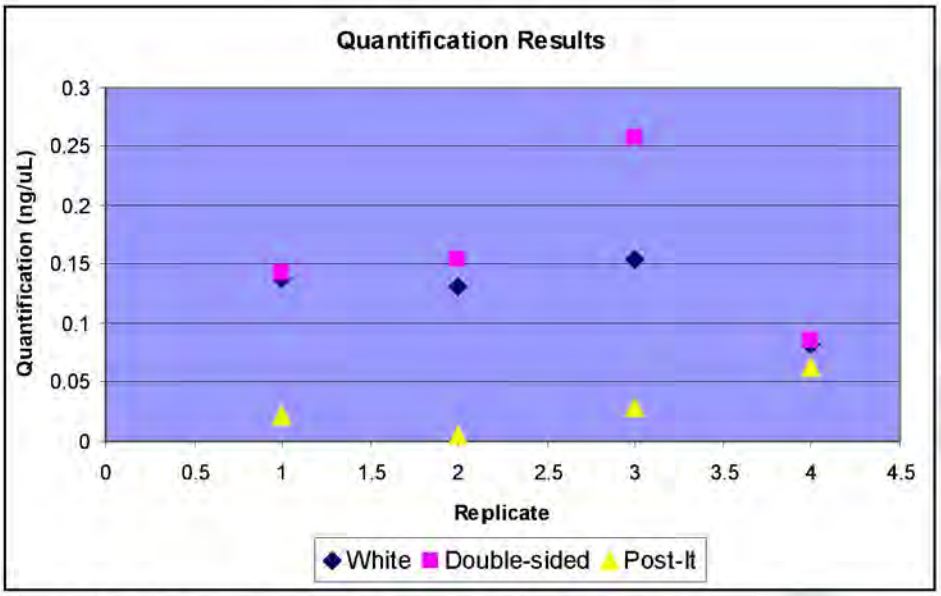

Figure 1. Quantification results for each replicate of each substrate type

As a general guide, a minimum quantification value of 0.05ng/µL is required for the addition of manufacturer-recommended minimum DNA template to the Profiler Plus amplification reaction.

Please note, ***these are preliminary results***. The results of analysis of the Profiler Plus amplified product (DNA results) will provide greater clarification of the results obtained. A more detailed analysis of results will be provided after amplification data has been analysed. There are limitations to the conclusions that can be drawn from the analysis carried out so far, and these will be elucidated in the final report.

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CA-85

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A CLINICAL AND STATEWIDE SERVICE

QPS Tapelift Trial

October 2008

DNA Analysis, Forensic and Scientific Services
Coopers Plains, Brisbane, QLD AUSTRALIA

Disclaimer
This report provides the results for a preliminary assessment and should not be considered as a validation of any kind. Further validation work is recommended in order to assess other variables.
Names of commercial manufacturers are provided for identification only. Inclusion in this report does not infer endorsement by DNA Analysis, Forensic and Scientific Services, Queensland Health.
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Aim

To compare the DNA yield obtained from three different types of tapelift materials that contain comparable amounts of cellular material.

Materials and Methods

Buccal cell collection
Buccal cells were collected from a female donor using the Cytobrush™ method. Briefly, two Cytobrush™ Plus Cell Collector devices (Cooper Surgical, Inc., Trumbull, CT, USA) were used to collect buccal cells from each cheek for 1 minute, then collected into 500µL of 0.9% saline solution (Baxter Healthcare, Old Toongabbie, NSW, Australia).

Sample creation
Three types of tapelift material were supplied by QPS and identified as:

- Post-It Flag (red tab) – 5 pieces;
- Double-sided tape – 5 pieces;
- White tape – 5 pieces.

Four pieces of each tapelift material were laid flat (sticky side facing up) in individual plastic Petri dishes in a Class II Biohazard Cabinet and spotted with 40µL of buccal cell suspension. Samples were allowed to dry at room temperature for 2 hours. The fifth piece of each tapelift material was kept as a substrate blank sample in its original packaging.

All tapelift samples (including substrate blanks) were cut into approximately 5mm x 5mm squares using scalpel blades and tweezers (sterilised by washing in 10% v/v bleach, 70% ethanol, followed by flaming using a Bunsen burner) and added to individual sterile 2mL tubes for processing.

DNA extraction and processing
Processing of samples was performed as per in-house protocols. DNA extraction was performed using the validated manual DNA IQ™ system (Promega Corp., Madison, WI, USA). Samples were quantified using the Quantifiler™ Human DNA Quantification Kit (Applied Biosystems, Foster City, CA, USA), followed by amplification using the AmpFℓSTR® Profiler Plus® kit (Applied Biosystems, Foster City, CA, USA). Fragment analysis was performed by capillary electrophoresis using an ABI Prism® 3130*xl* Genetic Analyzer instrument (Applied Biosystems, Foster City, CA, USA). Fragment data was analysed using GeneScan® v3.7.2 and Genotyper® v3.7.1 (Applied Biosystems, Foster City, CA, USA), with thresholds for heterozygous and homozygous peaks at 150 and 300 RFU respectively (as per routine casework samples). The allelic imbalance threshold was set at 70%.

Results and Discussion

Quantification results are presented in Table 1 below.

Table 1. Quantification and internal PCR control results.

Sample Description	Quant (ng/µL)	Average Quant (ng/µL)	IPC C_T
Post-It 40uL 1	0.021	0.029	27.69
Post-It 40uL 2	0.005		27.54
Post-It 40uL 3	0.028		27.47
Post-It 40uL 4	0.062		27.52
Post-It Blank	Undetermined		27.53
Double-sided 40uL 1	0.142	0.160	27.47
Double-sided 40uL 2	0.154		27.66
Double-sided 40uL 3	0.258		27.46
Double-sided 40uL 4	0.085		27.63
Double-sided Blank	Undetermined		27.68
White 40 uL 1	0.138	0.126	27.54
White 40uL 2	0.131		27.56
White 40uL 3	0.154		27.43
White 40uL 4	0.083		27.49
White 40uL Blank	Undetermined		27.55
Negative Control	Undetermined		27.4
Positive Control	0.453		27.43

A comparison of DNA quantification and DNA profile results are presented in Figure 1 below.

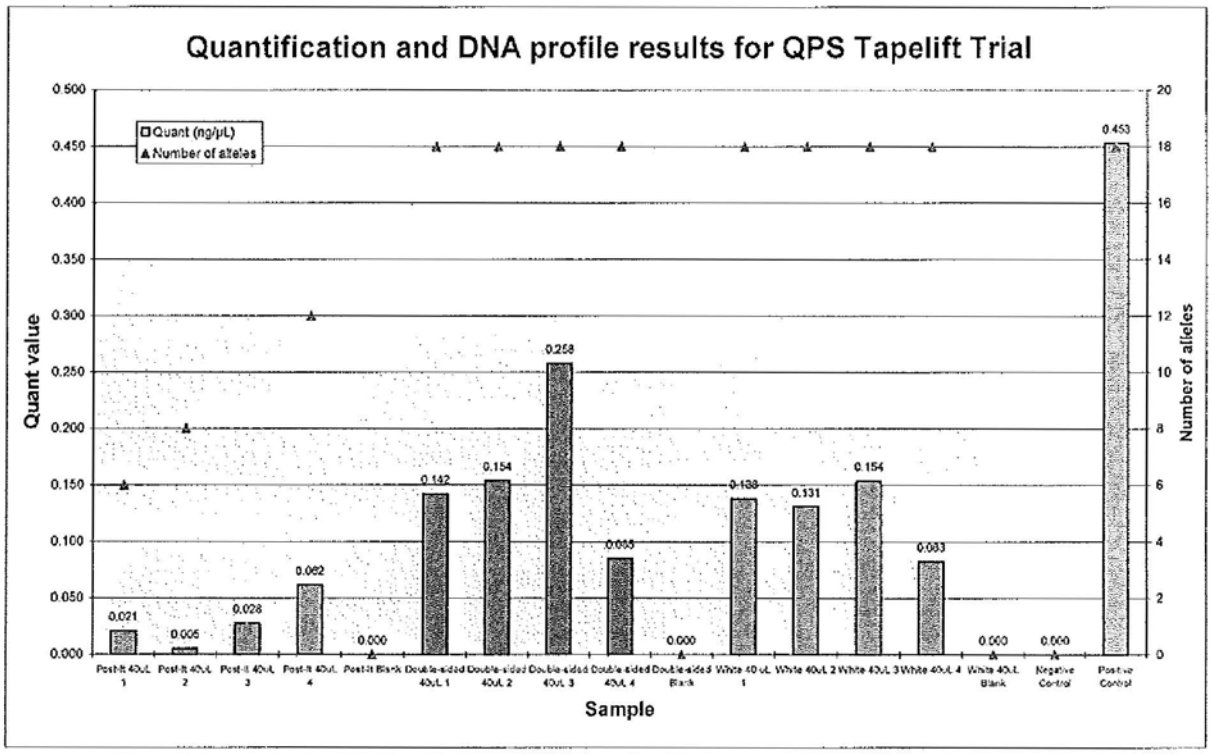

Figure 1. Results for the QPS Tapelift Trial. A full DNA profile (18/18 alleles) includes information on 9 loci (areas) with 18 pieces of inherited information (alleles).

Results obtained ***indicate*** the following:

- The DNA extraction process was free from contamination as shown by the negative control (with the positive control performing as expected).
- The tapelift substrate blank samples (containing no cellular material) did not result in a DNA quantification result, indicating the absence of human DNA material on the original tape materials.
- All DNA profiles were concordant with the expected donor profile. The positive control also generated the expected DNA profile, and the negative control did not result in a DNA profile.
- Inhibition of the quantification reaction was not detected, as indicated by the IPC C_T falling within the criteria for non-inhibited samples ($C_T \leq 30$).
- "Double-sided" and "white" tapelift material showed superior DNA yields compared with the "Post-It" material (Figure 1). As a general guide, a minimum quantification value of 0.05ng/µL is required to achieve the minimal amount of DNA template required for Profiler Plus® amplification.
- All "double-sided" and "white" tapelift samples generated full DNA profiles (18/18 alleles), whereas "Post-It" samples only produced partial DNA profiles (between 1-12 alleles) (Figure 1).

- Reduced DNA yields and concomitant partial DNA profiles exhibited by the "Post-It" samples may indicate that a component of the Post-It material has resulted in:
  - Inhibition of the DNA extraction process (i.e. interference in the binding of the DNA material to the DNA IQ™ resin);
  - Degradation of DNA material;
  - Inhibition of the PCR process that was not detected by the Quantifiler™ system (IPC C_T).

Conclusion

The QPS Tapelift Trial (October 2008) indicates that the "Post-It" tapelift material did not perform as well as the "double-sided" and "white" tapelift materials that were provided. Further testing of either "double-sided" or "white" tapelift materials should be performed to assess the suitability of these materials in a routine tapelift method, and compared to the standard tapelift material used in DNA Analysis, Forensic and Scientific Services (Brisbane, QLD, AUSTRALIA). Immediate further testing could include assessing the recovery of human DNA material from a cotton shirt (spotted with controlled amounts of human cellular material). This would provide information as to the suitability of each tapelift type in actually recovering material from mocked crime scene items.

CaSS | Forensic and Scientific Services
A CLINICAL AND STATEWIDE SERVICE

QPS Tapelift Trial: Part 2

Recovery Success using various Tapelift Materials

October 2008

DNA Analysis, Forensic and Scientific Services
Coopers Plains, Brisbane, QLD AUSTRALIA

Disclaimer
This report provides the results for a preliminary assessment and should not be considered as a validation of any kind. Further validation work is recommended in order to assess other variables.
Names of commercial manufacturers are provided for identification only. Inclusion in this report does not infer endorsement by DNA Analysis, Forensic and Scientific Services, Queensland Health.
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Aim

To compare the success in recovering DNA material using various tapelift materials, from constant amounts of human cellular material spotted onto a clothing substrate.

Materials and Methods

Buccal cell collection
Buccal cells were collected from a male donor using the Cytobrush™ method. Briefly, two Cytobrush™ Plus Cell Collector devices (Cooper Surgical, Inc., Trumbull, CT, USA) were used to collect buccal cells from each cheek for 1 minute, then collected into 500µL of 0.9% saline solution (Baxter Healthcare, Old Toongabbie, NSW, Australia) in a sterile 2mL tube. Two collections were made over two consecutive mornings, ensuring that the donor did not consume any food prior to the collections. The resulting cell suspensions were vortexed thoroughly and pooled into one sterile 2mL tube, resulting in a final buccal cell suspension with 1mL total volume. The buccal cells were stored at 4°C until use.

Washing and decontamination of clothing substrate
A piece of clothing substrate (100% white cotton t-shirt), approximately 50cm x 30cm in dimension, was washed and decontaminated using a combination of bleach, sodium sulfite and water. Briefly, the clothing material was washed in 2L of 10% (v/v) bleach on a platform shaker (set at medium shaking) for approximately 2hrs. After washing in bleach, 2L of 0.1343M Na_2SO_3 was added to the mixture and washing continued for approximately another 2hrs. The clothing material was then transferred to 4L sterile nanopure water and washed 3 times for a total of 1hr (using fresh water for every wash). Drying was performed overnight by hanging the clothing material inside a Class II biohazard cabinet.

Sample creation (spotting buccal cells)
The dried clothing substrate was laid out inside a Class II biohazard cabinet, slightly suspended above sheets of clean blotting paper. Seventeen squares (4cm x 4cm) were marked on the material using Chinagraph pencil and numbered 1-17 (Figure 1). To each square, 40µL of donor buccal cell suspension was added and allowed to absorb into the clothing material (without absorbing into the blotting paper). Spots were allowed to dry in the biohazard cabinet for at least 3hrs.

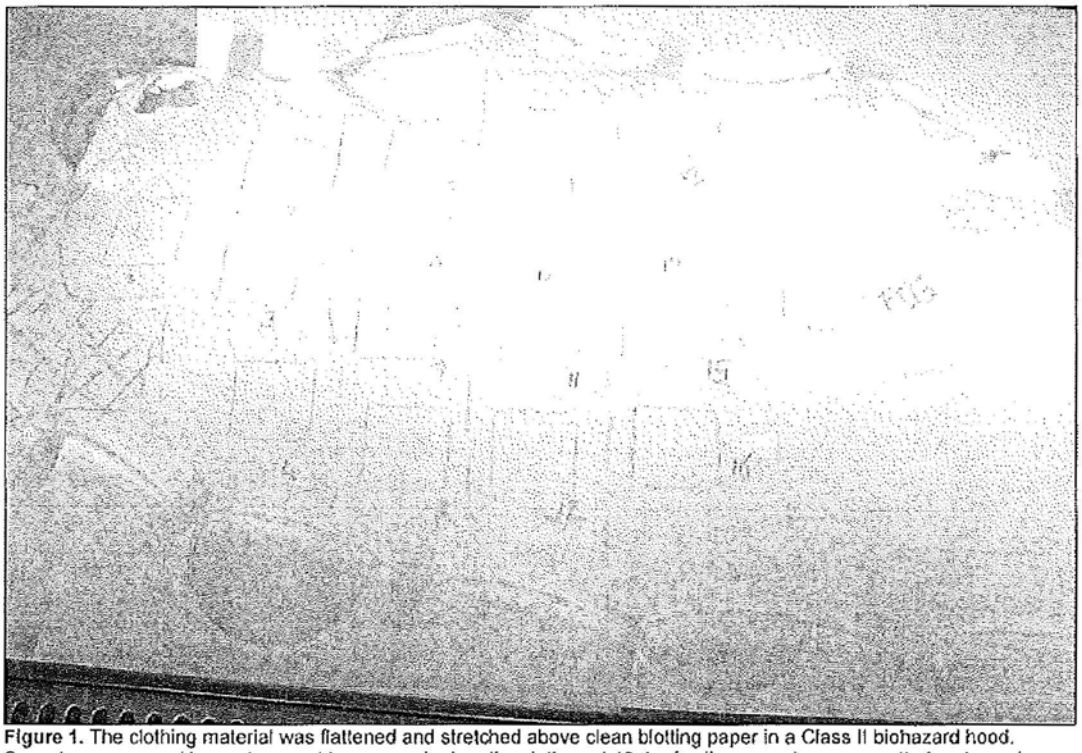


Figure 1. The clothing material was flattened and stretched above clean blotting paper in a Class II biohazard hood. Seventeen squares (4cm x 4cm each) were marked on the cloth, and 40µL of cell suspension was spotted on to each square.

Sampling using various tapelift materials

Three types of tapelift material were supplied by QPS and identified as:

- Post-It Flag (red tab) – 5 pieces;
- Double-sided tape – 5 pieces;
- White tape – 5 pieces.

An experienced staff member from the Evidence Recovery Team (DNA Analysis) sampled each square using a specific piece of tape (Table 1). Tape was used to lift material from the clothing substrate until the adhesive quality of the tape was lost. The tape was rolled (sticky-side facing inwards) and put inside a sterile 2mL tube. The fifth piece of each tape type was kept as a substrate blank sample (no sampling was performed), and the tape added directly to a sterile 2mL tube). For the purposes of comparison, the in-house FSS Tesa Tape was also used to sample a set of squares. A 2cm x 2cm square was cut out from the centre of sample square number 17 and served as the positive control. In total, 17 samples (including 4 substrate blank samples) were resulted from the sampling regime. Cutting tools used for sampling were sterilised in 70% ethanol, followed by flaming using a Bunsen burner.

Table 1. List of sample squares that were sampled using specific tapelift materials.

Sample description	Sample square number
Post-It 1	1
Post-It 2	2
Post-It 3	3
Post-It 4	4
Double-sided 1	5
Double-sided 2	6
Double-sided 3	7
Double-sided 4	8
White 1	9
White 2	10
White 3	11
White 4	12
FSS 1	13
FSS 2	14
FSS 3	15
FSS 4	16
Positive control (cut out)	17

DNA extraction and processing

Processing of samples was performed as per in-house protocols. DNA extraction was performed using the validated manual DNA IQ™ system (Promega Corp., Madison, WI, USA), with slight modifications: samples 1-2 for each tape type were subjected to lysis with 300µL Extraction Buffer, and samples 3-5 were extracted with 500µL Extraction buffer. For incubation on the Thermomixer at 37°C for 45mins, shaking was performed at 1400rpm, with vortexing performed before and after incubation.

Extracted samples were quantified using the Quantifiler™ Human DNA Quantification Kit (Applied Biosystems, Foster City, CA, USA), followed by amplification using the AmpFℓSTR® Profiler Plus® kit (Applied Biosystems, Foster City, CA, USA). Fragment

analysis was performed by capillary electrophoresis using an ABI Prism® 3130*xl* Genetic Analyzer instrument (Applied Biosystems, Foster City, CA, USA). Fragment data was analysed using GeneMapper ID-X® v1.0 (Applied Biosystems, Foster City, CA, USA), with thresholds for heterozygous and homozygous peaks at 50 and 200 RFU respectively. The allelic imbalance threshold was set at 50%.

Results and Discussion

The yield results obtained from tapelifting using various material types are presented in Figure 2 below.

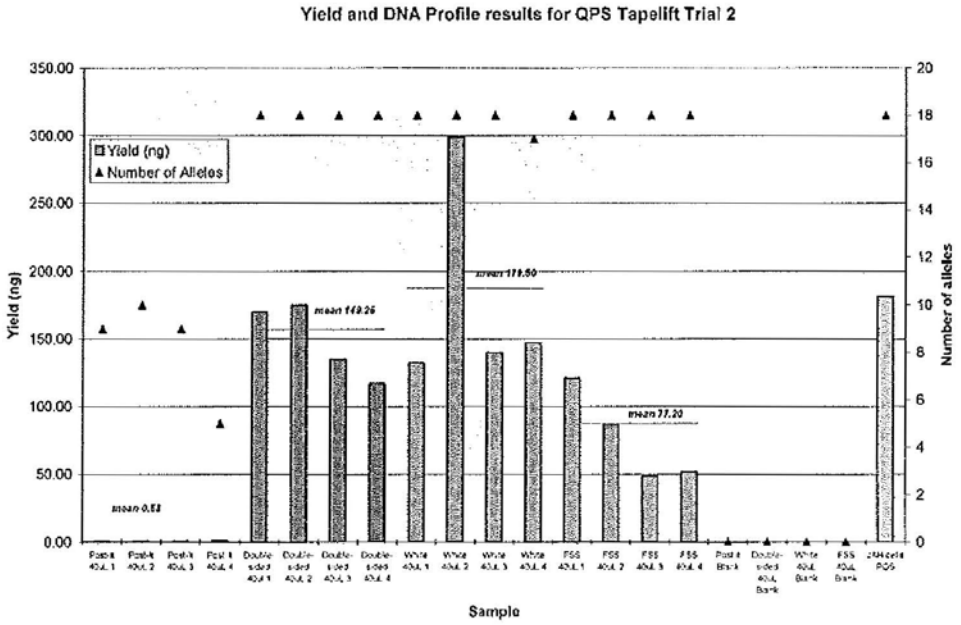


Figure 2. Quantitation and DNA profiles results from the QPS Tapelift Assessment Part 2, displaying the yield and number of alleles obtained using various tapelift materials.

High yields were obtained from all tapelift types, except the Post-It material. The yields obtained are sufficient to perform PCR amplification to obtain a DNA profile (approximately 1.2ng of DNA is required for successful amplification using the Profiler Plus® system). All positive and negative controls gave the expected results with the exception of the White tape extraction negative control. The DNA profile for this control had no reportable alleles but contained visible peaks below threshold (Figure 3). It is expected that this DNA profile may have been present on the tape before DNA extraction.

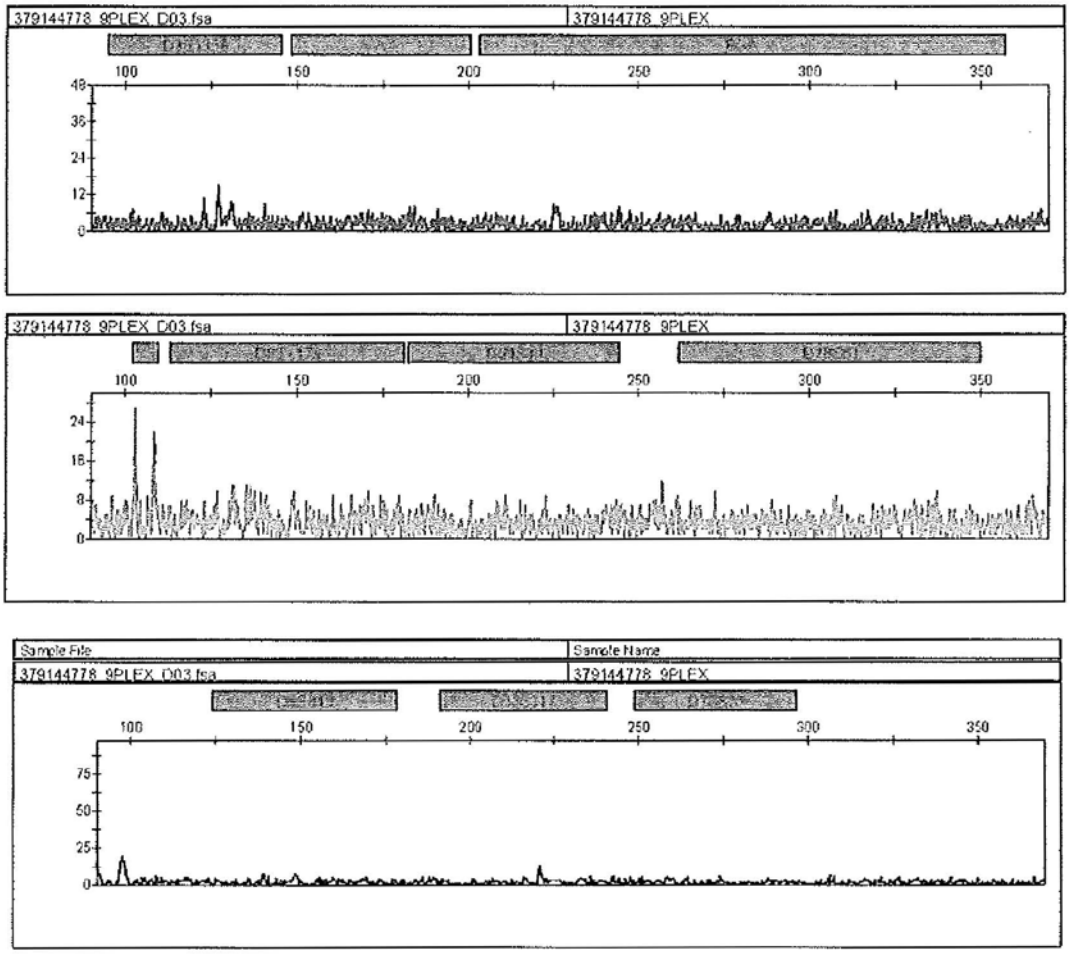
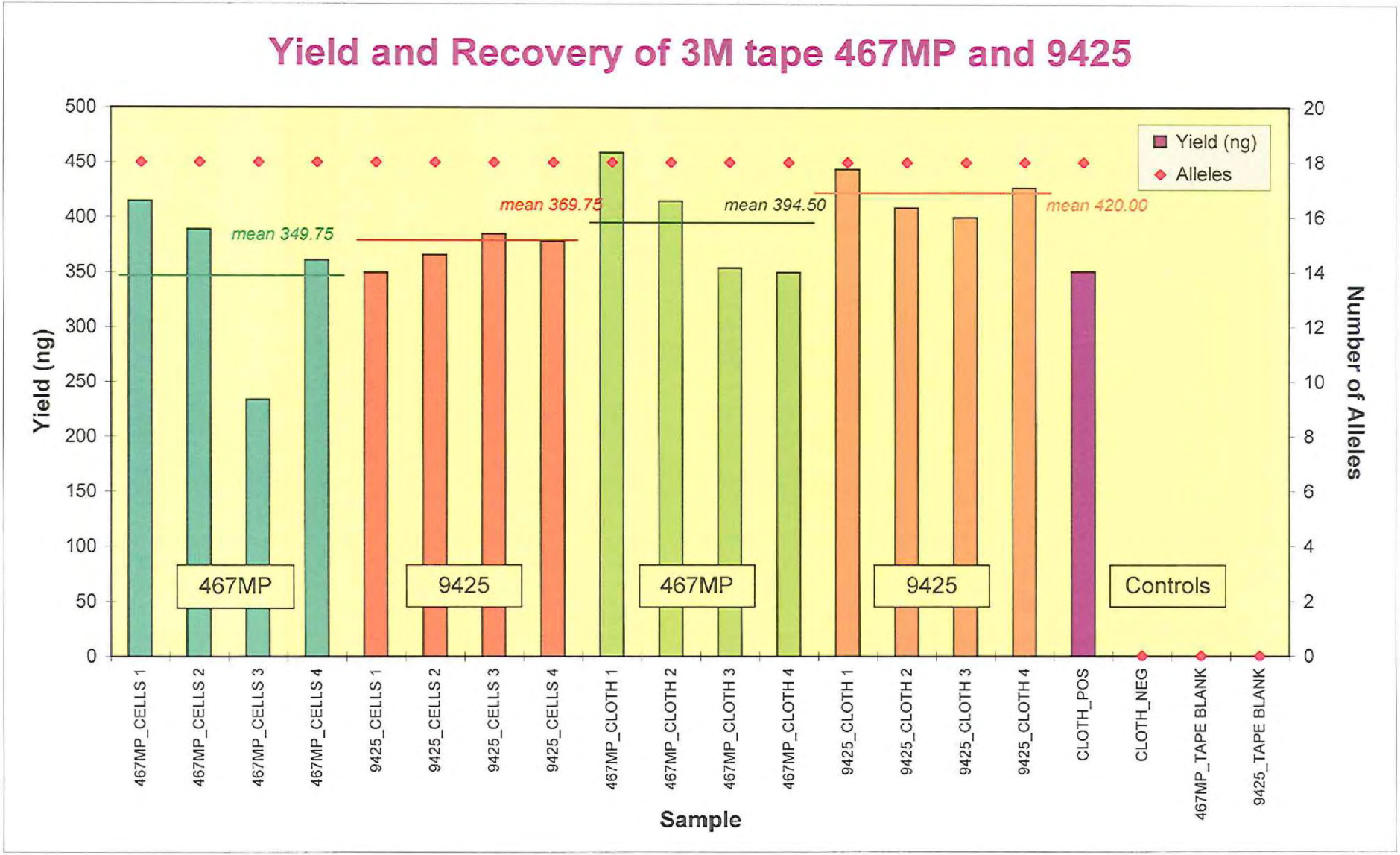


Figure 3 – White Blank DNA profile result

Conclusion

Based on these preliminary results, the Post-It material is not suitable for tapelifting due to consistent observation of low yields and partial DNA profiles. All other tapelift materials produced consistent DNA profiles and yields for tapelifting high concentrations of cellular material from a clothing substrate in a controlled experiment.



WIT.0019.0012.2060

QPS Tapelift 3							
	Barcode	Sample ID	[DNA]	Yield (ng)	Mean	SD	Alleles
AUSLAB	[redacted]	[redacted]	4.150000	415	349.75	80.26	18
AUSLAB			3.890000	389			18
AUSLAB			2.340000	234			18
AUSLAB			3.610000	361			18
AUSLAB			3.500000	350	369.75	15.33	18
AUSLAB			3.660000	366			18
AUSLAB			3.850000	385			18
AUSLAB			3.780000	378			18
AUSLAB			4.590000	459	394.50	52.28	18
AUSLAB			4.150000	415			18
AUSLAB			3.540000	354			18
AUSLAB			3.500000	350			18
AUSLAB			4.440000	444	420.00	19.54	18
AUSLAB			4.090000	409			18
AUSLAB			4.000000	400			18
AUSLAB			4.270000	427			18
AUSLAB			3.510000	351			18
AUSLAB			0	0			0
AUSLAB			0	0			0
AUSLAB			0	0			0
			2.61	261			
			0	0			
			2.13	213			
			0	0			

Case managed by: _____ Date: _____

Reviewed By: _____ Date: _____ Page 1 of 1

WIT.0019.0012.2061

Sample ID	Sample Description	Shirt Area
[redacted]		1
		2
		3
		4
		N/A
		5
		6
		7
		8
		N/A
		9
		10
		11
		12
		N/A
		13
		14
		15
		16
		N/A
		Cut out

[redacted]

TAPELIFTING
PERFORMED
BY JENNY MUNOZ -
10/10/2008

WIT.0019.0012.2062

Sample ID	Sample Description	Shirt Area
[redacted]	Post-It 40uL 1	1
	Post-It 40uL 2	2
	Post-It 40uL 3	3
	Post-It 40uL 4	4
	Post-It 40uL Blank	N/A
	Double-sided 40uL 1	5
	Double-sided 40uL 2	6
	Double-sided 40uL 3	7
	Double-sided 40uL 4	8
	Double-sided Blank	N/A
	White 40uL 1	9
	White 40uL 2	10
	White 40uL 3	11
	White 40uL 4	12
	White Blank	N/A
	FSS 40uL 1	13
	FSS 40uL 2	14
	FSS 40uL 3	15
	FSS 40uL 4	16
	FSS 40uL Blank	N/A
	UAH cells POS	Cut out

WIT.0019.0012.2063

Lab Number : [redacted] Received : ??:?? 16-Oct-08
UR/Case No : [redacted] DOB :
Name : TAPE LIFT Assessment* Client : Forensic Biolog*

Lab No.	Id	External Id	Received	Specimen	Specimen Descrip	Relation	Tests	Status
[redacted]	10		16-Oct-2008	DNA	Double-sided 40uL -4			.....
	9		16-Oct-2008	DNA	Double-sided 40uL -3			.....
	8		16-Oct-2008	DNA	Double-sided 40uL -2			.....
	7		16-Oct-2008	DNA	Double-sided 40ul -1			.....
	6		16-Oct-2008	DNA	Post it Blank			.....
	5		16-Oct-2008	DNA	Post-It 40uL -4			.....
	4		16-Oct-2008	DNA	Post-It 40uL -3			.....
	3		16-Oct-2008	DNA	Post-It 40uL - 2			.....
	2		16-Oct-2008	DNA	Post-It 40uL -1			.....
	1		16-Oct-2008	Cells	JAH in saline 2			.....

| | Nominate Dept SF5 Specimen Search SF7 Print Reports SF8 Find Test

Lab Number : [redacted] Received : ??:?? 16-Oct-08
UR/Case No : [redacted] DOB :
Name : TAPE LIFT Assessment* Client : Forensic Biolog*

Lab No.	Id	External Id	Received	Specimen	Specimen Descrip	Relation	Tests	Status
[redacted]	22		16-Oct-2008	DNA	JAH cells POS			.....
	21		16-Oct-2008	DNA	FSS 40uL Blank			.....
	20		16-Oct-2008	DNA	FSS 40uL 4			.....
	19		16-Oct-2008	DNA	FSS 40uL 3			.....
	18		16-Oct-2008	DNA	FSS 40uL 2			.....
	17		16-Oct-2008	DNA	FSS 40uL 1			.....
	16		16-Oct-2008	DNA	White 40uL Blank			.....
	15		16-Oct-2008	DNA	White 40uL -4			.....
	14		16-Oct-2008	DNA	White 40uL -3			.....
	13		16-Oct-2008	DNA	White 40uL -2			.....
	12		16-Oct-2008	DNA	White 40uL -1			.....
	11		16-Oct-2008	DNA	Double-sided 40uL Bla			.....

| | Nominate Dept | SF5 Specimen Search | SF7 Print Reports | SF8 Find Test

Lab No.	Id	External Id	Received	Specimen	Specimen Descrip	Relation	Tests	Status
[redacted]	18		02-Oct-2008	VALE	Positive Control		9PLEX	....M
	17		02-Oct-2008	VALE	Negative Control		9PLEX	....M
	16		02-Oct-2008	VALE	White 40uL Blank		9PLEX	....M
	15		02-Oct-2008	VALE	White 40uL 4		9PLEX	....M
	14		02-Oct-2008	VALE	White 40uL 3		9PLEX	....M
	13		02-Oct-2008	VALE	White 40uL 2		9PLEX	....M
	12		02-Oct-2008	VALE	White 40 uL 1		9PLEX	....M
	11		02-Oct-2008	VALE	Double-sided Blank		9PLEX	....M
	10		02-Oct-2008	VALE	Double-sided 40uL 4		9PLEX	....M
	9		02-Oct-2008	VALE	Double-sided 40uL 3		9PLEX	....M
	8		02-Oct-2008	VALE	Double-sided 40uL 2		9PLEX	....M
	7		02-Oct-2008	VALE	Double-sided 40uL 1		9PLEX	....M
	6		02-Oct-2008	VALE	Post-It Blank		9PLEX	....M
	5		02-Oct-2008	VALE	Post-It 40uL 4		9PLEX	....M
	4		02-Oct-2008	VALE	Post-It 40uL 3		9PLEX	....M
	3		02-Oct-2008	VALE	Post-It 40uL 2		9PLEX	....M
	2		02-Oct-2008	VALE	Post-It 40uL 1		9PLEX	....M
	1		01-Oct-2008	Cells	CJA Buccal Cell Suspe			.....

[redacted]

[redacted]

Printed: 13:34 16-Oct-08

WIT.0019.0012.2066

Cell Extraction Worksheet

[redacted]

Batch Number: [redacted]
Created by: ten1
Creation Date: 08:21 17-Oct-08

[redacted]

#	Lab Number	Processing Comment	#	Lab Number	Processing Comment
1	[redacted]	Pos	21	[redacted]	
2			22		Negative Extraction Ctrl
3		300µl Extraction Buffer	23		extb
4			24		
5		300µl Extraction Buffer	25		
6			26		
7			27		
8			28		
9		300µl Extraction Buffer	29		
10		300µl Extraction Buffer	30		
11			31		
12			32		
13		300µl Extraction Buffer	33		
14		300µl Extraction Buffer	34		
15			35		
16			36		
17			37		
18		300µl Extraction Buffer	38		
19			39		
20		300µl Extraction Buffer	40		

Operator:	GSL / DW	Date & Time:	17.10.08
Sample Located By:	DW	Sequence Checked:	CW 17.10.08
Chelex Prepared By:	N/A	Date Prepared:	N/A
Transfer Tube Sequence Checked:	CW 17.10.08	Nanopure Water Lot No:	
Chelex Lot No.:	N/A	Proteinase K lot No:	[redacted]
Twirled By:	N/A	Waterbath Temp:	37 °C 65°C

Total Number of Samples : 23

18.2 **Reagent & Batch details recording tables (DNA IQ™ Lysis Batch & Extraction Batch)**

Off Deck Lysis Batch ID:	DNA IQ Extraction Batch ID:

Lysis batch:

Samples located by:	
Sample set 1	**Sample set 2**
Operator: GSL	Operator:
Sequence check performed by:	Sequence check performed by:
Transfer tubes sequence checked:	Transfer tubes sequence checked:
37°C Incubation temp:	37°C Incubation temp:
65°C Incubation temp:	65°C Incubation temp:

Extraction Buffer made by:	TNE Buffer Lot#: EL 01.07.08
40% Sarcosyl Lot#: 047K0191 BUA/KAL	Proteinase K Lot#: 028K8623
Comments: 24.6.08	

Extraction batch:

Plate Lot#:	Lysate/STORstar Operators:
Nunc tube/STORstar Operators:	Lysate Logfile uploaded:
Nunc Logfile uploaded:	
Comments:	

MultiPROBE Platform:	Operator:
Date and Start time:	

Kit Lot#: 252296	1xWash Buffer Lot#: 23730922
Lysis Buffer Lot#: 24437105	DTT Lot#: # 084K13071
Resin Lot#: 24343204	Elution Buffer Lot#: 24661603
MP II Logfile uploaded:	Results file uploaded:
Comments:	

URGENT

CE/GeneScan Worksheet

URGENT



Amp Batch ID:	CE Batch ID:	Genotyper Batch ID:
[redacted]	[redacted]	[redacted]

CE Batch Created By: paf3 **Creation Date:** 16:45 19-Nov-08

Plate Preparation Details:

3130xl B

3100/3100xl Operator: BUA	Date & Time: 20.11.08
MPII Operator: Manual prep: BUA	Date & Time: 20.11.08
HiDi Lot Number: 07015G0	Sequence Checked By/Date: BM 20.11.08
ROX Lot Number: 08012P0	Hot Block Temp: 95 °C
Ladder Lot Number: 0710005	Plate Map Imported & Checked By/Date: BUA 20.11.08

Genescanning Details:

GeneScan By/Date:

LADDERS:

Ladder 1	Ladder 2	Ladder 3	Ladder 4	Ladder 5	Ladder 6
Pass/Fail/Not used	Pass/Fail/Not used	Pass/Fail/Not used	Pass/Fail/Not used	Pass/Fail/Not used	Pass/Fail/Not used

Comments: _____

AMPLIFICATION POSITIVE CONTROL: Correct number of peaks present & above threshold? YES / NO

	Casework		Reference		Reference FTA	
	No. Peaks	Peak Height	No. Peaks	Peak Height	No. Peaks	Peak Height
Profiler Plus	15	D3 >= 1200 RFU D7 >= 600 RFU	15	D3 >= 1200 RFU D7 >= 600 RFU	18	Heterozygote - 75RFU
COfiler	12		12		12	Homozygote - 150RFU

AMPLIFICATION NEGATIVE CONTROL: Peaks present? NO / YES

EXTRACTION NEGATIVE CONTROLS: Peaks present? NO / YES / N/A

Control Comments: (If positive control fails, or peaks present in negative controls advise supervisor & instigate investigation.)

SAMPLE ANALYSIS: Samples are analysed in Genescan. Record samples that need to be repeated and reason. (Record problems that may not be readily detected in a routine Genotyper read).

Folder No	Sample ID	Reason/Action taken	Re-Genescan test ordered?	.fsa Files moved to Re-Genescan sub folder?

Accept Run ☐ **Reject** Run ☐ Comment _____ (Advise supervisor & instigate investigation)

Amplification Worksheet

URGENT URGENT

Batch Number: [redacted]
Created by: sesf1
Creation Date: 15:07 19-Nov-08

#	[redacted]	Processing Comment	#	Lab Number	Processing Comment
1			49		
2			50		
3			51		
4			52		
5			53		
6			54		
7			55		
8			56		
9			57	Ladder 4	
10			58		
11			59		
12			60		
13			61		
14			62		
15			63		
16			64		
17			65		
18			66		
19			67		
20			68		
21			69		
22			70		
23			71		
24		Neg Control	72		
25			73	Ladder 5	
26		Extraction Positive Blood	74		
27		Negative Extraction Ctrl	75		
28		Positive Extraction Ctrl	76		
29			77		
30			78		
31			79		
32			80		
33			81		
34			82		
35			83		
36			84		
37			85		
38			86		
39			87		
40			88		
41	Ladder 3		89	Ladder 6	
42			90		
43			91		
44			92		
45			93		
46			94		
47			95		
48			96		

Operator: PA/VH
Date & Time: 19.11.08 15:35
Sequence Checked By/Date: SES 19.11.08
Thermalcycler: E
TAQ Lot No: KP0789 G37 + G36
Volume: 36µL (n x 1uL)
Reaction Mix Lot No: [redacted]
Volume: 756µL (n x 21uL)
[redacted]
Volume: 396µL (n x 11uL)
[redacted] 80628DF ALIQ: AC 19/11/08
Positive Control Lot No: 0805061 (G3)

Total Number of Samples : 26

DNA Extraction Worksheet

[redacted]

QPS Tape lifts

Batch Number: [redacted]
Created by: famf3
Creation Date: 16:22 17-Nov-08

[redacted]

#	Lab Number	#	Lab Number
1	[redacted]	49	
2		50	
3		51	
4		52	
5		53	
6		54	
7		55	
8		56	
9		57	
10		58	
11		59	
12		60	
13		61	
14		62	
15		63	
16		64	
17		65	
18		66	
19		67	
20		68	
21	Neg Ctl	69	
22	Pos Ctl	70	
23	Neg Ctl	71	
24	Pos Ctl	72	
25		73	
26		74	
27		75	
28		76	
29		77	
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31		79	
32		80	
33		81	
34		82	
35		83	
36		84	
37		85	
38		86	
39		87	
40		88	
41		89	
42		90	
43		91	
44		92	
45		93	
46		94	
47		95	
48		96	

VALIQLYS20081117_04

Sample No	Lab No	9PLUR	9PLSAM	Operator
1	[redacted]			CI
2				CI
3				CI
4				CI
5				CI
6				CI
7				CI
8				CI
9				CI
10				CI
11				CI
12				CI

Sample No	Lab No	9PLUR	9PLSAM	Operator
1	[redacted]			MLH
2				MLH
3				MLH
4				MLH
5				MLH
6				MLH
7				MLH
8				MLH
9				MLH
10				MLH
11				MLH
12				MLH

VALIQLYS20081117_04

Set - 1 -

Sample No	Lab No	9PLUR	9PLSAM	Operator
1				CI
2				CI
3				CI
4				CI
5				CI
6				CI
7				CI
8				CI
9				CI
10				CI
11				CI
12				CI

Set - 2 -

Sample No	Lab No	9PLUR	9PLSAM	Operator
1				MLH
2				MLH
3				MLH
4				MLH
5				MLH
6				MLH
7				MLH
8				MLH
9				MLH
10				MLH
11				MLH
12				MLH

18.2 Reagent & Batch details recording tables (DNA IQ™ Lysis Batch & Extraction Batch)

Off Deck Lysis Batch ID:	DNA IQ Extraction Batch ID:

Lysis batch:

Samples located by:	
Sample set 1	**Sample set 2**
Operator: CL	Operator: MLH
Sequence check performed by: BVA 18-11-08	Sequence check performed by: BVA 18-11-08
Transfer tubes sequence checked: BVA 18-11-08	Transfer tubes sequence checked: BVA 18-11-08
37°C Incubation temp: 37°C	37°C Incubation temp: 37°C
65°C Incubation temp: 65°C	65°C Incubation temp: 65°C

Extraction Buffer made by: MLH.	TNE Buffer Lot#: EL20080701-01
40% Sarcosyl Lot#: 0478191	Proteinase K Lot#: 077K8609 SH 20080702-01
Comments: BVA/KAC26C608	

Extraction batch:

Plate Lot#:	Lysate/STORstar Operators:
Nunc tube/STORstar Operators:	Lysate Logfile uploaded:
Nunc Logfile uploaded:	
Comments:	

MultiPROBE Platform:	Operator:
Date and Start time:	

Kit Lot#: 255146	1xWash Buffer Lot#: 24809214
Lysis Buffer Lot#: 24963606	DTT Lot#: 0861C 13071 SH 20080820-01
Resin Lot#: 25398001	Elution Buffer Lot#: 24661606
MP II Logfile uploaded:	Results file uploaded:
Comments:	

CA-86

Paula Brisotto

From: Cathie Allen
Sent: Thursday, 12 June 2014 11:44 AM
To: Paula Brisotto; Justin Howes
Subject: RE: Ownership of Items

Hi Paula & Justin

For a few of those on the list, there is no details whatsoever - so it worries me that there were details there that didn't transfer across.

Also for a few of them - there is something listed in the Forensic Relationship field - for [redacted] - its A - for Admission / Intelligence (Principal Exhibit). So are we asking SSLU to confirm the Forensic Relationship status with QPS? As we should be doing this given they have provided some information to us.

Cheers
Cathie

From: Paula Brisotto
Sent: Thursday, 12 June 2014 11:27 AM
To: Cathie Allen; Justin Howes
Subject: RE: Ownership of Items

Hi Cathie,

I don't think there has been a noticeable improvement in the last month. The ELF (item ownership) list was implemented only two weeks ago, and currently there are 12 items from 3 different cases (received within the last two days) that SSLU need to chase up on. SSLU regularly remove these items from the list, so if they are currently on the ELF list, they have only recently been added.

Thanks
Paula

Paula Brisotto
Team Leader - Evidence Recovery & Quality
Forensic DNA Analysis | Police Services Stream | Forensic & Scientific Services, HSSA
Department of Health | Queensland Government
[redacted]
t. [redacted] m [redacted]
e. [redacted] | www.health.qld.gov.au



From: Cathie Allen
Sent: Thursday, 12 June 2014 11:19 AM
To: Justin Howes; Paula Brisotto
Subject: FW: Ownership of Items

Hi Justin & Paula

I'm thinking that communication of ownership of items hasn't changed over the past month - do you agree?

Cheers
Cathie

From: [redacted] [mailto: [redacted]]
Sent: Wednesday, 4 June 2014 2:12 PM
To: Cathie Allen
Subject: Ownership of Items

Hi Cathie

Just following up to see if this issue has improved in the last month or so. At the time, I sent a statewide email to all forensic officers with the following information:

*To enable a faster turnaround for DNA results, please ensure sufficient information is recorded in the 'Exhibit Notes and QHFSS Advice' field on the FR 'Exhibit Record' to allow scientists at QHFSS to determine the **owner** or **wearer** of an item.*

*In cases where the exhibit is taken directly from the suspect or victim, the appropriate 'Relationship' checkbox (Suspect or Victim) is **also** to be selected on the Exhibit Record.*

*On occasions where the forensic officer has reason to believe an item belongs to a particular person (but has not been collected directly from that person), **this information should be included in the 'Exhibit Notes and QHFSS Advice', e.g. "Shoe from wardrobe of Joe Bloggs".***

When this information is conveyed to QHFSS via the FR, the scientist can expedite results by employing the correct interpretation methodology without seeking further clarification. The information can also assist in deciding the best re-work strategy and whether to report for intell purposes.

Could you let me know if your staff are still having issues regarding ownership of items. If so, I will take it further.

Thanks

David Neville
Inspector
Quality Manager
Ph [redacted] **Mob** [redacted]

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From: Cathie Allen [mailto: [redacted]]
Sent: Monday, 28 April 2014 4:38 PM

To: Neville.DavidH[OSC]
Subject: Ownership of Items

Hi Dave

Recently it's been raised to my attention that the staff in Forensic DNA Analysis spend a fair amount of time requesting information from QPS regarding the ownership of items. It appears that not a lot of that detail is transferred across to QH, despite the mechanism being available.

Are you able to request that all items of clothing have information regarding ownership supplied at the time of submission? If ownership is unknown, then 'ownership unknown' would be greatly appreciated. This will help us to differentiate between items where its been forgotten.

The ownership of items is more important these days - due to the use of STRmix. As PP21 is more sensitive and we are detecting more mixed DNA profiles, this means that we are putting this mixtures through STRmix. In STRmix you're able to condition on a person (ie suspect) and this greatly helps the end result. By having this information available at time of submission, it reduces time required to follow-up for the information when the results are ready for STRmix.

Cheers
Cathie

Cathie Allen BSc. MSc (Forensic Science)
Managing Scientist for Forensic Chemistry & Forensic DNA Analysis
Police Services Stream | Forensic & Scientific Services | Health Services Support Agency
Department of Health | Queensland Government
[redacted]
t. [redacted]
m. [redacted]
e. [redacted] | www.health.qld.gov.au



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Paula Brisotto

From: Justin Howes
Sent: Wednesday, 14 February 2018 11:52 AM
To: [redacted]
Cc: Paula Brisotto
Subject: Ownership information

Hi Dave

One piece of information that we regularly request of QPS is 'ownership' information. This means, information on from whom the item was taken from eg. swab of arm of SMITH; shorts from JONES.

This allows us to apply the best interpretation to these DNA profiles being a conditioned/remaining situation. With these interpretations, by factoring in the 'conditioned' contribution, we can have an improved ability to obtain a 'remaining' DNA profile that could be put to NCIDD to identify possible POIs for QPS. For example:

- 2 person mixture where both people have contributed evenly. If we could condition the profile, which is effectively removing the 'owner's' DNA from the mix, we could have a profile remaining that could be loaded to NCIDD. This is obviously important in unknown offender cases where potentially that profile could be loaded and linked to a profile on the database.

Is there some way that QPS could look at their processes to make it clear to us for items (and these would be the parent items from which QPS have subsampled) who the 'owner' is. If there is doubt, it should be 'unknown' eg. when a shirt is located on the floor.

Any assistance on this would be appreciated and hopefully with this refresher, we can improve our abilities to send intelligence to QPS more efficiently.

Regards
Justin

Justin Howes
Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

p | [redacted] m | [redacted]
a | [redacted]
w | Queensland Health e | [redacted]

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Paula Brisotto

From: Justin Howes
Sent: Wednesday, 14 February 2018 12:36 PM
To: Paula Brisotto
Subject: FW: Ownership information

FYI

Justin Howes
Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

p | [redacted] m | [redacted]
a | [redacted]
w | Queensland Health e | [redacted]

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From: Keatinge.DavidJ[OSC] [mailto:[redacted]
Sent: Wednesday, 14 February 2018 12:27 PM
To: Justin Howes
Subject: RE: Ownership information

Thanks Justin – much appreciated. We will attempt to get an email out to the troops to remind them of this very soon.

Regards
Dave

David Keatinge

Inspector | Quality Manager | Forensic Services Group | Queensland Police Service

[redacted] | [redacted] | **Email:** [redacted]

From: Justin Howes [mailto:[redacted]
Sent: Wednesday, 14 February 2018 11:52 AM
To: Keatinge.DavidJ[OSC] <[redacted]>
Cc: Paula Brisotto <[redacted]>
Subject: Ownership information

Hi Dave

One piece of information that we regularly request of QPS is 'ownership' information. This means, information on from whom the item was taken from eg. swab of arm of SMITH; shorts from JONES.

This allows us to apply the best interpretation to these DNA profiles being a conditioned/remaining situation. With these interpretations, by factoring in the 'conditioned' contribution, we can have an improved ability to obtain a 'remaining' DNA profile that could be put to NCIDD to identify possible POIs for QPS. For example:

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Is there some way that QPS could look at their processes to make it clear to us for items (and these would be the parent items from which QPS have subsampled) who the 'owner' is. If there is doubt, it should be 'unknown' eg. when a shirt is located on the floor.

Any assistance on this would be appreciated and hopefully with this refresher, we can improve our abilities to send intelligence to QPS more efficiently.

Regards
Justin

Justin Howes
Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

p | [redacted] m | [redacted]
a | [redacted]
w | Queensland Health e | [redacted]

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Paula Brisotto

From: Allan McNevin
Sent: Thursday, 15 May 2014 10:35 AM
To: Emma Caunt; Allan McNevin; Amanda Reeves; Cathie Allen; Justin Howes; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone
Subject: Item ownsership - proposed new process (reply by COB Mon 19th May)

Hi all,

After a number of discussions about item ownership, I have developed a proposed new process with SSLU.

There is an available list that has a catchy name - the "ELF" list (I am logging a job to have it renamed "Item Ownership" from the current name).

The proposal is for ERT or any CM'er to simply list insert any sample where item ownership information is required, and once a day SSLU would e-mail QPS with a list of samples that need the information. SSLU would then put the answer back into the UR notes and scan the e-mail (like they do now).

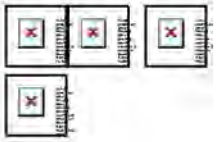
The rule for ERT will be - for any item (tube or whole item) that is either a body swab or item of clothing & there are reference samples associated with the case & there is no information regarding item ownership then it will be list inserted to the ELF list for SSLU to follow up. Whilst this won't catch everything (as sometimes the Ref samples come in later), it will save people following up on things where we may never get the appropriate ref samples, but will save time for cases where we do have them.

Andrea said that SSLU would give QPS 3 days to get back to them with an answer as there are times where SOCO's or IO's need to be contacted and they can be on days off etc. SSLU would then follow up a second time (they will manage this).

so, if you are happy with us moving forwards and implementing this minor change (or not) can you please reply with the above voting buttons by COB Monday.

ta
Al

Allan McNevin
Supervising Scientist Evidence Recovery - Forensic DNA Analysis
Police Services Stream | Forensic and Scientific Services | Health Services Support Agency
Department of Health | Queensland Government
[redacted]
t [redacted]
e [redacted] | www.health.qld.gov.au/hssa/



Paula Brisotto

From: Allan McNevin
Sent: Tuesday, 20 May 2014 3:05 PM
To: Allan McNevin; Amanda Reeves; Cathie Allen; Justin Howes; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone
Cc: Emma Caunt
Subject: RE: Ownership of Items list - process implementation

I meant to put "Monday the 26th May"

cheers
Al

From: Allan McNevin
Sent: Tuesday, 20 May 2014 3:03 PM
To: Allan McNevin; Amanda Reeves; Cathie Allen; Justin Howes; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone
Cc: Emma Caunt
Subject: Ownership of Items list - process implementation

Hi all,

Given that everyone who has replied to my e-mail on Thursday is happy with the use of the "ELF" list for item ownership, I will liaise with Andrea to start the use of this list on Monday (

The for to get the list name change has only been completed by myself today, but I don't see this as an impediment to implementation.

So, I will leave it up to each line manager to communicate this change to their teams, and I will update the minor changes log on Monday.

cheers
Al

Allan McNevin
Senior Scientist Evidence Recovery - Forensic DNA Analysis
Police Services Stream | Forensic and Scientific Services | Health Services Support Agency
Department of Health | Queensland Government
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Customers first Ideas into action Unleash potential Be courageous Empower people Queensland Government
Great state. Great opportunity.

CA-87

Cathie Allen

From: McNab.BruceJ[OSC] <[redacted]>
Sent: Friday, 14 February 2020 7:10 AM
To: Cathie Allen
Cc: John Doherty; Neville.DavidH[OSC]
Subject: RE: Request for information

Hi Cathie,

We've had a look at this issue from our end.

In short, it was changed from our end unintentionally, as such, much of FSG we were unaware until advised by your team. Those who located it, did so whilst performing their normal duties of scanning the FR to either see the progress, or the results of your examinations. No action was taken with any of the information that could be seen, as soon as you advised us, we changed it back so no one could see. I am confident with the departure of Tim, and the movement of all work over to BDNA till the commercialisation process is completed that such an issue will not arise again.

We accept that his unintentional change took place at our end.

In conclusion it shows that they greater degree of cooperation and information sharing between our departments is ensuring that the people of Queensland are being well served.

Have a great weekend.

Bruce McNab BM
Superintendent 7417
Operations Commander
Forensic Services Group
OPERATIONS SUPPORT COMMAND
Queensland Police Service
[redacted]

Yammer - Forensic Services Group

Did you know? – Over 70% of volume crime is solved by Forensic Services Group.



From: Cathie Allen <[redacted]>
Sent: Wednesday, 12 February 2020 16:13

To: McNab.BruceJ[OSC] <[redacted]>
Cc: John Doherty <[redacted]>
Subject: Request for information

Hi Supt McNab

Thank you for your time today on the teleconference regarding access by QPS staff members to Forensic DNA Analysis results that may have not been through the peer review process (via Exhibit Testing Table and Profile Data Analysis page).

Forensic DNA Analysis are accredited through NATA, under ISO17025. Under Section 7.11 – Control and data and information management, there appears to have been a breach ('...changes need to be authorised, documented and validated before implementation.' And 'LIMS must be: be protected from unauthorised access; LIMS must be maintained in a manner which ensures the integrity of the data and information'). An investigation, including corrective actions, regarding this will need to be conducted to advise NATA. This is normal for a breakdown in accreditation requirements and is not intended to be adversarial. Documenting an investigation and addressing the root cause is a requirement under any quality system.

To assist us to address this corrective action report, can you please provide either John or myself with the following information:

- How did it occur that QPS staff who have Results Management or Quality access were also provided with access to Forensic DNA Analysis Exhibit Testing and Profile Data assessment information?
- When did this change occur? (noting the removal of access was on Wednesday, 12th of Feb, prior to or at 2pm).
- What did the QPS staff do with the information that they had available to them?
- Who authorised the change to occur?
- Why was FSS not advised of this change prior to it occurring?

This will inform a risk-based assessment of the issue and allow us to demonstrate to NATA that we took appropriate action to address the issue and the root cause.

Cheers
Cathie

Cathie Allen
Managing Scientist

Police Services Stream, Forensic & Scientific Services
Health Support Queensland, Queensland Health

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Health Support Queensland
EXECUTIVE DIRECTOR BRIEFING NOTE

CA-88

C-ECTF-20/XXXX
Forensic and Scientific Services

SUBJECT: Forensic Register, user access and explicit images

☐ Approved ☐ Not approved ☐ Noted ☐ Further information required (see comments)	John Doherty, Executive Director, Forensic and Scientific Services Comments:

ACTION REQUIRED BY
30 October 2020

RECOMMENDATIONIt is recommended the Executive Director:

- **Endorse** the continuation of the current image process in the Forensic Register (FR), whereby images that are explicit are marked as such and Forensic and Scientific Services (FSS) staff can gain access to those images without requesting them.
- **Advocate** with the Queensland Police Service (QPS) the continuation of the current image process with respect to explicit images being marked as such.
- **Approve** FR access of images to be utilised from the Forensic Pathologists' own desktop.
- **Approve** Dr Naylor or appropriate delegate from Forensic Pathology to provide communication to Forensic Pathologists regarding access to the FR and how password resets are gained.

ISSUES

1. Recently, some Forensic DNA Analysis staff were exposed to explicit crime scene images on the FR, as a QPS officer had not marked the image as explicit. Marking of the image as explicit means that the thumbnail image is hidden, and a warning is provided to the user prior to opening the image.
2. Continued exposure to explicit images could be harmful to staff members from both FSS and the QPS.
3. Forensic DNA Analysis and Forensic Pathology staff access location images and crime scene images for a variety of reasons, including cross checking these images with the description of the item assists with quality assurance. Both location images and crime scene images can be explicit.
4. The QPS have provided the following feedback:
   4.1. Crime scene images on a compact disc were no longer going to be provided to Forensic Pathologists, given Forensic Pathologists had been provided with access to the FR from their desktop.
   4.2. Forensic Pathologists prefer to request access to the images via the QPS officers' FR access as these QPS officers are located with the FSS Mortuary.
   4.3. Forensic Pathologists advised the QPS that although they had access to the FR, they were no longer able to access it after the first three months. [This is likely to be due to Forensic Pathologists requiring a password reset, as their password had expired due to not accessing the FR for that period.]

BACKGROUND

5. Forensic Property Point (FPP), Scientific Services Liaison Unit (SSLU) and Forensic Chemistry went live with the FR on 16 May 2016. Forensic DNA Analysis went live with the FR on 15 June 2017. Forensic Pathology staff (26) were provided access to the FR in late 2017. Training by the Scientific Services Development Unit (SSDU) has been undertaken with all staff that have access to the FR.
6. The QPS require two forms to be completed, which are accompanied by a Justice of the Peace certified copy of their driver's licence and their Queensland Health identification badge. The QPS then undertake a criminal history check prior to providing access to the staff member.
7. Each year, the Managing Scientist – Police Services Stream completes an audit of all FSS staff members with FR access to ensure that their access is required to be continued for another year.
8. The QPS undertook a review which highlighted that the only staff that required crime scene images to be provided on a disc and delivered to them was Forensic Pathologists. At this point, the QPS advised that it would no longer provide images in this manner, given the Forensic Pathologists had desktop access to the FR to view the images.
9. FSS mortuary staff members are required to enter a small amount of data into the FR for autopsy samples that require DNA analysis. Damien Cass, Mortuary Manager, has advised that the mortuary staff don't have the time to enter the data or cannot remember how to enter the data into the FR. This means that FPP staff members enter this data when the items are delivered to FPP.
10. The password for the FR must be changed every three months, and the FR must be accessed at least once in a three-month period to remain an active user.

11. The FR Training Manual (QIS #33744) details how to reset your own password via the QPS Password Manager application or by contacting the Managing Scientist – Police Services Stream for a reset.

RESULTS OF CONSULTATION

12. Ilce Ristanovski, A/Coordinator FPP has provided feedback from the group that it would be rare that they would review location or scene images prior to or during the receipt process for an item.
13. The Forensic Chemistry Management Team have provided the following feedback – use of crime scene images assists with sample prioritisation, advice on chemicals or materials found at a scene (including explosives and/or CBR manufacture), comparison of labelling and packaging of an exhibit before and after delivery for quality issues and provision of advice on destruction of items that have not been submitted to FSS. The team's preference was to have the images available, rather than having to request them.
14. I verbally consulted with Paula Brisotto, Team Leader for Evidence Recovery & Quality Team and it was agreed that there was a need for crime scene images for quality purposes, as once an item has begun processing with a particular barcode, any changes to the unique identifier (barcode) cannot be made.

RESOURCE/FINANCIAL IMPLICATIONS

15. If a process was implemented whereby crime scene images were made available only on request, this will have impacts on human resources for both FSS and the QPS.

SENSITIVITIES/RISKS

16. The nature of the crime scene images are sensitive.

ATTACHMENTS

Nil

Author	**Cleared by (Principal Advisor)**	
Name: Cathie Allen Position: Managing Scientist – Police Services Stream Business/Branch: Forensic & Scientific Services Tel No: [redacted] Date Drafted: 23 Oct 2020	Name: Alison Slade Position: Principal Advisor Business/Branch: Forensic & Scientific Services Tel No: [redacted] Date Cleared: 23 October 2020 **Note clearance contact is also key contact for brief queries**	

CA-89

Allison Lloyd

From: Cathie Allen
Sent: Tuesday, 18 February 2020 4:20 PM
To: Allison Lloyd
Cc: Justin Howes
Subject: RE: QPS Manuscript Feedback given via phone call 17/02/2020

Thanks Allison, much appreciated.

Cheers
Cathie

Cathie Allen
Managing Scientist

Police Services Stream, Forensic & Scientific Services
Health Support Queensland, Queensland Health

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a [redacted]
e [redacted] w www.health.qld.gov.au/healthsupport

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From: Allison Lloyd <[redacted]>
Sent: Tuesday, 18 February 2020 1:34 PM
To: Cathie Allen <[redacted]>
Cc: Justin Howes <[redacted]>
Subject: QPS Manuscript Feedback given via phone call 17/02/2020

Hi Cathie,

Here is a breakdown of the feedback I gave to Dr Matt Krosch yesterday morning via phone call regarding the 'Variation in Forensic DNA profiling... ' manuscript.

Points discussed:

1. Page 4/Methods – We were still using Profiler Plus for volume crime samples for the most part of 2017 which was not mentioned. This also had implications for results obtained in the second paragraph of Methods as we were using a binary method of interpretation which would affect the profiles that could be counted as a 'successful' profile.
2. Page 4/Methods – QIA symphony was not mentioned
3. Page 5/Methods, line 1: Sub-threshold information (<150rfu) was incorrect and different for the different kits used.

4. Page 4/Methods, bottom line: (no DNA+full) what does this mean? This is when a 'NO DNA' result line was released and most likely the quant was not right, the batch requanted and corrected results released. I said these results should be considered as being the 'updated/corrected' results.
5. General discussion on what was considered a 'full' profile/mixed/partial. These results were taken directly from result lines in the FR. I offered to go through them in more detail. In my opinion, Dr Krosch did not have a particularly strong understanding of the results or what they meant.
6. General discussion on what was considered a 'successful' profile. I said that in my opinion, obtaining a profile regardless of whether is was able to be interpreted would be considered successful. It is my understanding that the QPS version of a successful result was obtaining a suspect identification/LR favouring contribution for a suspect (Page 6, 1st paragraph). I suggested that some definitions around 'success' and even the types of results such as 'full/mixed/partial etc' were put in the manuscript to avoid ambiguity.
7. General discussion that the processes/reworking strategies that DNA Analysis used were not vital to the manuscript as this was generally looking at different sampling methods and the different types of results obtained from those sampling methods and substrates and the point of the paper was for SOCOs to have some printed advice to take to Investigators for discussions as to why certain samples might not be as worthwhile as others (as per the anecdotal experience mentioned on page 3/Introduction). I expressed enthusiasm for this as I could see that might be less complex or uninterpretable profiles and our analysts could focus more time on potentially meaningful samples which would benefit us all. The impression I got from this was that we were both on the same wavelength.
8. General discussion on the success of the tape lifts (page 7/Discussion). I gave anecdotal stories of where I had seen unexpected profiles obtained on objects such as tapelifted rocks/bricks and that the success of the tapelifts was pleasantly surprising.

Thanks,

Allison Lloyd
A/Senior Scientist - Intelligence Team

Forensic DNA Analysis, Police Services Stream
Forensic & Scientific Services, Health Support Queensland, Queensland Health

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Cathie Allen

From: Cathie Allen
Sent: Friday, 17 December 2021 9:52 AM
To: Lara Keller
Cc: Justin Howes; 'Paula Brisotto'
Subject: FW: Enquires from Ms Kirsty Wright
Attachments: Email re FSS inclusion on QPS journal article.pdf; Email re QPS journal article_July 2021.pdf

Hi Lara

It's extremely disappointing that the journal article written by a QPS staff member is now looking to be used against the laboratory. Both Allison Lloyd and myself gave significant verbal feedback to Dr Matt Krosch regarding the deficiencies within the draft version of the paper, however none of our concerns were taken onboard.

I escalated this issue to John Doherty, as the paper contains duplicate samples (at the very least) so has at least 1 flaw scientifically. My understanding was that John was working with Supt Bruce McNab on this and despite my repeated follow-up, no outcome was provided to me. Until I found the journal article myself in July of this year. I was never advised that the QPS were proceeding to publishing.

The acknowledgement of myself on the paper is reprehensible, as it appears that I support the paper, when I verbally expressed to the author that I did not support the draft as it was. I wished I'd been provided a copy of the paper to be published, as I would have directed the author to remove my name from the acknowledgements as I do not wish to be associated with it.

Acknowledgments

The author would like to thank Inspectors David Keatinge and David Neville (QPS), and Allisor Cathie Allen (QHFSS) for their review of the manuscript and valuable comments and discussi Middleton (QPS) assisted extraction of DNA results from the LIMS.

Tim Middleton was a QPS contractor that was working on the Forensic Register, so had access to pull data from the FR, without the knowledge of FSS. FSS were not involved in the setting the parameters for collecting the DNA data.

It appears that Insp Neville has authorised Dr Krosch to proceed with publishing, despite our concerns and requests for changes.

My plan is to email the Inspector back and thank him for advising us of the enquiries, advise that FSS had raised concerns to the author prior to publishing and to request that if further enquiries are made that we are advised of them.

Cheers
Cathie



Cathie Allen BSc, MSc (Forensic Science) (She/Her*)
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health

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a [redacted]
e [redacted] w www.health.qld.gov.au/fss

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*If you're wondering about the use of pronouns She/Her on this signature block, I encourage you to read some resources available here



From: Neville.DavidH[OSC] <[redacted]>
Sent: Friday, 17 December 2021 8:32 AM
To: Cathie Allen <[redacted]>
Cc: Lara Keller <[redacted]>
Subject: Enquires from Ms Kirsty Wright

This email originated from outside Queensland Health. DO NOT click on any links or open attachments unless you recognise the sender and know the content is safe.

Hi Cathie
I need to give you a heads up on an enquiry made by Kirsty Wright recently. The email string below is fairly self-explanatory. We wont be providing her any further comment.

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
Ph: [redacted]
Mob: [redacted]
[redacted]

From: Kirsty Wright <[redacted]>
Sent: Thursday, 16 December 2021 11:08
To: Krosch.MattN[OSC] <[redacted]>
Cc: Neville.DavidH[OSC] <[redacted]>
Subject: Re: Some Further Analysis from your Paper

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Hi Matt,

Thank you for your response and clarifying the sexual assault samples. I understand your comments about not using the data to make comment about the lab's efficiency, and will respect your position on that. There are some very interesting results in there that may indicate there are issues in the lab though. The breast, oral and penis swabs are essentially clinical samples (taken from either the victim or offender by a GMO). To get such high amounts of 'no DNA' from those swabs is a concern (eg 52% of penis swabs getting no DNA, when you would expect to always at least get the donor).

Thanks again and have a lovely Christmas.

Dr Kirsty Wright

Visiting Fellow

Genomics Research Centre,

Institute of Health and Biomedical Innovation

From: Krosch.MattN[OSC] <[redacted]>
Sent: Thursday, December 16, 2021 9:14 AM
To: Kirsty Wright <[redacted]>
Cc: Neville.DavidH[OSC] <[redacted]>
Subject: RE: Some Further Analysis from your Paper

Dear Kirsty,

Thank you for your inquiry. Regarding your specific questions, sexual assault sample results included both fractions (where relevant), and I am not sure about AP/microscopy results for the semen swabs. More broadly, however, the purpose of the paper was to provide some insight for crime scene examiners about the likelihood of generating a useable profile from a particular sample type based on the substrate and collection technique and thereby inform their decision-making at the point of collection. The study was not designed to evaluate the efficacy of the testing laboratory and it would be inappropriate to use the data for that purpose. Any attempt to do so would be significantly flawed. There are numerous caveats around these data and the appropriateness or otherwise of comparing these with previous studies, many of which are discussed in the paper. It would not be appropriate for me to comment more broadly on these matters.

Kind regards,
Matt

Dr Matt Krosch
Research Officer
Quality Management Section
Forensic Services Group
Operation Support Command
Queensland Police Service
Ph: [redacted] | Mobile: [redacted]



Members of QMS will at times be working from home during the COVID-19 crisis. If my office phone goes unanswered, please call me on the mobile above if you need to speak with me.

From: Kirsty Wright <[redacted]>
Sent: Monday, 13 December 2021 08:21
To: Krosch.MattN[OSC] <[redacted]>
Subject: DNA Profiling Success Article

CAUTION: This email originated from outside of Queensland Police Service. Do not click links or open attachments unless you recognise the sender and know the content is safe.

Hi Matt,

I'm doing some research into the lab issues that were affecting the BLACKBURN case after the introduction of PP21 and STRMix. I found your 2020 paper in AJFS about DNA profiling success rates. I don't want to draw any incorrect or unfair conclusions from the data, so can I ask you some questions just to clarify a couple of points? Eg for the sexual assault samples, were these only the male fractions? For semen samples, were these AP+ and micro+? Please let me know if this is OK, and when would be a good time to talk.

Best wishes

Dr Kirsty Wright

Visiting Fellow

Genomics Research Centre,

Institute of Health and Biomedical Innovation

Allison Lloyd

From: Allison Lloyd
Sent: Friday, 14 February 2020 3:25 PM
To: Cathie Allen
Subject: RE: DNA success rates manuscript

Hi Cathie,

My apologies, it won't happen again.

Thanks,

Allison

From: Cathie Allen <[redacted]>
Sent: Friday, 14 February 2020 3:22 PM
To: Allison Lloyd <[redacted]>
Cc: Justin Howes <[redacted]>
Subject: FW: DNA success rates manuscript

Hi Allison

I've just received the below email back from Insp Neville at the QPS.

I'm surprised that you forwarded the email that I had written to you onto Dr Matt Krosch. From my perspective, the information I provided to you was for your information only and I hadn't intended for Dr Matt Krosch to be aware of what I had expressed to you and how I expressed it to you.

In future circumstances like this, can you please ensure that the QPS aren't forwarded emails from me in this way.

Cheers
Cathie

Cathie Allen
Managing Scientist

Police Services Stream, Forensic & Scientific Services
Health Support Queensland, Queensland Health

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From: Allison Lloyd <[redacted]>
Sent: Friday, 14 February 2020 10:31

To: Krosch.MattN[OSC] <[redacted]>
Subject: FW: DNA success rates manuscript

Hi Matt,

I've been asked to go through your manuscript. I've given it a good read and have a few questions/comments... I'm more than happy to meet up or talk on the phone, whatever suits you better.

My number is [redacted] or [redacted]

Looking forward to working with you on this.

Kind regards,

Allison Lloyd
A/Senior Scientist - Intelligence Team

Forensic DNA Analysis, Police Services Stream
Forensic & Scientific Services, Health Support Queensland, Queensland Health

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a [redacted]
e [redacted] w www.health.qld.gov.au/healthsupport/businesses/forensic-and-scientific-services

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From: Cathie Allen <[redacted]>
Sent: Tuesday, 11 February 2020 12:04 PM
To: Allison Lloyd <[redacted]>
Cc: Justin Howes <[redacted]>; Paula Brisotto <[redacted]>
Subject: FW: DNA success rates manuscript

Hi Allison

Thanks so much for agreeing to be the FSS collaborator on this paper – I really appreciate it, given your busy role.

Attached is the manuscript and also the raw data.

I've discussed with Matt that the Government would be expecting a collaboration on this, given the significant investment they have made in the Forensic DNA Analysis lab to undertake DNA testing solely for the purpose of the QPS. I appreciate that Matt has driven this work himself and has focussed on sampling, however my perspective is that the lab has tailored it's processes to ensure success for a sample that's submitted, so it's a collaboration and Matt readily agreed. Matt has done all of the evaluation of the data to date, so I suggested that perhaps the FSS rep (as we spoke on Friday, prior to offering you the opportunity so wasn't able to name you) would be able to review some data, as I believe he hasn't taken into account any microcons that we've done to achieve the profiles. So they may need to run the report in the FR again, to capture the post extraction techniques so that we can review them to see if they have affected the outcome. If the report needs to be re-run, Matt will be able to achieve that, given he's within the QPS.

Please let me know if you have any questions. I'm excited that we're able to collaborate with the QPS on this and am excited for you to be given this opportunity, given your vast experience with profiles and NCIDD.

Cheers
Cathie



Cathie Allen
Managing Scientist

Police Services Stream, Forensic & Scientific Services
Health Support Queensland, Queensland Health

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e [redacted] w www.health.qld.gov.au/healthsupport

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From: Krosch.MattN[OSC] <[redacted]
Sent: Tuesday, 7 January 2020 1:02 PM
To: Cathie Allen <[redacted]>
Cc: Keatinge.DavidJ[OSC] <[redacted]>
Subject: DNA success rates manuscript

Dear Cathie,

Over the latter months of last year I spent some time summarising FR data for DNA results with a view to establish percentage successes for common items/substrates and collection methods. This was essentially a self-driven project that grew out of conversations with SOCOs and OICs and so the focus was on our side of the process to ensure we're making the best decisions on sampling to maximise success in the lab. In a nutshell it involved pulling information on the DNA results for every exhibit that was submitted over a set time period and searching the item description/location fields for keywords that allowed extraction of specific items/substrate results. The aim was to develop an evidence base on the success rates of sampling certain items to inform procedures and make recommendations to our officers on which collection methods were most effective for specific items based on recent data from actual casework.

I've now completed the analysis and have written the results up as a short paper that I hope to submit to AJFS as I believe this information is important to communicate to the forensic community. However, because the paper necessarily contains information about DNA profiling in Queensland we wish to offer you the opportunity to review the draft manuscript before submission to ensure that you and QHFSS are happy for the contents to be published. Please find attached the draft manuscript as a word document and the tables both at the end of the manuscript and as a separate excel file on individual sheets.

If you would like any further explanation on the methods or outcomes, please don't hesitate to get in touch.

Kind regards,

Matt

Dr. Matt Krosch
Research Officer
Quality Management Section, Forensic Services Group
Queensland Police Service
Ph: [redacted] | M: [redacted] | Email: [redacted]

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Cathie Allen

From: Cathie Allen
Sent: Friday, 14 February 2020 3:14 PM
To: John Doherty
Subject: FW: DNA success rates manuscript

Importance: High

Hi John

Seems that Dr Matt Krsoch has had a change of mind or been influenced to change his mind (probably due to the request of doing more data mining).

From my perspective, their rationale of being focussed on sampling is incorrect. They have not tested different sampling methods and have used crime scene samples for this paper.

From my perspective, this is unacceptable to exclude us as an author and won't represent the data accurately if post-extraction methods are taken into account (as they could vary the success rate!!!).

Could you please discuss this with Supt McNab.

Cheers
Cathie

Cathie Allen
Managing Scientist

Police Services Stream, Forensic & Scientific Services
Health Support Queensland, Queensland Health

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From: Neville.DavidH[OSC] <[redacted]>
Sent: Friday, 14 February 2020 2:42 PM
To: Cathie Allen <[redacted]>
Cc: Krosch.MattN[OSC] <[redacted]>; McNab.BruceJ[OSC] <[redacted]>; Keatinge.DavidJ[OSC] <[redacted]>
Subject: FW: DNA success rates manuscript

Hi Cathie

Matt has forwarded me the below email and we have had a discussion in relation to this. Thanks for taking the time to review his work. This paper is aimed at crime scene examiners to help them better focus their sampling methodology. It is not aimed at the laboratory and the introduction of additional lab factors might unnecessarily complicate the matter. It is important that the possible the impact of micron be covered in the discussion, however I don't think it is necessary for us to rerun the data. In this instance we were looking to provide QHFSS an acknowledgement in the paper, however it was not anticipated that the article would be become lab focused. As a result, a general review is probably all that is needed, if possible please.

Regards

David Neville

From: Allison Lloyd <[redacted]>
Sent: Friday, 14 February 2020 10:31
To: Krosch.MattN[OSC] <[redacted]>
Subject: FW: DNA success rates manuscript

Hi Matt,

I've been asked to go through your manuscript. I've given it a good read and have a few questions/comments... I'm more than happy to meet up or talk on the phone, whatever suits you better.

My number is [redacted] or [redacted]

Looking forward to working with you on this.

Kind regards,

Allison Lloyd
A/Senior Scientist - Intelligence Team

Forensic DNA Analysis, Police Services Stream
Forensic & Scientific Services, Health Support Queensland, Queensland Health

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From: Cathie Allen <[redacted]>
Sent: Tuesday, 11 February 2020 12:04 PM
To: Allison Lloyd <[redacted]>

Cc: Justin Howes <[redacted]>; Paula Brisotto <[redacted]>
Subject: FW: DNA success rates manuscript

Hi Allison

Thanks so much for agreeing to be the FSS collaborator on this paper – I really appreciate it, given your busy role.

Attached is the manuscript and also the raw data.

I've discussed with Matt that the Government would be expecting a collaboration on this, given the significant investment they have made in the Forensic DNA Analysis lab to undertake DNA testing solely for the purpose of the QPS. I appreciate that Matt has driven this work himself and has focussed on sampling, however my perspective is that the lab has tailored it's processes to ensure success for a sample that's submitted, so it's a collaboration and Matt readily agreed. Matt has done all of the evaluation of the data to date, so I suggested that perhaps the FSS rep (as we spoke on Friday, prior to offering you the opportunity so wasn't able to name you) would be able to review some data, as I believe he hasn't taken into account any microcons that we've done to achieve the profiles. So they may need to run the report in the FR again, to capture the post extraction techniques so that we can review them to see if they have affected the outcome. If the report needs to be re-run, Matt will be able to achieve that, given he's within the QPS.

Please let me know if you have any questions. I'm excited that we're able to collaborate with the QPS on this and am excited for you to be given this opportunity, given your vast experience with profiles and NCIDD.

Cheers
Cathie

Cathie Allen
Managing Scientist

Police Services Stream, Forensic & Scientific Services
Health Support Queensland, Queensland Health

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From: Krosch.MattN[OSC] <[redacted]>
Sent: Tuesday, 7 January 2020 1:02 PM
To: Cathie Allen <[redacted]>
Cc: Keatinge.DavidJ[OSC] <[redacted]>
Subject: DNA success rates manuscript

Dear Cathie,

Over the latter months of last year I spent some time summarising FR data for DNA results with a view to establish percentage successes for common items/substrates and collection methods. This was essentially a self-driven project that grew out of conversations with SOCOs and OICs and so the focus was on our side of the process to

ensure we're making the best decisions on sampling to maximise success in the lab. In a nutshell it involved pulling information on the DNA results for every exhibit that was submitted over a set time period and searching the item description/location fields for keywords that allowed extraction of specific items/substrate results. The aim was to develop an evidence base on the success rates of sampling certain items to inform procedures and make recommendations to our officers on which collection methods were most effective for specific items based on recent data from actual casework.

I've now completed the analysis and have written the results up as a short paper that I hope to submit to AJFS as I believe this information is important to communicate to the forensic community. However, because the paper necessarily contains information about DNA profiling in Queensland we wish to offer you the opportunity to review the draft manuscript before submission to ensure that you and QHFSS are happy for the contents to be published. Please find attached the draft manuscript as a word document and the tables both at the end of the manuscript and as a separate excel file on individual sheets.

If you would like any further explanation on the methods or outcomes, please don't hesitate to get in touch.

Kind regards,

Matt

Dr. Matt Krosch
Research Officer
Quality Management Section, Forensic Services Group
Queensland Police Service
Ph: [redacted] | M: [redacted] | Email: [redacted]

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Cathie Allen

From: Lara Keller
Sent: Thursday, 14 July 2022 6:56 AM
To: Cathie Allen; Helen Gregg
Subject: Emailing: Taylor & Francis 220704
Attachments: Taylor & Francis 220704.pdf

FYI Ladies
Sent recently.
Thanks
Lara

Queensland
Government

4 July 2022

Pathology Queensland and Forensic & Scientific Services
Prevention Division

Department of
Health

Taylor & Francis
[redacted]

Dear Sir/ Madam

I am writing to express concern on behalf of this organisation, regarding two instances of Acknowledgements in two journal articles where Dr Matt N Krosch has been a common author. Acknowledgements of Queensland Health Forensic and Scientific Services (QHFSS) staff members have been made; however, my staff report that they had not been notified of the acknowledgement nor had they granted their permission to be acknowledged.

The first journal article was: '*Variation in forensic DNA profiling success among sampled items and collection methods: a Queensland perspective*', published in May 2020. Acknowledgements were provided to Allison Lloyd and Cathie Allen. Both Allison and Cathie advise that they provided extensive feedback, however no aspect of their feedback was incorporated. Neither staff member was provided with a copy of the final article so that they could verify the context of their contribution or grant their permission for acknowledgment.

The second journal article was: '*Casework comparison of DNA sampling success from steering wheels and car seats in tropical Australia*', published in November 2021. Acknowledgment was provided to Justin Howes. Justin has reported that he has had no contact with the named authors regarding this article. He was not provided with a copy of the final article so that he could verify the context of his contribution or grant his permission for acknowledgement.

It is generally accepted that permission from named contributors is granted before acknowledging them in research outputs, since acknowledgement may imply a contributor's endorsement of the research output. According to my staff, this did not occur for either journal article.

I therefore respectfully request that these instances are investigated, and a response provided please.

Yours sincerely

[redacted]

Lara Keller
A/Executive Director
Queensland Health Forensic and Scientific Services
[redacted]

Forensic and Scientific Services
[redacted]
Website www.health.qld.gov.au

CA-90

TRACE DNA DETECTION ON PENILE SWABS IN SEXUAL ASSAULT CASES, AN INVESTIGATION OF QUEENSLAND DATA

Lloyd, A[1], McNevin, A[1], Allen, C[1]

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Trace or touch DNA located on penile swabs of offenders can provide useful information in sexual assault cases, potentially establishing a degree of contact between an alleged victim and offender.

Under ideal conditions, DNA profiles can be obtained from minimal amounts of trace DNA, however in forensic scenarios, these conditions are not always favourable. DNA can be removed, transferred or degraded and sampling success may not be uniform between samplers or sample donors. Resulting profiles may be unsuitable for interpretation or for application by statistical programs due to low levels of cellular material available or complexity of the profile including assessment of the number of potential contributors.

This work examined data from twelve months of penile swab samples submitted to the Forensic DNA Analysis laboratory in Queensland and reports on the types of DNA profiles obtained. Analysis compared the differences between results of separately extracted wet and dry swabs of the same penile area and investigated the results of swabs submitted for a differential extraction if scenarios indicated the subjects had previous intercourse.

The remainder of the analysis aimed to look at a breakdown of all DNA results obtained and report the variation in the profiles. This includes samples where no DNA was detected, DNA was insufficient for further processing, single source profiles, complex profiles where interpretation was unsuitable and mixed DNA profiles. Mixed DNA profiles are further interrogated to show the percentage of samples that were able to be deconvoluted using STRmix™ to provide likelihood ratio for evidence samples within a case.

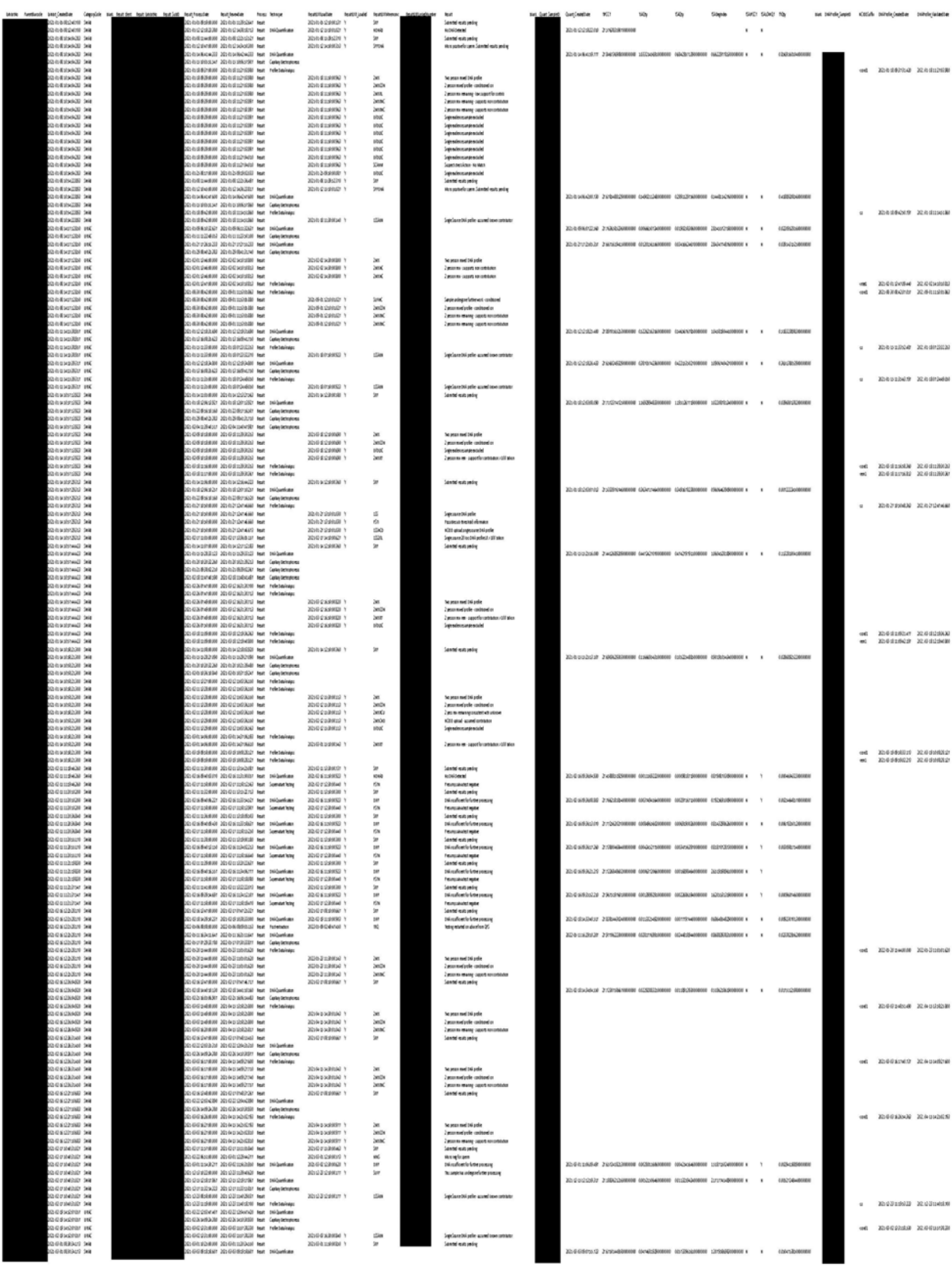
This analysis showed that DNA profiles and consequent statistical interpretations obtained from penile swabs in Queensland remain an important source of information for investigators. The analysis of these samples can be complex, and the ability to obtain DNA profiles and the assessment of what is informative or non-informative information is multi-layered.

Instructions (delete these before submission):

- Save this file as a .doc or .docx file for submission. Abstracts must be saved with the following filename - **'Surname_Initial'**. If you are submitting more than one abstract, please also include subsequent numbers in the filename, e.g. **'Surname_Initial_1'**.
- Please use capital letters for the abstract title
- Make sure you include all the authors and their affiliations in the abstract as there will be no opportunity to add these after acceptance
- Your abstract will appear on the internet and in the program book exactly as submitted

- Please refer to the Abstract Submission Guidelines for further information

CA-91



23/07/2022 11:16
Data for the ASCE Symposium poster
Data for profiles retrieved from previous visits.
Count values, dependent on visits, hypothetical and imported visits/time.

Cases: not 'Training'
Service Occupied between: 01/01/2021 - 31/12/2021
Imported Visits: are reviewed, (and not marked incorrect)
Profile Status: Validated (and not marked incorrect/imposed)
Service Description: contains 'trimmed', or 'mow, and, and/shrub/cut, or Cleft and mulch/weed/strim/strim/pass, (and, or not an environmental exception)

Site Ref No	Parent Site Ref No	Service Commencement	Category Code	Visit Ref	Visit Site Ref	Visit Site Name	Visit Type	Visit Planned Date	Visit Planned Week	Process	Visit Purpose	Visit Visit Status Name	Visit Visit Status	Visit Visit Locked	Visit Visit Reference	Visit Visit Visit Outcome Name	Visit	Visit Count_Category	Count_Count Name	WC1	SA Qty	EA Qty	SS Weight Mm	SSA FC1	SSA Cm2	YSA	Visit	Visit Profile_Category	VC Visit Ref	Visit Profile_Created Date	Visit Profile_Validated Date
[redacted]		2021-03-04 to 2021-09-24	3 mth	[redacted]	[redacted]	[redacted]	Inspect	2021-03-04 to 22:28:24	2021-09-24 to 22:28:24	Inspect	Courtesy Site Inspections																[redacted]			
		2021-03-01 to 21:26:31	3 mth				Inspect	2021-03-22 to 26:28:22		Inspect	Courtesy Site Inspections																			
		2021-03-23 to 24:08:00	3 mth				Inspect	2021-04-16 to 21:27:28		Inspect	Prefer Date Inspect																			
		2021-03-23 to 24:08:00	3 mth				Inspect	2021-04-16 to 21:27:43		Inspect	Prefer Date Inspect																			
		2021-03-24 to 06:21:30	3 mth				Inspect	2021-07-16 to 07:24:45		Inspect	Courtesy Site Inspections																			
		2021-07-07 to 10:48:00	3 mth				Inspect	2021-07-07 to 12:23:19		Inspect					2021-07-07 to 12:23:19		Mixed Shrub profile													
		2021-07-07 to 10:48:00	3 mth				Inspect	2021-07-07 to 12:23:19		Inspect					2021-07-07 to 12:23:19		Mix - supports non-contractor													
		2021-07-07 to 10:48:00	3 mth				Inspect	2021-07-07 to 12:23:19		Inspect					2021-07-07 to 12:23:19		Mix - KCEG upload													
		2021-07-01 to 01:25:00	3 mth				Inspect	2021-07-01 to 11:21:39		Inspect					2021-07-01 to 11:21:39		Submitted results pending													
		2021-03-01 to 08:45:00	3 mth				Inspect	2021-03-01 to 08:45:00		Inspect	Shrub Quantification																			
		2021-03-04 to 21:28:24	3 mth				Inspect	2021-04-16 to 21:28:24		Inspect	Courtesy Site Inspections																			
		2021-03-04 to 21:28:24	3 mth				Inspect	2021-04-16 to 21:27:43		Inspect	Courtesy Site Inspections																			
		2021-03-24 to 06:21:30	3 mth				Inspect	2021-07-16 to 07:24:45		Inspect	Courtesy Site Inspections																			
		2021-03-01 to 21:26:31	3 mth				Inspect	2021-03-22 to 26:28:22		Inspect	Courtesy Site Inspections																			
		2021-03-23 to 24:08:00	3 mth				Inspect	2021-04-16 to 21:27:43		Inspect	Prefer Date Inspect																			
		2021-03-01 to 01:25:00	3 mth				Inspect	2021-07-01 to 11:21:39		Inspect					2021-07-01 to 11:21:39		Submitted results pending													
		2021-03-01 to 08:45:00	3 mth				Inspect	2021-03-01 to 08:45:00		Inspect	Shrub Quantification																			
		2021-03-04 to 21:28:24	3 mth				Inspect	2021-04-16 to 21:28:43		Inspect	Courtesy Site Inspections																			
		2021-07-07 to 10:48:00	3 mth				Inspect	2021-07-07 to 12:23:19		Inspect	Prefer Date Inspect																			
		2021-07-07 to 10:48:00	3 mth				Inspect	2021-07-07 to 12:23:19		Inspect					2021-07-07 to 12:23:19		Mixed Shrub profile													
		2021-07-07 to 10:48:00	3 mth				Inspect	2021-07-07 to 12:23:19		Inspect					2021-07-07 to 12:23:19		KCEG upload - assumed contractor													
		2021-07-07 to 10:48:00	3 mth				Inspect	2021-07-07 to 12:23:19		Inspect					2021-07-07 to 12:23:19		Assumed contractor													
		2021-07-07 to 10:48:00	3 mth				Inspect	2021-07-07 to 12:23:19		Inspect					2021-07-07 to 12:23:19		Mix - supports non-contractor													
		2021-03-01 to 01:26:00	3 mth				Inspect	2021-03-01 to 11:22:44		Inspect					2021-03-01 to 11:22:44		Submitted results pending													
		2021-03-01 to 08:45:00	3 mth				Inspect	2021-03-01 to 08:45:00		Inspect	Shrub Quantification																			
		2021-03-04 to 21:28:24	3 mth				Inspect	2021-04-16 to 21:28:43		Inspect	Courtesy Site Inspections																			
		2021-03-23 to 24:08:00	3 mth				Inspect	2021-03-23 to 24:08:00		Inspect	Courtesy Site Inspections																			
		2021-03-04 to 06:39:00	3 mth				Inspect	2021-04-16 to 21:28:43		Inspect	Courtesy Site Inspections				2021-04-16 to 21:28:43		Complete mixed profile unsuitable for referring on or compaction													
		2021-03-01 to 01:26:00	3 mth				Inspect	2021-03-01 to 11:22:44		Inspect	Shrub Quantification																			
		2021-03-01 to 08:45:00	3 mth				Inspect	2021-03-01 to 08:45:00		Inspect	Shrub Quantification																			
		2021-03-04 to 21:28:24	3 mth				Inspect	2021-04-16 to 21:28:43		Inspect	Courtesy Site Inspections																			
		2021-03-01 to 08:45:00	3 mth				Inspect	2021-03-01 to 08:45:00		Inspect	Shrub Quantification																			
		2021-03-04 to 21:28:24	3 mth				Inspect	2021-04-16 to 21:28:43		Inspect	Courtesy Site Inspections																			
		2021-03-01 to 08:45:00	3 mth				Inspect	2021-03-01 to 08:45:00		Inspect	Shrub Quantification

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Data for the ASCE Symposium poster
Data for profiles retrieved from anemometer.
Quantities, degradation index, hysteresis and reported results time.

Cases not Training
Selected Created between 01/01/2021 - 31/12/2021
Reported Results are Reviewed (and not marked incorrect)
Profile Status = Validated (and not marked incorrect/rejected)
Selected Description contains Entered Cement, or Fresh, and Undisturbed, or Cliff, and Undisturbed (in notes/plans), (and, or not an environmental sample)

Selected No.	Parent Barcode	Selected Created Date	Category Code	Asset	Asset Client	Asset Sub-Site	Asset Sub-Unit	Result Protocol Date	Result Created Date	Process	Test Purpose	Result Validation Date	Result Validated	Result Validated Name	Asset	Quant_Layer.id	Quant_Created Date	WC1	%Qty	Qty	Qty Uncertainty	Shift Cl	Shift Cl2	%Qty	Asset	Shift Profile_Layer.id	ACMS Suffix	Shift Profile_Created Date	Shift Profile_Validated Date
[redacted]		2021-10-21 10:39:00.000	01 HC	[redacted]				2021-10-21 16:09:00.000	2021-10-26 10:19:34.707	Import	Profile Evaluations															[redacted]		2021-10-21 10:39:00.000	2021-10-26 10:19:34.707
		2021-10-21 10:39:00.000	01 HC					2021-10-21 16:09:00.000	2021-10-26 10:19:34.707	Import		2021-10-26 10:19:00.000	1	Z4H																
		2021-10-21 10:39:00.000	01 HC					2021-10-21 16:09:00.000	2021-10-26 10:19:34.707	Import		2021-10-26 10:19:00.000	1	Z4H3C																
		2021-10-21 10:39:00.000	01 HC					2021-10-21 16:09:00.000	2021-10-26 10:19:34.707	Import		2021-10-26 10:19:00.000	1	W50C																
		2021-10-21 10:39:00.000	01 HC					2021-10-21 16:09:00.000	2021-10-26 10:19:34.707	Import																				
		2021-10-21 12:39:00.000	01 HC					2021-10-27 12:09:00.000	2021-10-27 11:03:22.943	Import	Profile Evaluations															[redacted]		2021-10-21 12:39:00.000	2021-10-27 11:03:22.943
		2021-10-21 12:39:00.000	01 HC					2021-10-27 12:09:00.000	2021-10-27 11:03:22.960	Import		2021-10-27 11:03:00.000	1	S4HC																
		2021-10-21 12:39:00.000	01 HC					2021-10-27 12:09:00.000	2021-10-27 11:03:22.960	Import		2021-10-27 11:03:00.000	1	Z4H																
		2021-10-21 12:39:00.000	01 HC					2021-10-27 12:09:00.000	2021-10-27 11:03:22.960	Import		2021-10-27 11:03:00.000	1	Z4H2M																
		2021-10-21 12:39:00.000	01 HC					2021-10-27 12:09:00.000	2021-10-27 11:03:22.960	Import		2021-10-27 11:03:00.000	1	Z4H3C																
		2021-10-21 12:39:00.000	01 HC					2021-10-27 12:09:00.000	2021-10-27 11:03:22.960	Import		2021-10-27 11:03:00.000	1	Z4H4C																
		2021-10-21 15:09:00.000	04 HA					2021-10-21 21:09:00.000	2021-10-21 19:09:18.820	Import		2021-10-21 19:09:00.000	1	SHY																
		2021-10-21 09:37:12.000	04 HA					2021-10-21 09:37:12.000	2021-10-21 10:09:18.962	Import	Shift Quantification						2021-10-20 20:37:30.000	21.0	0.1	0.0	0.0	0	0	0.1						
		2021-10-21 12:39:00.000	04 HA					2021-10-21 16:09:00.000	2021-10-21 14:09:28.671	Import	Cautley Interference																			
		2021-10-21 14:09

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Data for ArcGIS Symposium poster
Data for profiles retrieved from postcrete.
Quant values, degradation index, % quant and imported mass/vol.

Cases: not 'Training'
Session Created: between 01/01/2021 - 31/12/2021
Imported Results: unreviewed (and not marked incorrect)
Profile Status: Validated (and not marked incorrect/rejected)
Session Description: contains 'mineral' (peroxi, or mins, and undifferentiated, or CAH and undifferentiated) in name (case), (and) or not environmental sample)

Session	Session Description	Session Created Date/Time	Category Code	Client	Result Client	Result Site Name	Result Code	Result Process Date	Result Process Time	Process	Technique	Result ROI Modified Date	Result ROI Created	Result ROI Reference	Result ROI Classification	Result	Client	Quant Sample	Quant Created Date	WCF	%Qty	%Qty Error	%Degradation	SI of CT	%Qty Min	%Qty Max	Client	Result Profile Sample	ACADEMy No	Result Profile Created Date	Result Profile Validated Date
[redacted]	[redacted]	2021-06-11 08:39:45.000	Sand	[redacted]	[redacted]	[redacted]	[redacted]	2021-06-11 12:25:14.000	2021-06-11 12:25:14.000	Import						Non-Asbestos material (as assigned	[redacted]	[redacted]									[redacted]	[redacted]			
		2021-06-11 09:04:04.647	Sand					2021-06-11 09:04:04.647	2021-06-11 10:17:16.262	Import						Submitted results pending															
		2021-06-11 09:04:04.663	Sand					2021-06-14 16:37:28.020	2021-06-14 16:37:28.020	Import	Shell Quantification							2021-06-14 16:36:12.253.242	2.45896428E-06	0.010274494000000	0.012731741000000	0.008307941000000	N	0.010274494	0.012731741000000					
		2021-06-11 09:04:04.663	Sand					2021-06-23 12:07:21.743	2021-06-23 12:09:23.257	Import	Capillary Electrophoresis																			
		2021-06-11 09:04:04.663	Sand					2021-06-11 13:47:34.443	2021-06-11 13:48:34.617	Import	Shell Quantification							2021-06-21 13:42:24.228	2.34685905E-06	0.009628135000000	0.010439697210000	0.008816573000000	N	0.009628135	0.010439697210000					
		2021-06-11 09:04:04.663	Sand					2021-06-09 11:28:31.017	2021-06-09 12:06:43.540	Import	Capillary Electrophoresis																			
		2021-06-11 09:04:04.663	Sand					2021-12-02 14:42:49.000	2022-02-01 12:43:14.820	Import	Profiler Embedologics																			
		2021-06-11 09:04:04.663	Sand					2021-12-02 14:42:49.000	2022-02-01 12:43:14.820	Import			2022-02-01 12:43:14.820	1	2 min	Trimm passes round 2 min profile														
		2021-06-11 09:04:04.663	Sand					2021-12-02 14:42:49.000	2022-02-01 12:43:14.820	Import			2022-02-01 12:43:14.820	1	2min02m	2 passes round profile - continued on														
		2021-06-11 09:04:04.663	Sand					2021-12-02 14:42:49.000	2022-02-01 12:43:14.820	Import			2022-02-01 12:43:14.820	1	2min30sec	2 passes min remaining - supports non-contributor														
		2021-06-11 09:04:04.663	Sand					2021-06-11 09:04:04.647	2021-06-11 09:05:13.283	Import			2021-06-11 10:10:05.047	1	3 PF	Submitted results pending														
		2021-06-11 09:04:04.663	Sand					2021-06-14 16:23:28.200	2021-06-14 16:37:44.217	Import	Shell Quantification		2021-06-14 16:23:28.200	1	3 PF	3 Min insufficient for further processing		2021-06-14 16:36:12.253.210	2.46289145E-06	0.005102744000000	0.005882201000000	0.004322864000000	N	1	0.005102744	0.005882201000000					
		2021-06-11 09:04:04.663	Sand					2021-06-14 16:23:28.200	2021-06-14 16:37:44.217	Import			2021-06-14 16:23:28.200	1	3 PF	Submitted results pending		2021-06-21 13:17:52.282	2.42436426E-06	1.87492E-06	0.000000000000	1.96422e+12	0.000000000000	0.014	1.87492E-06	1.96422e+12					
		2021-06-11 09:04:04.663	Sand					2021-06-11 12:25:22.299	2021-06-11 12:25:22.299	Import	Shell Quantification																			
		2021-06-11 09:04:04.663	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-11 09:04:04.663	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-11 09:04:04.663	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	4 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	5 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	6 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	7 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	8 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	9 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	10 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	11 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	12 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	13 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	14 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	15 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	16 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	17 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	18 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	19 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	20 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	21 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	22 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	23 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	24 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	25 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	26 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	27 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	28 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	29 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	30 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	31 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	32 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	33 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	34 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	35 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-27 12:09:00.000	2021-08-04 16:21:43.191	Import	Profiler Embedologics																			
		2021-06-14 12:39:24.403	Sand					2021-06-23 12:09:23.257	2021-06-23 12:09:23.257	Import			2021-07-21 16:39:07.777	1	36 PF	Submitted results pending														
		2021-06-14 12:39:24.403	Sand					2021-06-24 12:46:12.702	2021-06-24 13:21:19.527	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021-07-14 16:46:24.200	2021-07-14 16:46:24.217	Import	Capillary Electrophoresis																			
		2021-06-14 12:39:24.403	Sand					2021

[redacted]

Event Log Export

Data for event ID: [redacted]

Data for profiles: [redacted]

Export status: Applied event filters, layout and redacted mask rules.

Query run: Yesterday

Selected Occurred between: 01-01-2020 - 31-12-2020

Reported Results: sent forwarded, [and] not marked as incorrect

Profile Status: Validated [and] not marked as incorrect

Selected Description contains: forward, [and] or, Press, [and] child fatalities, or, Child, [and] unaffiliated [with] victim [data], [and] a, not an environmental, [and] accident

Subscriber	EventID	Subscriber	Category Code	Event	Result_Event	Result_Subscriber	Result_Event	Result_EventDate	Result_EventDate	Process	Technique	ResultEXIFLocation	ResultEXIF_LocalId	ResultEXIFReferences	ResultEXIFLocationNumber	Result	Event_Event	Event_Event	Event_EventDate	WGS1	SADy	SADy	SADy	SADy	SADy	Event	EXIFProfile_Computed	ACCESSoffs	EXIFProfile_CreatedDate	EXIFProfile_ValidatedDate
[redacted]			0 FAC			[redacted]		2021-09-01 12:23:49.000	2021-09-01 07:27:29.000	Import	Child Quantification	2021-09-01 07:27:29.000	1	EXIF		Data insufficient for further processing	[redacted]		2021-09-01 12:23:34.538	21.7128.0.1.1354.0.1.538	21.7128.0.1.1354.0.0.0.0.0.0.0.0.0.0.0	1.6.1.2.7.2.1.2.0.0.0.0.0.0.0.0	1.6.1.2.7.2.1.2.0.0.0.0.0.0.0.0	1.6.1.2.7.2.1.2.0.0.0.0.0.0.0.0	1.6.1.2.7.2.1.2.0.0.0.0.0.0.0.0	x	1	0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0				
			0 FAC					2021-09-01 12:23:49.000	2021-09-01 12:23:49.000	Import		2021-09-01 12:23:49.000	1	EXIF		Submitted results pending														
			0 FAC					2021-09-01 12:23:36.672	2021-09-01 12:23:36.672	Import	Child Quantification	2021-09-01 12:23:36.672	1	NOAID		Archived/Unsolved			2021-09-01 12:23:36.672	21.7128.0.1.1354.0.0.0.0.0.0.0.0.0.0.0					x	x				
			0 FAC					2021-09-01 12:24:00.000	2021-09-01 12:24:00.000	Import		2021-09-01 12:24:00.000	1	NFI		Item has been reserved/Location accepted														
			0 FAC					2021-09-01 12:23:00.000	2021-09-01 12:23:00.000	Import		2021-09-01 12:23:00.000	1	EXIF		Submitted results pending														
			0 FAC					2021-09-01 12:23:49.000	2021-09-01 12:24:49.000	Import	Child Quantification	2021-09-01 12:24:49.000	1	NOAID		Archived/Unsolved			2021-09-01 12:24:49.000	21.7128.0.1.1354.0.0.0.0.0.0.0.0.0.0.0					x	x				
			0 FAC					2021-09-01 12:24:00.000	2021-09-01 12:24:00.000	Import		2021-09-01 12:24:00.000	1	NFI		Item has been reserved/Location accepted														
			0 FAC					2021-09-01 12:23:49.000	2021-09-01 12:24:49.000	Import		2021-09-01 12:24:49.000	1	EXIF		Submitted results pending														
			0 FAC					2021-09-01 12:23:36.672	2021-09-01 12:24:36.672	Import	Child Quantification	2021-09-01 12:24:36.672	1	NOAID		Archived/Unsolved			2021-09-01 12:24:36.672	21.7128.0.1.1354.0.0.0.0.0.0.0.0.0.0.0					x	x				
			0 FAC					2021-09-01 12:24:00.000	2021-09-01 12:24:00.000	Import		2021-09-01 12:24:00.000	1	NFI		Item has been reserved/Location accepted														
			0 FAC					2021-09-01 12:24

23/07/2022 11:16
Data for ANZCS symposium poster
Data for profiles retrieved from anesmonedc
Count values, dependance on date, % count and reported mean time.

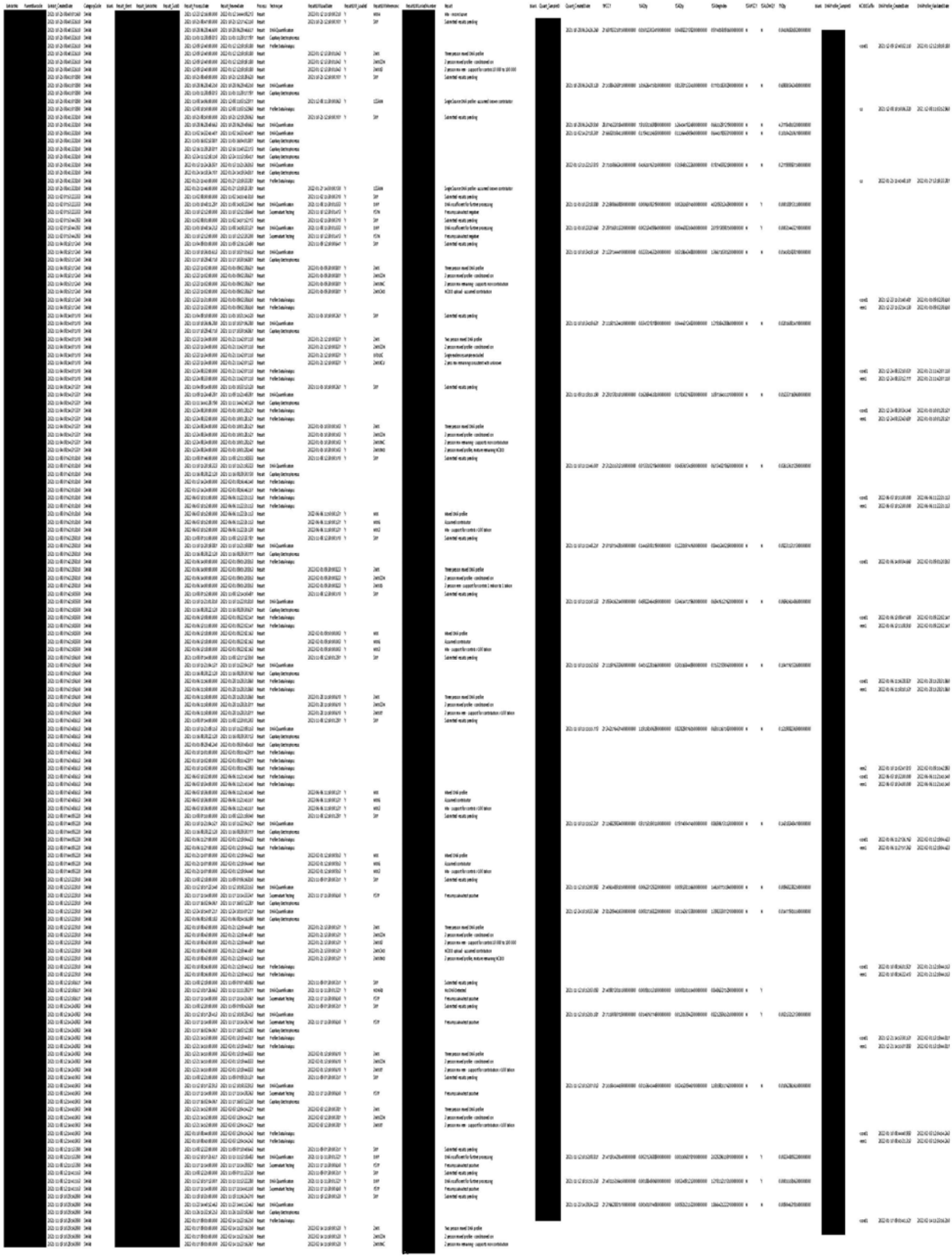
Cases not Training
Session Created between 01 of Jul 2021 - 31 of Jul 2021
Reported Results and Reviewed (and not reviewed incorrect)
Profile Status Validated (and not reviewed incorrect/missed)
Session Description contains Interventional (anesmon, or Hemo, and Undifferentiated, or Cath and Undifferentiated) in interventional, Cath is not an interventional anesmon

SessionNo	FromSession	SessionCreatedDate	CategoryScale	Num	Result_Event	Result_SessionNo	Result_SessionDate	Result_ElapsedDate	Persons	TestAnswer	ResultAllValueDate	ResultAllCorrectAnswer	ResultAllAnswerAnswer	Result	Num	Count_CategoryId	Count_CreatedDate	MCC	TotQty	EstQty	EstUpdateDate	EstMCC	TotQty	Num	EstProfile_CategoryId	ACSIGCodes	EstProfile_CreatedDate	EstProfile_ValidatedDate
[redacted]		2021-08-01 11:16:49.0000	24 HR		[redacted]	2021-08-01 11:24:53.2533	2021-08-01 11:24:53.2533	Result	Supervised Testing	2021-08-01 11:30:07.7642	Y	YCN		Intubated patient negative														
		2021-08-01 11:16:49.0000	24 HR			2021-08-01 14:28:27.1112	2021-08-01 21:27:42.2577	Result	Email Questionnaire	2021-08-01 21:30:07.0627	Y	DFF		Intubated insufficient for further processing			2021-08-02 04:20:24.0000	0.1250833344000000	0.0025000000000000	0.0025000000000000	2021-08-02 04:20:24.0000	0.1250833344000000	1.0000000000000000	0.0025000000000000			
		2021-08-01 11:16:50.0250	24 HR			2021-08-01 22:08:00.0000	2021-08-01 14:08:18.1612	Result	Supervised Testing	2021-08-01 22:30:07.0152	Y	DFF		Submitted results pending														
		2021-08-01 11:16:50.2250	24 HR			2021-08-01 12:24:08.0000	2021-08-01 12:24:24.4287	Result	Supervised Testing	2021-08-01 22:30:07.0742	Y	YCN		Previously assessed as positive														
		2021-08-01 11:16:50.2250	24 HR			2021-08-01 14:28:20.0420	2021-08-01 21:27:42.2577	Result	Email Questionnaire	2021-08-01 21:30:07.0627	Y	DFF		Intubated insufficient for further processing			2021-08-02 04:20:24.0000	0.1250833344000000	0.0025000000000000	0.0025000000000000	2021-08-02 04:20:24.0000	0.1250833344000000	1.0000000000000000	0.0025000000000000			
		2021-08-01 11:16:50.4583	24 HR			2021-08-01 22:08:00.0000	2021-08-01 14:08:18.1612	Result	Supervised Testing	2021-08-01 22:30:07.0152	Y	DFF		Submitted results pending														
		2021-08-01 11:16:50.4583	24 HR			2021-08-01 12:24:08.0000	2021-08-01 12:24:24.4287	Result	Supervised Testing	2021-08-01 22:30:07.0742	Y	YCN		Previously assessed as positive														
		2021-08-01 11:16:50.4583	24 HR			2021-08-01 14:28:20.0420	2021-08-01 21:27:42.2577	Result	Email Questionnaire	2021-08-01 21:30:07.0627	Y	HOHAE		Intubated Interested			2021-08-02 04:20:24.0000	0.1250833344000000	0.0025000000000000	0.0025000000000000	2021-08-02 04:20:24.0000	0.1250833344000000	1.0000000000000000	0.0025000000000000			
		2021-08-01 11:16:50.4847	24 HR			2021-08-01 14:42:27.7417	2021-08-01 21:42:27.7417	Result	Email Questionnaire	2021-08-01 21:45:07.0627	Y	LBYFB		Previously assessed as pos. Submitted results pending														
		2021-08-01 11:16:50.5583	24 HR			2021-08-01 09:47:08.4000	2021-08-01 09:47:24.1210	Result	Email Questionnaire	2021-08-01 09:50:07.0727	Y	HMG		Micro-org for germ														
		2021-08-01 11:16:50.5583	24 HR			2021-08-01 09:49:08.3612	2021-08-01 09:49:24.4612	Result	Email Questionnaire								2021-08-02 09:49:24.2177	27.2228828.0000000	0.0104038240000000	0.0042000000000000	27.4228828.0000000	0.0104038240000000	1.0000000000000000	0.0042000000000000			
		2021-08-01 11:16:50.5583	24 HR			2021-08-01 12:44:08.0000	2021-08-01 12:44:25.2260	Result	Supervised Testing	2021-08-01 22:30:07.0833	Y	YCN		Previously assessed as positive														
		2021-08-01 11:16:50.5583	24 HR			2021-08-01 12:24:52.7447	2021-08-01 12:24:52.7447	Result	Cardiac Electrophysiology				[redacted]															
		2021-08-01 11:16:50.5583	24 HR			2021-08-01 14:28:27.2412	2021-08-01 14:28:27.2412	Result	Cardiac Intra-Images																			
		2021-08-01 11:16:50.5583	24 HR			2021-08-01 14:28:27.2412	2021-08-01 14:28:27.2412	Result		2021-08-27 14:28:30.0372	Y	LSSAN		Single Source Unit profile - assumed known contractor														
		2021-08-01 11:16:50.5583	24 HR			2021-08-01 14:28:27.2412	2021-08-01 14:28:27.2412	Result		2021-08-27 14:28:30.0372	Y	YCH		Hypotension threshold information														
		2021-08-01 11:16:50.5583	24 HR			2021-08-01 14:28:27.2412	2021-08-01 14:28:27.2412	Result		2021-08-01 22:30:07.0729	Y	DFF		Submitted results pending														
		2021-08-01 12:47:13.8212	24 HR			2021-08-01 12:47:13.8212	2021-08-01 12:47:13.8212	Result	Email Questionnaire								2021-08-02 12:47:13.8212	0.1250775262500000	0.0075000000000000	0.0075000000000000	2.1250775262500000	0.1250775262500000	1.0000000000000000	0.0075000000000000			
		2021-08-01 12:47:13.8212	24 HR			2021-08-01 12:47:13.8212	2021-08-01 12:47:13.8212	Result	Cardiac Electrophysiology																			
		2021-08-01 12:47:13.8212	24 HR			2021-08-01 12:47:13.8212	2021-08-01 12:47:13.8212	Result	Cardiac Intra-Images																			
		2021-08-01 12:47:13.8212	24 HR			2021-08-01 12:47:13.8212	2021-08-01 12:47:13.8212	Result	Cardiac Electrophysiology

23/07/2022 11:16
Data for the NICE Symposium poster
Data for profiles retrieved from previous visits.
Count values, dependent on visits, hypothetical and imported visits time.

Cases not Training
Session Created between 01-07-2021 - 31-12-2021
Imported Results and Reviewed (and not reviewed incorrect)
Profile Status = Validated (and not reviewed incorrect imported)
Session Description contains Stressful Lament, or Stress and Untidy Routine, or Cold and Unsatisfactory Kitchen Chairs, Sand, or Intravenous Insurance Lawyer)

Session No	Parent Session No	Session Created Date	Category Code	Visit No	Result Client No	Result Session No	Result Created Date	Result Process Date	Result Observation Date	Process Type	Test Version	Result Visit Duration	Result Visit Length	Result Visit Reference No	Result Visit Location Number	Result	Visit No	Count Completed	Count Completed Date	WHO 1	WHO 2	WHO 3	WHO 4	WHO 5	Visit No	Child Profile Completed Date/Time	ACMS Suffix	Child Profile Created Date	Child Profile Validated Date
[redacted]		2021-09-27 14:44:27.2403	EMOC		[redacted]		2021-11-09 12:26:09.000	2021-11-09 15:28:26.2133	2021-11-09 15:28:26.2133	Import	Profile Evaluation Apps														[redacted]			
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:26:09.000	2021-11-09 15:28:26.2264	2021-11-09 15:28:26.2264	Import						Time pressure mood 2 Hot profile												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:26:09.000	2021-11-09 15:28:26.2341	2021-11-09 15:28:26.2341	Import					2 HotCPA	2 pressure mood profile - continued on												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:26:09.000	2021-11-09 15:28:26.2419	2021-11-09 15:28:26.2419	Import					2 HotSE	2 pressure mo - support for control 1 reborn to 1 broken												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.2634	2021-11-09 15:28:26.2634	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:26:09.000	2021-11-09 15:28:26.2734	2021-11-09 15:28:26.2734	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.2841	2021-11-09 15:28:26.2841	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.2934	2021-11-09 15:28:26.2934	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.3041	2021-11-09 15:28:26.3041	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.3141	2021-11-09 15:28:26.3141	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.3241	2021-11-09 15:28:26.3241	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.3341	2021-11-09 15:28:26.3341	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.3441	2021-11-09 15:28:26.3441	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.3541	2021-11-09 15:28:26.3541	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.3641	2021-11-09 15:28:26.3641	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.3741	2021-11-09 15:28:26.3741	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.3841	2021-11-09 15:28:26.3841	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.3941	2021-11-09 15:28:26.3941	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.4041	2021-11-09 15:28:26.4041	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.4141	2021-11-09 15:28:26.4141	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.4241	2021-11-09 15:28:26.4241	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.4341	2021-11-09 15:28:26.4341	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.4441	2021-11-09 15:28:26.4441	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.4541	2021-11-09 15:28:26.4541	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.4641	2021-11-09 15:28:26.4641	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.4741	2021-11-09 15:28:26.4741	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.4841	2021-11-09 15:28:26.4841	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.4941	2021-11-09 15:28:26.4941	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.5041	2021-11-09 15:28:26.5041	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.5141	2021-11-09 15:28:26.5141	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.5241	2021-11-09 15:28:26.5241	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.5341	2021-11-09 15:28:26.5341	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.5441	2021-11-09 15:28:26.5441	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.5541	2021-11-09 15:28:26.5541	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.5641	2021-11-09 15:28:26.5641	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.5741	2021-11-09 15:28:26.5741	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.5841	2021-11-09 15:28:26.5841	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.5941	2021-11-09 15:28:26.5941	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.6041	2021-11-09 15:28:26.6041	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.6141	2021-11-09 15:28:26.6141	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.6241	2021-11-09 15:28:26.6241	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.6341	2021-11-09 15:28:26.6341	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.6441	2021-11-09 15:28:26.6441	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.6541	2021-11-09 15:28:26.6541	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.6641	2021-11-09 15:28:26.6641	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.6741	2021-11-09 15:28:26.6741	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.6841	2021-11-09 15:28:26.6841	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.6941	2021-11-09 15:28:26.6941	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.7041	2021-11-09 15:28:26.7041	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.7141	2021-11-09 15:28:26.7141	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.7241	2021-11-09 15:28:26.7241	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.7341	2021-11-09 15:28:26.7341	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.7441	2021-11-09 15:28:26.7441	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.7541	2021-11-09 15:28:26.7541	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.7641	2021-11-09 15:28:26.7641	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.7741	2021-11-09 15:28:26.7741	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.7841	2021-11-09 15:28:26.7841	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.7941	2021-11-09 15:28:26.7941	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.8041	2021-11-09 15:28:26.8041	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.8141	2021-11-09 15:28:26.8141	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.8241	2021-11-09 15:28:26.8241	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.8341	2021-11-09 15:28:26.8341	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.8441	2021-11-09 15:28:26.8441	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.8541	2021-11-09 15:28:26.8541	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.8641	2021-11-09 15:28:26.8641	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.8741	2021-11-09 15:28:26.8741	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.8841	2021-11-09 15:28:26.8841	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.8941	2021-11-09 15:28:26.8941	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.9041	2021-11-09 15:28:26.9041	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.9141	2021-11-09 15:28:26.9141	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.9241	2021-11-09 15:28:26.9241	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.9341	2021-11-09 15:28:26.9341	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.9441	2021-11-09 15:28:26.9441	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.9541	2021-11-09 15:28:26.9541	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.9641	2021-11-09 15:28:26.9641	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.9741	2021-11-09 15:28:26.9741	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.9841	2021-11-09 15:28:26.9841	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:26.9941	2021-11-09 15:28:26.9941	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.0041	2021-11-09 15:28:27.0041	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.0141	2021-11-09 15:28:27.0141	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.0241	2021-11-09 15:28:27.0241	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.0341	2021-11-09 15:28:27.0341	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.0441	2021-11-09 15:28:27.0441	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.0541	2021-11-09 15:28:27.0541	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.0641	2021-11-09 15:28:27.0641	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.0741	2021-11-09 15:28:27.0741	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.0841	2021-11-09 15:28:27.0841	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.0941	2021-11-09 15:28:27.0941	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.1041	2021-11-09 15:28:27.1041	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.1141	2021-11-09 15:28:27.1141	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.1241	2021-11-09 15:28:27.1241	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.1341	2021-11-09 15:28:27.1341	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.1441	2021-11-09 15:28:27.1441	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.1541	2021-11-09 15:28:27.1541	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.1641	2021-11-09 15:28:27.1641	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.1741	2021-11-09 15:28:27.1741	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.1841	2021-11-09 15:28:27.1841	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.1941	2021-11-09 15:28:27.1941	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.2041	2021-11-09 15:28:27.2041	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.2141	2021-11-09 15:28:27.2141	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.2241	2021-11-09 15:28:27.2241	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.2341	2021-11-09 15:28:27.2341	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.2441	2021-11-09 15:28:27.2441	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.2541	2021-11-09 15:28:27.2541	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.2641	2021-11-09 15:28:27.2641	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.2741	2021-11-09 15:28:27.2741	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.2841	2021-11-09 15:28:27.2841	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.2941	2021-11-09 15:28:27.2941	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.3041	2021-11-09 15:28:27.3041	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.3141	2021-11-09 15:28:27.3141	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.3241	2021-11-09 15:28:27.3241	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.3341	2021-11-09 15:28:27.3341	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.3441	2021-11-09 15:28:27.3441	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.3541	2021-11-09 15:28:27.3541	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.3641	2021-11-09 15:28:27.3641	Import					2 HotCMC	2 pressure mo - rehearsing - supports non-combatant												
		2021-09-27 14:44:27.2403	EMOC				2021-11-09 12:27:09.000	2021-11-09 15:28:27.3741	2021-11-09 15:28:27.3741	Import					2 HotSE	2 pressure mo - rehearsing - supports non-combatant										



23/07/2022 11:16
Data for the ASCE Symposium poster
Data for profiles retrieved from anemometry.
Quant values, dependent on inlet, hypothetical reported maximum.

Cases not 'missing'
Session Created between 01/01/2021 - 31/12/2021
Reported Results are Reviewed (and not reviewed incorrect)
Profile Status = Validated (and not reviewed incorrect reviewed)
Session Description contains Entered Session, or Fence, and Undisturbed, or Cliff, and Unidirectional, or Inlet (Open), (and) or not an anemometric sample)

SessionNo	EventDateTime	SessionCreatedBy	CategoryCode	Inlet	Report_Result	Report_SessionNote	Result_Status	Result_CreatedBy	Result_CreatedDate	Result_SessionNote	Persons	Technique	ResultUKCMeanSpeed	ResultUKCGustSpeed	ResultUKCGustDuration	ResultUKCGustFactor	Result	Inlet	Quant_SampleID	Quant_CreatedBy	Quant_CreatedDate	WC1	TAQty	EAQty	EAAngle	EAWC1	EAUWC2	YAQty	Inlet	UnitProfile_SampleID	UKCASEuRo	UnitProfile_CreatedDate	UnitProfile_ValidatedDate
[redacted]									2021-11-10 10:58:00.000	2021-11-10 11:07:10.540	Report						Submitted results pending															
									2021-11-23 14:40:00.827	2021-11-24 10:31:20.970	Report	Field Quantification					Site is insufficient for further processing				2021-11-23 14:39:41.237	2.4438622266000000	0.0010600781000000	0.0042721202000000	1.1664497910000000	0	1	0.0035282864000000				
									2021-10-05 10:40:00.000	2021-10-05 10:40:44.620	Report	Fluctuanalysis					Testing restarted on subsurface QFS															
									2021-10-05 12:10:28.204	2021-10-05 12:24:28.201	Report	Field Quantification									2021-10-05 12:24:11.237	2.4438622266000000	0.0010600781000000	0.0042721202000000	1.1664497910000000	0	1	0.0035282864000000				
									2021-10-06 10:41:28.229	2021-10-06 10:42:28.203	Report	Cyanbey Instruments																				
									2021-10-07 10:07:00.000	2021-10-07 10:07:44.620	Report	Profile Stabalisinga																				
									2021-10-11 14:40:00.000	2021-10-11 14:40:44.620	Report				2021-10-12 12:10:00.520	1	2nd		Two pressure mixed 3rd/4 profile															
									2021-10-11 14:40:00.000	2021-10-11 14:40:44.620	Report				2021-10-12 12:10:00.520	1	2nd/2nd		2 pressure mixed profile - conditioned on															
									2021-10-11 14:40:00.000	2021-10-11 14:40:44.620	Report				2021-10-12 12:10:00.520	1	2nd/3rd		3 pressure mixed profile - conditioned on															
									2021-10-11 14:40:00.000	2021-10-11 14:40:44.620	Report				2021-10-12 12:10:00.520	1	2nd/3rdC		3 pressure mix remaining - supports micro orientation															
									2021-10-11 12:10:00.000	2021-10-11 12:10:20.640	Report				2021-10-12 12:10:00.520	1	3rd		Submitted results pending															
									2021-10-11 12:10:00.000	2021-10-11 12:10:20.640	Report	Field Quantification			2021-10-12 12:10:00.520	1	3rd		Site is insufficient for further processing															
									2021-10-11 12:10:00.000	2021-10-11 12:10:20.640	Report	Fluctuanalysis			2021-10-12 12:10:00.520	1	3rd/2nd		Testing restarted on subsurface QFS															
									2021-10-11 12:10:00.000	2021-10-11 12:10:20.640	Report	Cyanbey Instruments																				
									2021-10-11 12:10:00.000	2021-10-11 12:10:20.640	Report	Profile Stabalisinga																				
									2021-10-11 12:10:00.000	2021-10-11 12:10:20.640	Report				2021-10-12 12:10:00.520	1	3rd/3rd		Two pressure mixed 3rd/4 profile															
									2021-10-11 12:10:00.000	2021-10-11 12:10:20.640	Report				2021-10-12 12:10:00.520	1	3rd/3rdC		3 pressure mixed profile - conditioned on															
									2021-10-11 12:10:00.000	2021-10-11 12:10:20.640	Report				2021-10-12 12:10:00.520	1	3rdC		3 pressure mix remaining - supports micro orientation															
									2021-10-11 12:10:00.000	2021-10-11 12:10:20.640	Report	Profile Stabalisinga																				
									2021-10-11 12:10:00.000	2021-10-11 12:10:20.640	Report	Cyanbey Instruments																				
									2021-10-11 12:10:00.000	2021-10-11 12:10:20.640	Report	Profile Stabalisinga																				
									2021-10-11 12:10:00.000	2021-10-11 12:10:20.640	Report				2021-10-12 12:10:00.520	1	3rd		Submitted results pending

23/07/2022 15:16
Data for ward02 symposium poster
Data for profiles retrieved from previous visits.
Count values, dependance on date, % count and reported reaction time.

Cases: not 'missing'
Lesion Created between 01/01/2021 - 31/12/2021
Reported Results: are reviewed (and not reverted incorrect)
Profile Status: Validated (and not reverted incorrect/rejected)
Lesion Description contains: browed (severe), or Hevo, and (mild/moderate), or CAM and (mild/moderate/blank/not taken), (and, or not severe/anemia (severe)

LesionNo	FormStatus2b	LesionCreatedDate	CategoryScore	Exam	Result_Short	Result_LesionNo	Result_Guid	ResultCreatedDate	ResultLastModifiedDate	Process	TestGroup	ResultEntryStatusShort	ResultEntryFlagged	ResultEntryReferenceLesion	ResultEntryExcludeFromAnalysis	Result	Exam	Count_CategoryId	Count_CreatedDate	WBC1	%Qty	EAQty	EAAnalyte	EAAFC1	EAUnit2	YQty	Exam	EntryProfile_CategoryId	AC005Suffix	EntryProfile_CreatedDate	EntryProfile_ValidatedDate
[redacted]		2021-12-23 09:20:20.0200000	3mild		[redacted]			2022-01-07 11:22:20.347	2022-01-07 11:22:20.3500000	Result	Cardiac Electrosensitivity																			
		2021-12-23 09:20:20.0200000	3mild					2022-02-02 12:33:24.277	2022-02-02 12:33:25.2180000	Result	Cardiac Electrosensitivity																			
		2022-02-02 16:44:44.0500000	3mild					2022-02-02 16:45:48.0377000		Result		2022-02-02 16:45:59.0500000	1	WAQ05		No further work required as per above Non QPS														
		2021-12-23 09:20:20.0200000	3mild					2021-12-23 12:49:28.4649000	2021-12-23 12:49:28.4649000	Result		2021-12-23 12:49:28.4649000	1	3FF		Submitted results pending														
		2021-12-23 09:20:20.0200000	3mild					2021-12-23 12:49:44.5630000		Result	EntryQuantification							2021-12-23 12:49:44.2300000	2.41489E+12	2.33000000	4.53216E+12	0.0000000	0.0000000	x	x	0.2054597527000000				
		2022-01-07 11:22:20.347	3mild					2022-01-07 11:22:20.3500000		Result	Cardiac Electrosensitivity																			
		2022-02-02 16:44:44.0500000	3mild					2022-02-02 16:45:48.6970000		Result		2022-02-02 16:45:59.0500000	1	WAQ05		No further work required as per above Non QPS														
		2021-12-23 12:49:28.4700000	3mild					2021-12-23 12:49:44.5630000		Result	EntryQuantification							2021-12-23 12:49:44.2300000	2.41489E+12	2.33000000	4.53216E+12	0.0000000	0.0000000	x	x	0.2054597527000000

CA-92

[redacted]
Study for MHOTE Symposium poster
Data Source/Files obtained from participants.
Event value_dependent on Index, if event omitted: imputed mus 0 mus.

Cases: red "Training"
Exhibit Cases between 25/02/2023 - 30/12/2023
Imputed Results are Reviewed (and not marked incorrect)
Profile Data is Verified (and not marked incorrect/replaced)

Below data is the Test and control criteria combined
- 2nd version 25/09/2023 - MHOT 2019094 - Exhibit Description/Located Description contains the word "panic/panic", or Located Description contains "SHA" and Exhibit Description/Located Description contains "shaft/chaos/mould", (and is not a non-environmental sample)
- 02/09/2023 - RECOVD 2019094 - Exhibit Description/Located Description contains the word "scotting/glass/shovel/scotting/autlay", Exhibit Description/Located Description contains the word "Eight/Hot" and Located Description contains "SHA" and Exhibit Description/Located Description bloss not contain "negative" (and is not a non-environmental sample)

2288 Records

| Exhibit_Date | Person_Description | Exhibit_Category_Code | Exhibit_Description | Located_Description | Blank | Result_Subject_Volume | Result_Buffer_Volume | Result_Cell_Count | Result_Process_Status | Result_Review_Status | Process | Technique | Result_DNA_Quantification | Result_DNA_Concentration | Result_DNA_Concentration_Unit | Result_DNA_Measurement | Result_DNA_Measurement_Unit | Result_DNA_Manufacturer | Result_Comments | Blank | Control_Sample_Id | Control_Check_Status | Control_Check_Date | Control_Check_Time | Control_Check_Comments | Control_Check_Operator | Control_Check_Reason | Control_Check_Reason_Comments | Control_Check_Reason_Operator | Control_Check_Reason_Date | Control_Check_Reason_Time

ELVIRA 2022 | DI-HC
Study for HAIRS Symposium poster
Data Source Files obtained from participants.
Query value_degradation Index, 1 query used, exported results 0 rows.

Query: val_"Training"
Exhibit 1A Created between 25/01/2021 - 30/12/2021
Reported Results are Reviewed (and not marked Incorrect)
Profile Data is Verified (and not marked Incorrect/Duplicate)

Below data is the Text and second value is combined
- 2nd version 25/01/2021 - 14:07:39.1970 - Exhibit1DescriptionLicensed Description contains the word "panic/panic", or Licensed Description contains "SHA" and Exhibit1DescriptionLicensed Description contains "SHA/Obese/Assault", (and is not an environmental sample)
- 25/01/2021 - 30/12/2021 - 09:37:09.1970 - Exhibit1DescriptionLicensed Description contains the word "cocktail/glass/shrewd/vanishing/autocar," Exhibit1DescriptionLicensed Description contains the word "Eight/Hot" and Licensed Description contains "SHA" and Exhibit1DescriptionLicensed Description Excess not contains "neglect" (and is not an environmental sample)

2288 Records

Exhibit1Key	ParentBarcodeID	Exhibit1_CreatedAtDate	CategoryCode	Exhibit1DescriptionValue	LicensedDescriptionValue	Blank1	Result1_Value1	Result1_Exhibit1Key	Result1_ExhibitID	Result1_PhysicianDate	Result1_ReviewedDate	Process	Technique	ResultDNAMeasureStatus	ResultDNA_Loaded	ResultDNAMeasurements	ResultDNAHeadNumber	Result1	Blank	Quant_SampleID	Quant_CheckedDate	TYPE	TotalQty	TSHQty	TSHQtyUnits	TSHPCT	TSHCONFZ	TSQty	Blank	DNAProfile_SampleID	NCBIBioProfile	DNAProfile_CreatedDate	DNAProfile_ValidatedDate
[redacted]		2021-02-17 12:40:55.1027	DNAC	pan kit	PM Sample Jess		[redacted]			2021-02-22 12:39:47.427	2021-02-22 12:39:47.427	Result	Profile Data Analysis																		co	2021-12-23 11:39:59.1223	2021-12-23 12:41:48.1192
		2021-02-19 14:13:07.1257	DNAC	pan kit	PM Sample Jess					2021-02-22 12:39:47.433	2021-02-22 12:39:47.433	Result	DNA Quantification																				
		2021-02-19 14:13:07.1257	DNAC	pan kit	PM Sample Jess					2021-02-22 12:39:47.43	2021-02-22 12:39:47.43	Result	CapillaryElectrophoresis																				
		2021-02-19 14:13:07.1257	DNAC	pan kit	PM Sample Jess					2021-02-22 12:39:47.398	2021-02-22 12:39:47.398	Result	Profile Data Analysis																		cm01	2021-03-02 20:13:33.1108	2021-03-02 20:17:38.1061
		2021-02-19 14:13:07.1257	DNAC	pan kit	PM Sample Jess					2021-02-22 12:39:50.083	2021-02-22 12:39:50.083	Result		DZ2-DI-22-1B-1B-1B

ELIDE 2022.3.0+C

Study for MAGIC Symposium poster

Data Source Files obtained from participants.

Quant value_degradation Indices, 3 quant.sf.sf. exported results files.

Cases: red, "Training"

Exhibit 3 Cases between 25/03/2022 - 30/12/2022.

Reported Results are Reviewed (and not marked incorrect).

Profile Data is not Exact (and not marked incorrect/replaced).

Below data is the Test and control criteria combined

– 2nd version 25/08/2022 - MVP 29/09/04 - Exhibit.Description.Lowered.Description contains the word "pos1x3 pos1c", or quoted.Description contains "DNA" and Exhibit.Description.Lowered.Description contains "DNA[Chaos.Found]", (and is not a non-environmental sample)

–12/09/2022 - SECOND OPINION - Exhibit.Description.Lowered.Description contains the word "control/gblanc/pcrneat/control/negative/ntc", Exhibit.Description.Lowered.Description contains the word "Duplicate" and Lowered.Description contains "DNA" and Exhibit.Description.Lowered.Description Does not contain "negative" (and is not a non-environmental sample)

2288 Records

Exhibit.Item	Parent.Item.Code	Exhibit.Created.Date	Category.Code	Exhibit.Description	Lowered.Description	Blank	Result_Intact	Result_Exhibit.Item	Result_Exhibit.Type	Result_Photos.Date	Result_Review.Name	Process	Technique	Result.DNA.Mean.Depth	Result.DNA_Loaded	Result.DNA.Mean.Height	Result.DNA.Mean.Area	Result.DNA.Mean.Area.Ratio	Result	Blank	Quant_Sample.ID	Quant_Created.Date	TAPE	TAQty	TSHQty	TSHQ.ratio	TSHPCT	TSHCONF	YHQty	Blank	DNAProfile_Sample.ID	NCBIBioProj	DNAProfile_Created.Date	DNAProfile_Validated.Date
[redacted]		2022-04-20 21:53:28.788	TAPE	glass dry	SWA					2022-05-28 21:49:08.000	2022-05-31 22:05:55.757	Result		2022-05-28 22:18:00.541	P	2669.90																		
[redacted]		2022-04-20 21:53:28.788	TAPE	glass dry	SWA					2022-05-28 21:49:08.000	2022-05-31 22:05:55.757	Result		2022-05-28 22:18:00.541	P	2662.00																		
[redacted]		2022-04-20 21:53:28.802	TAPE	stored saliva wet	SWA					2022-04-28 21:19:00.000	2022-04-30 21:10:00.000	Result		2022-04-30 22:48:02.746	P	89																		
[redacted]		2022-04-20 21:53:28.802	TAPE	stored saliva wet	SWA					2022-04-27 22:06:00.000	2022-04-27 22:54:28.000	Result	DNAQuantification																					
[redacted]		2022-04-20 21:53:28.802	TAPE	stored saliva wet	SWA					2022-04-28 21:49:40.705	2022-04-28 22:06:45.737	Result	DNAQuantification																					
[redacted]		2022-04-20 21:53:28.802	TAPE	stored saliva wet	SWA					2022-04-28 21:49:40.705	2022-04-28 22:06:44.467	Result	CapillaryElectrophoresis																					
[redacted]		2022-04-20 21:53:28.802	TAPE	stored saliva wet	SWA					2022-04-28 21:35:21.153	2022-04-28 22:04:07.280	Result	CapillaryElectrophoresis																					
[redacted]		2022-04-20 21:53:28.802	TAPE	stored saliva wet	SWA					2022-04-28 21:34:41.213	2022-04-28 22:04:07.280	Result	Profile Data Analysis																					
[redacted]		2022-04-20 21:53:28.802	TAPE	stored saliva wet	SWA					2022-04-28 21:34:41.213		Result		2022-05-28 22:18:00.541	P	2686			Two person mixed DNA profile															
[redacted]		2022-04-20 21:53:28.802	TAPE	stored saliva wet	SWA					2022-04-28 21:34:41.213		Result		2022-05-28 22:18:00.541	P	2662.24			3 person mixed profile - deviled case on															
[redacted]		2022-04-20 21:53:28.802	TAPE	stored saliva wet	SWA					2022-04-28 21:34:41.213		Result		2022-05-28 22:18:00.541	P	2669.90			3 person mix+ening - supports non contribution															
[redacted]		2022-04-20 21:53:28.802	TAPE	stored saliva wet	SWA					2022-04-28 21:33:47.985	2022-04-28 22:04:07.280	Result		2022-05-28 22:18:00.541	P	89			Submitted results pending															
[redacted]		2022-04-20 21:53:28.847	TAPE	stored saliva dry	SWA					2022-04-27 22:06:00.000	2022-04-27 22:54:28.000	Result	DNAQuantification																					
[redacted]		2022-04-20 21:53:28.847	TAPE	stored saliva dry	SWA					2022-04-28 21:49:40.705	2022-04-28 22:06:45.737	Result	CapillaryElectrophoresis																					
[redacted]		2022-04-20 21:53:28.847	TAPE	stored saliva dry	SWA					2022-04-28 21:49:40.705	2022-04-28 22:06:44.467	Result	CapillaryElectrophoresis																					
[redacted]		2022-04-20 21:53:28.847	TAPE	stored saliva dry	SWA					2022-04-28 21:35:21.153	2022-04-28 22:04:07.280	Result	CapillaryElectrophoresis																					
[redacted]		2022-04-20 21:53:28.847	TAPE	stored saliva dry	SWA					2022-04-28 21:34:41.213	2022-04-28 22:04:07.280	Result	Profile Data Analysis																					
[redacted]		2022-04-20 21:53:28.847	TAPE	stored saliva dry	SWA					2022-04-28 21:34:41.213		Result		2022-05-28 22:18:00.541	P	2686			Two person mixed DNA profile															
[redacted]		2022-04-20 21:53:28.847	TAPE	stored saliva dry	SWA					2022-04-28 21:34:41.213		Result		2022-05-28 22:18:00.541	P	2662.24			3 person mixed profile - deviled case on															
[redacted]		2022-04-20 21:53:28.847	TAPE	stored saliva dry	SWA					2022-04-28 21:34:41.213		Result		2022-05-28 22:18:00.541	P	2669.90			3 person mix+ening - supports non contribution															
[redacted]		2022-04-20 21:53:28.847	TAPE	stored saliva dry	SWA					2022-04-27 22:06:00.000	2022-04-27 22:54:28.000	Result	DNAQuantification																					
[redacted]		2022-04-20 21:53:28.847	TAPE	stored saliva dry	SWA					2022-04-28 21:49:40.705	2022-04-28 22:06:45.737	Result	CapillaryElectrophoresis																					
[redacted]		2022-04-20 21:53:28.847	TAPE	stored saliva dry	SWA					2022-04-28 21:49:40.705	2022-04-28 22:06:44.467	Result	CapillaryElectrophoresis																					
[redacted]		2022-04-20 21:53:28.847	TAPE	stored saliva dry	SWA					2022-04-28 21:35:21.153	2022-04-28 22:04:07.280	Result	CapillaryElectrophoresis																					
[redacted]		2022-04-20 21:53:28.847	TAPE	stored saliva dry	SWA					2022-04-28 21:34:41.213	2022-04-28 22:04:07.280	Result	Profile Data Analysis																					
[redacted]		2022-04-20 21:53:28.847	TAPE	stored saliva dry	SWA					2022-04-28 21:34:41.213		Result		2022-05-28 22:18:00.541	P	2686			Two person mixed DNA profile															
[redacted]		2022-04-20 21:53:28.847	TAPE	stored saliva dry	SWA					2022-04-28 21:34:41.213		Result		2022-05-28 22:18:00.541	P	2662.24			3 person mixed profile - deviled case on															
[redacted]		2022-04-20 21:53:28.847	TAPE	stored saliva dry	SWA					2022-04-28 21:34:41.213		Result		2022-05-28 22:18:00.541	P	2669.90			3 person mix+ening - supports non contribution															
[redacted]		2022-04-20 21:53:28.847	TAPE	stored saliva dry	SWA					2022-04-28 21:33:47.985	2022-04-28 22:04:07.280

ELIGIBILITY CRITERIA
Study: The MAGNETIC Symposium: poster
Data: Records/Files obtained from participants.
Query: value_degradation Index, 0, quantized, imputed mice 0 rows.

Query: visit "Screening"
(with 0 clauses between 25/03/2023 - 30/12/2023)
Repeated Results are Reviewed (and not marked incorrect)
Profile Data: is not blank (and not marked incorrect/replaced)

Below data is the Text and consent vitals combined
- 2nd version 25/03/2023 - 14:07:39.139 hr - (with 1 Description/Located Description contains the word "penile/penis", or a Located Description contains "SMA" and (with 0 Description/Located Description contains "shaft/base/head", (and is not a non-environmental sample)
- 02/09/2023 - 30/12/2023 07:39:19 hr - (with 0 Description/Located Description contains the word "urethra/glans/prepuce/urethra/urine/tissue", (with 0 Description/Located Description contains the word "Eligible" and Located Description contains "SMA" and (with 0 Description/Located Description does not contain "negative" (and is not a non-environmental sample)

2288 Records

| [redacted] | [redacted] | [redacted] |

ELIXIR 2022 Q4 HE
Study for HUMOR Symposium poster
Data Source Files obtained from participants.
Experiment data_degradation Index, 3 experiment reported results files.

Cases: incl "Training"
Batch 1 Cases between 25/01/2021 - 31/12/2021
Reported Results are Reviewed (and not marked Incorrect)
Profile Data is Verified (and not marked Incorrect/Duplicate)

Below data is the Test and control arms in combined
- Test version 25/01/2021 - 14:07:39.1970 - Batch1 Description/Lysosomal Description contains the word "pool in lysosic", or Lysosomal Description contains "Shell" and Batch1 Description/Lysosomal Description contains "Shell/Ocean/Hazard", (and is not a non-environmental sample)
- 25/01/2021 - 30/12/60 23:59:59 - Batch1 Description/Lysosomal Description contains the word "Lysosic" and Batch1 Description/Lysosomal Description contains "Shell" and Batch1 Description/Lysosomal Description Ocean not contain "negative", (and is a non-environmental sample)

2288 Records

Batch1_Key	Reason Description	Batch1_Created_Status	Category Code	Batch1 Description	Lysosomal Description	Ring 1_Result_Subset	Ring 2_Result_Subset	Batch1_Key_Reason_Result	Process	Technique	Result Batch Lysosomal Date	Result Batch_Lysosomal	Result Batch Reference Id	Result Batch Manufacturer	Result	Blank	Quant_Sample Id	Quant_Created Date	TWCT	TWQty	TSHQty	TSHQty Analysis	TSHWCT	TSHCWCT	TSQty	Blank	DNAProfile_Sample Id	NCBI Staff a	DNAProfile_Created Date	DNAProfile_Val Validated Date
[redacted]		25/01/2021 14:07:39.1970	SHAL	Sh- Shell Mollis Swabs	Mucus	[redacted]		25/01/2021 14:07:39.1970	Result		25/01/2021 14:07:39.1970	Result	NT		Skin+ Axe Storm Insertion(s) Lab sample id															
		25/01/2021 14:07:40.1927	SWAB	wet dry				25/01/2021 14:07:40.1930	Result		25/01/2021 14:07:40.1930	Result	P	SHP	Submitted results pending															
		25/01/2021 14:07:40.1927	SWAB	wet dry				25/01/2021 14:07:40.1930	Result	DNA Quantification	25/01/2021 14:07:40.1930	Result	P	SHP	DNA Insufficient For further processing		1	25/01/2021 14:07:40.1930	21.7024	0.0025000000	0.0025	0.0025000000	N	F	0.0025					
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result	DNA Quantification	25/01/2021 14:07:40.1930	Result	P	SHP	Submitted results pending															
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result	DNA Quantification								25/01/2021 14:07:40.1930	21.7024	0.0025000000	0.0025	0.0025000000	N	N	0.0025		[redacted]			
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result	CapillaryElectrophoresis																			
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result	Profile Data Analysis																			
		25/01/2021 14:07:40.1927	SWAB	wet wet		[redacted]		25/01/2021 14:07:40.1930	Result		25/01/2021 14:07:40.1930	Result	P	25949	Single Source DNA profile - assumed Forever contributor															
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result		25/01/2021 14:07:40.1930	Result	P	25963	NCIDD upload single source DNA profile															
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result		25/01/2021 14:07:40.1930	Result	P	RES	Possible Lab threshold Information															
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result		25/01/2021 14:07:40.1930	Result	P	SHP	Submitted results pending															
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result	DNA Quantification																			
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result	CapillaryElectrophoresis																			
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result	DNA Quantification																			
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result	CapillaryElectrophoresis																			
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result	Profile Data Analysis																			
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result		25/01/2021 14:07:40.1930	Result	P	25949	Single Source DNA profile - assumed Forever contributor															
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result		25/01/2021 14:07:40.1930	Result	P	RES	Possible Lab threshold Information															
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result		25/01/2021 14:07:40.1930	Result	P	SHP	Submitted results pending															
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result	DNA Quantification																			
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result	CapillaryElectrophoresis																			
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result	Profile Data Analysis																			
		25/01/2021 14:07:40.1927	SWAB	wet wet		[redacted]		25/01/2021 14:07:40.1930	Result		25/01/2021 14:07:40.1930	Result	P	25949	Single Source DNA profile - assumed Forever contributor															
		25/01/2021 14:07:40.1927	SWAB	wet wet				25/01/2021 14:07:40.1930	Result		25/01/2021 14:07:40.1930	Result	P	25963	NCIDD upload single source DNA profile

ELVIS 2022.3.0.42
Study for MAGPIE Symposium poster
Data Source Files obtained from participants.
Query value_degradation Index, 1 query used, exported results 0 rows.

Query: not "Training"
Birth Dt Created between 01/01/2021 - 31/12/2021
Repeated Results are Reviewed (and not marked Incorrect)
Profile Status is Verified (and not marked Incorrect/replaced)

Below data is the Text and second value is combined
- 2nd version 01/09/2022 - MVP 29/09/4 - Birth Dt Description/Located Description contains the word "parish/county", or second Description contains "NHS" and Birth Dt Description/Located Description contains "Unit/Ward/Road", (and is not a non-environmental sample)
- 02/09/2022 - SECOND DRAFT - Birth Dt Description/Located Description contains the word "catchment/glen/stream/waterbody/surface", Birth Dt Description/Located Description contains the word "Clyde/Firth" and Located Dt Description/Located Description does not contain "region" (and is not a non-environmental sample)

2288 Records

Birth Dte	Parent Barcode	Birth Dt_Created Status	Category of Data	Birth Dt Description	Located Description	Blank	Result_Cohort	Result_Birth Dte	Result_Birth Dte	Result_Created Date	Result_Review Status	Process	Test Value	Result DNA Count Data	Result DNA Count Data	Result DNA Mean Insert	Result DNA Mode Number Insert	Result	Blank	Query_Sample Id	Query_Created Date	TAPE	TAQ Qty	TAQ Qty	TAQ Degradation	TAPE Cl	TAQ Ratio	YQ Qty	Blank	DNA Profile_Sample Id	NCBI Staff Id	DNA Profile_Created Date	DNA Profile_Verification Date
[redacted]		2021-08-02 21:09:20.237	1844	wet commercial surface	5444	[redacted]		2021-07-29 22:28:28.743	2021-07-30 22:28:28.743	Result	DNA Quantification								[redacted]	2021-07-30 21:05:13.523	2.718749791000000	0.449459791000000	1.039160400000000	0.782830200000000	N	N	0.458349401000000					
		2021-08-02 21:09:20.237	1844	wet commercial surface	5444			2021-07-30 20:28:39.490	2021-07-30 20:28:40.676	Result	Capillary Electrophoresis																						
		2021-08-02 21:09:20.237	1844	wet commercial surface	5444			2021-08-02 21:10:20.000	2021-08-02 21:10:39.977	Result	Profile Data Analysis																						
		2021-08-02 21:09:20.237	1844	wet commercial surface	5444			2021-07-29 21:10:20.000	2021-08-02 21:09:39.977	Result				2021-08-02 21:09:40.403	F	2646		Two person mixed DNA profile															
		2021-08-02 21:09:20.237	1844	wet commercial surface	5444			2021-07-29 21:10:20.000	2021-08-02 21:09:39.977	Result				2021-08-02 21:09:40.403	F	2662CN		2 person mixed profile - dandelion tar															
		2021-08-02 21:09:20.237	1844	wet commercial surface	5444			2021-07-29 21:10:20.000	2021-08-02 21:09:39.982	Result				2021-08-02 21:09:40.403	F	2660L		2 person mix remaining - low support for rare nb															
		2021-08-02 21:09:20.237	1844	wet commercial surface	5444			2021-07-29 21:10:20.000	2021-08-02 21:09:39.986	Result				2021-08-02 21:09:40.403	F	2660MC		2 person mix remaining - suspects non contribution															
		2021-08-02 21:09:20.237	1844	wet commercial surface	5444			2021-07-29 21:10:20.000	2021-08-02 21:09:39.990	Result				2021-08-02 21:09:40.403	F	2660MC		2 person mix remaining - suspects non contribution															
		2021-08-02 21:09:20.237	1844	wet commercial surface	5444			2021-07-29 21:10:20.000	2021-08-02 21:09:39.993	Result				2021-08-02 21:09:40.403	F	2660MC		2 person mix remaining - suspects non contribution															
		2021-08-02 21:09:20.237	1844	wet commercial surface	5444			2021-07-29 22:14:00.000	2021-07-30 22:49:14.923	Result				2021-07-31 14:10:20.000	F	899		Submit Batch results pending															
		2021-08-02 21:09:20.115	1844	dry coastal surface	5444			2021-07-30 22:21:00.000	2021-07-30 22:21:03.187	Result	DNA Quantification									2021-07-27 20:29:14.000	21.752317200000000	0.182330240000000	0.182317629000000	1.000069510000000	N	N	0.000339189000000					
		2021-08-02 21:09:20.115	1844	dry coastal surface	5444			2021-07-30 22:21:00.000	2021-08-02 21:09:41.982	Result	Capillary Electrophoresis																						
		2021-08-02 21:09:20.115	1844	dry coastal surface	5444			2021-08-02 21:10:20.000	2021-08-02 21:10:40.837	Result	Profile Data Analysis																						
		2021-08-02 21:09:20.115	1844	dry coastal surface	5444			2021-08-02 21:10:20.000	2021-08-02 21:10:40.837	Result	Profile Data Analysis																						
		2021-08-02 21:09:20.115	1844	dry coastal surface	5444			2021-07-29 21:10:20.000	2021-08-02 21:09:40.841	Result				2021-08-02 21:09:40.403	F	2646		Two person mixed DNA profile															
		2021-08-02 21:09:20.115	1844	dry coastal surface	5444			2021-07-29 21:10:20.000	2021-08-02 21:09:40.841	Result				2021-08-02 21:09:40.403	F	2662CN		2 person mixed profile - dandelion tar															
		2021-08-02 21:09:20.115	1844	dry coastal surface	5444			2021-07-29 21:10:20.000	2021-08-02 21:09:40.841	Result				2021-08-02 21:09:40.403	F	26607		2 person mix rem - support for contribution < 100 kit flow															
		2021-08-02 21:09:20.115	1844	dry coastal surface	5444			2021-07-29 21:10:20.000	2021-08-02 21:09:40.841	Result				2021-08-02 21:09:40.403	F	9105C		Single evidence sample excluded															
		2021-08-02 21:09:20.115	1844	dry coastal surface	5444			2021-07-29 21:10:20.000	2021-08-02 21:09:40.841	Result				2021-08-02 21:09:40.403	F	9105C		Single evidence sample excluded															
		2021-08-02 21:09:20.115	1844	dry coastal surface	5444			2021-07-30 21:10:20.000	2021-07-30 22:49:14.923	Result				2021-07-31 14:10:20.000	F	899		Submit Batch results pending															
		2021-08-02 21:09:20.110	1844	wet gravel peaty	5444			2021-07-30 22:21:00.000	2021-07-30 22:22:12.761	Result	DNA Quantification									2021-07-27 20:29:14.000	21.777533440000000	0.220307320000000	0.220277760000000	1.000134320000000	N	N	0.124398260000000					
		2021-08-02 21:09:20.110	1844	wet gravel peaty	5444			2021-08-02 21:09:41.845	2021-08-02 21:09:41.845	Result	Capillary Electrophoresis																						
		2021-08-02 21:09:20.110	1844	wet gravel peaty	5444			2021-08-02 21:10:20.000	2021-08-02 21:10:40.407	Result	Profile Data Analysis																						
		2021-08-02 21:09:20.110	1844	wet gravel peaty	5444			2021-07-29 21:10:20.000	2021-08-02 21:09

DLR(DLT(DLT)=4)
Study Ts=MUSTO Symposium poster
Data Source=Files obtained from participants.
Query=alias_degradation=false, F_query=and, reported results=false.

Cases: red, "Training"
Ref=0.5 (Accepted between 25/03/2023 - 30/12/2023)
Reported=Results are Reviewed (and not marked Incorrect)
Prof=Is Data is Verified (and not marked Incorrect/Duplicated)

Below data is the Text and second row is combined
- 2nd version 25/03/2023 - MUST 20.10.0 - Ref=0.5 Description/Located Description contains the word "pen's/penis", or located Description contains "Shift"and Ref=0.5 Description/Located Description contains "Shaft/base/head", (and is not a non-environmental sample)
- 02/09/2023 - SECOND OPINION - Ref=0.5 Description/Located Description contains the word "urethra/glans/prepuce/frenulum/urethra/scrotum/", Ref=0.5 Description/Located Description contains the word "Tip/shaft" and Located Description contains "Shaft" and Ref=0.5 Description/Located Description/Located Description bases not contain "vagina" (and is not an environmental sample)

2208 Records

Ref=0.5Flag	Parent=Barcode	Ref=0.5_Created=Date	Category=Code	Ref=0.5=Description	Located=Description	Blank1	Result_Value1	Result_Ref=0.5Flag	Result_Ref=0.5	Result_Method=Date	Result_Review=Date	Process	Technique	Result2DNAExtractDate	Result2DNA_Loaded	Result2DNAReference(s)	Result2DNAFreeform(s)	Result	Blank	Quant_Sample(s)	Quant_Created=Date	TAPE	TAQty	TAQUg	TAQ=ng/mLu	TAAMP2	TAQ=ng/mL	Blank	DNAPrcFlu_Sample(s)	NCBIBLAST%	DNAPrcFlu_Created=Date	DNAPrcFlu_Ref=0.5Flag	DNAPrcFlu_Ref=0.5=Date
[redacted]		2022-07-26 09:28:33.000	DNAC	glans penis excl.	Skin	[redacted]				2022-07-26 14:39:00.000	2022-08-09 14:44:42.827	Result	Puffin Data Analysis														[redacted]		2022-07-26 23:23:28.897	2022-08-09 14:44:42.827
		2022-07-26 09:28:33.000	DNAC	glans penis excl.	Skin					2022-07-26 14:39:00.000	2022-08-09 14:44:42.827	Result		2022-08-03 15:30:47.140	P	3NA	Three person mixed DNA profile																
		2022-07-26 09:28:33.000	DNAC	glans penis excl.	Skin					2022-07-26 14:39:00.000	2022-08-09 14:44:42.827	Result		2022-08-03 15:30:47.140	P	3NA2CN	3 person mixed profile - conditional on																
		2022-07-26 09:28:33.000	DNAC	glans penis excl.	Skin					2022-07-26 14:39:00.000	2022-08-09 14:44:42.827	Result		2022-08-03 15:30:47.140	P	3NAR3	3 person min - support for events 1 mil Tier to 1 bil Tier																
		2022-07-26 09:28:33.000	DNAC	glans penis excl.	Skin					2022-07-26 14:39:00.000	2022-08-09 14:44:42.827	Result		2022-08-03 15:30:47.140	P	3NAMC	3 person min remaining - supports non contributor																
		2022-07-26 09:28:33.000	DNAC	glans penis excl.	Skin					2022-07-26 14:39:00.000	2022-08-09 14:44:42.827	Result		2022-08-03 15:30:47.140	P	2NA2UB	NCBI upload - assumed contributor																
		2022-07-26 09:28:33.173	DNAC	glans penis skin	Skin					2022-07-26 17:17:21.863	Result	2NA Quantification					2NA - Insufficient Tier for further processing																
		2022-07-26 09:28:33.280	DNAC	external vulva wet	Skin					2022-07-26 12:39:52.277	2022-07-26 13:55:53.277	Result	DNA Quantification																				
		2022-07-26 09:28:33.280	DNAC	external vulva wet	Skin					2022-07-26 17:17:21.863	Result	Capillary Electrophoresis																				
		2022-07-26 09:28:33.280	DNAC	external vulva wet	Skin					2022-07-26 17:17:21.863	2022-08-03 23:54:21.987	Result	Puffin Data Analysis																				
		2022-07-26 09:28:33.280	DNAC	external vulva wet	Skin					2022-07-26 23:54:21.987	Result			2022-08-03 15:30:47.137	P	3NA	Three person mixed DNA profile																
		2022-07-26 09:28:33.280	DNAC	external vulva wet	Skin					2022-07-26 23:54:21.987	Result			2022-08-03 15:30:47.137	P	3NA2CN	3 person mixed profile - conditional on																
		2022-07-26 09:28:33.280	DNAC	external vulva wet	Skin					2022-07-26 23:54:21.987	Result			2022-08-03 15:30:47.137	P	3NAR3	3 person min - support for events 1 mil Tier to 1 bil Tier																
		2022-07-26 09:28:33.280	DNAC	external vulva wet	Skin					2022-07-26 23:54:21.987	Result			2022-08-03 15:30:47.137	P	3NAMC	3 person min remaining - supports non contributor																
		2022-07-26 09:28:33.280	DNAC	external vulva dry	Skin					2022-07-27 12:39:44.982	Result	2NA Quantification																				
		2022-07-26 09:28:33.340	DNAC	external vulva dry	Skin					2022-07-27 17:21.883	Result	Capillary Electrophoresis																				
		2022-07-26 09:28:33.340	DNAC	external vulva dry	Skin					2022-07-26 23:54:47.147	Result			2022-08-03 23:38:03.457	P	3NA	Mixed DNA profile																
		2022-07-26 09:28:33.340	DNAC	external vulva dry	Skin					2022-07-26 23:54:47.147	Result			2022-08-03 23:38:03.457	P	3NAE	Assumed contributor																
		2022-07-26 09:28:33.340	DNAC	external vulva dry	Skin					2022-07-26 23:54:47.147	Result			2022-08-03 23:38:03.457	P	3NAS	3Ms - supports non contributor																
		2022-07-26 09:28:33.340	DNAC	external vulva dry	Skin					2022-07-26 23:54:47.147	Result			2022-08-03 23:38:03.457	P	3NSS	3Ms - supports non contributor																
		2022-07-26 09:28:33.340	DNAC	external vulva dry	Skin					2022-07-26 17:17:21.863	Result	Puffin Data Analysis																				
		2022-07-26 09:29:04.555	TAMC	base of Penis wet	Skin					2022-07-26 17:17:21.863	2022-08-03 23:38:03.457	Result	Puffin Data Analysis																				
		2022-07-26 09:29:04.555	TAMC	base of Penis wet	Skin					2022-07-26 23:38:03.457	Result			2022-08-03 15:30:47.137	P	3NA	Three person mixed DNA profile																
		2022-07-26 09:29:04.555	TAMC	base of Penis wet	Skin					2022-07-26 23:38:03.457	Result			2022-08-03 15:30:47.137	P	3NA2CN	3 person mixed profile - conditional on																
		2022-07-26 09:29:04.555	TAMC	base of Penis wet	Skin					2022-07-26 23:38:03.457	Result			2022-08-03 15:30:47.137	P	3NAR3	3 person min - support for events 1 mil Tier to 1 bil Tier																
		2022-07-26 09:29:04.555	TAMC	base of Penis wet	Skin					2022-07-26 23:38:03.457	Result			2022-08-03 15:30:47.137	P	3NAMC	3 person min remaining - supports non contributor																
		2022-07-26 09:29:04.786	TAMC	base of Penis dry	Skin					2022-07-27 12:39:44.982	Result	2NA Quantification																				
		2022-07-26 09:29:04.786	TAMC	base of Penis dry	Skin					2022-07-27 17:21.883	Result	Capillary Electrophoresis																				
		2022-07-26 09:29:04.786	TAMC	base of Penis dry	Skin					2022-07-26 23:38:03.457	Result	Puffin Data Analysis																				
		2022-07-26 09:29:04.941	TAMC	shaft of Penis wet	Skin					2022-07-26 23:38:03.457	Result			2022-08-03 15:30:47.137	P	3NA	Three person mixed DNA profile																
		2022-07-26 09:29:04.941	TAMC	shaft of Penis wet	Skin					2022-07-26 23:38:03.457	Result			2022-08-03 15:30:47.137	P	3NAE	Assumed contributor																
		2022-07-26 09:29:04.941	TAMC	shaft of Penis wet	Skin					2022-07-26 23:38:03.457	Result			2022-08-03 15:30:47.137	P	3NAS	3Ms - supports non contributor																
		2022-07-26 09:29:04.941	TAMC	shaft of Penis wet	Skin					2022-07-26 23:38:03.457	Result			2022-08-03 15:30:47.137	P	3NSS	3Ms - supports non contributor																
		2022-07-26 09:29:05.138	TAMC	shaft of Penis dry	Skin					2022-07-27 12:39:44.982	Result	2NA Quantification																				
		2022-07-26 09:29:05.138	TAMC	shaft of Penis dry	Skin					2022-07-27 17:21.883	Result	Capillary Electrophoresis																				
		2022-07-26 09:29:05.138	TAMC	shaft of Penis dry	Skin					2022-07-26 23:54:47.147	Result	Puffin Data Analysis																				
		2022-07-26 09:29:05.340	TAMC	tip of Penis wet	Skin					2022-07-26 23:38:03.457	Result			2022-08-03 15:30:47.137	P	3NA	Three person mixed DNA profile																
		2022-07-26 09:29:05.340	TAMC	tip of Penis wet	Skin					2022-07-26 23:38:03.457	Result			2022-08-03 15:30:47.137	P	3NA2CN	3 person mixed profile - conditional on																
		2022-07-26 09:29:05.340	TAMC	tip of Penis wet	Skin					2022-07-26 23:38:03.457	Result			2022-08-03 15:30:47.137	P	3NAR3	3 person min - support for events 1 mil Tier to 1 bil Tier																
		2022-07-26 09:29:05.340	TAMC	tip of Penis wet	Skin					2022-07-26 23:38:03.457	Result			2022-08-03 15:30:47.137	P	3NAMC	3 person min remaining - supports non contributor																
		2022-07-26 09:29:05.340	TAMC	tip of Penis wet	Skin					2022-07-26 23:38:03.457	Result			2022-08-03 15:30:47.137	P	2NA2UB	NCBI upload - assumed contributor																
		2022-07-26 09:29:05.340	TAMC	tip of Penis wet	Skin					2022-07-26 23:38:03.457	Result			2022-08-03 15:30:47.137	P	2NA4S	Single Source DNA profile - assumed Known contributor																
		2022-07-26 09:29:05.340	TAMC	tip of Penis wet	Skin					2022-07-26 23:38:03.457	Result			2022-08-03 15:30:47.137	P	3NAR	Single Source DNA profile - assumed Known contributor																
		2022-07-26 09:29:05.340	TAMC	tip of Penis wet	Skin					2022-07-26 23:38:03.457	Result			2022-08-03 15:30:47.137	P	3NAS	3Ms - supports non contributor																
		2022-07-26 09:29:05.340	TAMC	tip of Penis wet	Skin					2022-07-26 23:38:03.457	Result			2022-08-03 15:30:47.137	P	3NSS	3Ms - supports non contributor																
		2022-07-26 09:29:05.340	TAMC	tip of Penis wet	Skin					2022-07-26 17:17:21.863	Result	Puffin Data Analysis																				
		2022-07-26 09:29:05.340	TAMC	tip of Penis wet	Skin					2022-07-26 23:38:03.457	Result	Puffin Data Analysis																				
		2022-07-26 09:29:05.340	TAMC	tip of Penis wet	Skin					2022-07-27 12:39:44.982	Result	2NA Quantification																				
		2022-07-26 09:29:05.340	TAMC	tip of Penis wet	Skin					2022-07-27 17:21.883	Result	Capillary Electrophores

01/09/2022 20:40
Data for ANATO Symposium poster
Data for profiles obtained from particle counts
Count value, degradation index, t-quant and mycelial mass/litre.

Cases not 'training'
Exhibit Unused between 01/01/2022 - 31/12/2022
Imported Results are Reviewed (and not marked Reviewed)
Profile Data is Validated (and not marked Invalid/Updated)

Active data is the first and second criteria combined
- first session 01/09/2022 - 19:07:20.170864 - Exhibit Description/Loaded Description contains the word 'parsley/parsley', or unused Description contains 'EMS' and Exhibit Description/Loaded Description contains 'shelf/beam/hook', (and is not an environmental sample)
- 01/09/2022 - 20:20:40.191964 - Exhibit Description/Loaded Description contains the word 'control/glass/stored/control/vial/ice', Exhibit Description/Loaded Description contains 'EMS' and Exhibit Description/Loaded Description does not contain 'negative' (and is not an environmental sample)

2288 Records

Exhibit No.	Person Exhibit	Exhibit_CreatedWhen	CategoryCode	Exhibit Description	LocationDescription	Event	Result_Taken	Result_ExhibitNo	Result_ExhibitNo	Result_ProcessDate	Result_ReviewedDate	Process	Technique	ResultDNAconcMeas	ResultDNA_quantified	ResultDNAInterpretation	Result	Event	Event_SampleID	Event_CreatedWhen	TAPCT	TotalQty	TSAQty	TSAOrganisms	TSAPCT	TSAQUANT	PCQty	Event	DNAProfile_SampleID	NCBIBLAST%	DNAProfile_CreatedWhen	DNAProfile_ValidatedWhen
[redacted]		2021-08-30 08:49:39.975	1998	dry base pens	504	[redacted]			2021-08-31 08:50:15.990	2021-08-31 08:50:15.990	Result	DNA Quantification							2021-08-30 08:49:42.787	21.917195636000000	0.009914179000000	0.010871500000000	8.742406138000000	N	N	0.023498900000000		[redacted]				
		2021-08-30 08:49:39.975	1998	dry base pens	504				2021-08-31 12:27:59.060	2021-08-31 12:27:59.060	Result	Capillary Electrophoresis																				
		2021-08-30 08:49:39.975	1998	dry base pens	504				2021-08-31 08:50:15.990	2021-08-31 08:50:15.990	Result	Profile Data Analysis																				
		2021-08-30 08:49:39.975	1998	dry base pens	504				2021-08-31 09:11:00.000	2021-08-31 09:11:52.980	Result	Profile Data Analysis																				
		2021-08-30 08:49:39.975	1998	dry base pens	504				2021-08-31 09:11:00.000	2021-08-31 09:11:52.997	Result			2021-11-30 12:00:00.047	F	DNA		Three person mixed DNA profile														
		2021-08-30 08:49:39.975	1998	dry base pens	504				2021-08-31 09:11:00.000	2021-08-31 09:11:52.997	Result			2021-11-30 12:00:00.047	F	DNA2CON		3 person mixed profile - conditional on														
		2021-08-30 08:49:39.975	1998	dry base pens	504				2021-08-31 09:11:00.000	2021-08-31 09:11:52.997	Result			2021-11-30 12:00:00.047	F	DNA3T		3 person mixed - support for contributor 1 3DS1Tsa														
		2021-08-31 08:15:22.283	1998	pants	Mattamyia Unit 9				2021-08-31 08:15:40.480	2021-08-31 12:00:15.497	Result			2021-08-31 12:00:00.047	F	DNP		Submitted results pending														
		2021-08-31 08:15:22.283	1998	pants	Mattamyia Unit 9				2021-08-31 08:15:40.480	2021-08-31 08:15:41.266	Result			2021-08-31 08:00:00.143	F	DNA2PCR4		Mixture positive for sperm. Submitted results pending														
		2021-08-31 08:15:22.283	1998	pants	Mattamyia Unit 9				2021-08-31 08:15:40.480	2021-08-31 09:15:12.157	Result	DNA Quantification							2021-08-31 08:15:42.535	26.828277772000000	1.099867420000000	1.213531420000000	8.606974960000000	N	N	1.826049341000000						
		2021-08-31 08:15:22.283	1998	pants	Mattamyia Unit 9				2021-08-31 08:15:40.480	2021-08-31 09:15:12.157	Result	Capillary Electrophoresis																				
		2021-08-31 08:15:22.283	1998	pants	Mattamyia Unit 9				2021-08-31 08:15:40.480	2021-08-31 09:15:12.157	Result	Profile Data Analysis																				
		2021-08-31 08:15:22.283	1998	pants	Mattamyia Unit 9				2021-08-31 08:15:40.480	2021-08-31 12:39:39.063	Result			2021-09-13 12:00:00.490	F	2NA		Two person mixed DNA profile														
		2021-08-31 08:15:22.283	1998	pants	Mattamyia Unit 9				2021-08-31 08:15:40.480	2021-08-31 12:39:39.063	Result			2021-09-13 12:00:00.490	F	2NA2CN		2 person mixed profile - conditional on														
		2021-08-31 08:15:22.283	1998	pants	Mattamyia Unit 9				2021-08-31 08:15:40.480	2021-08-31 12:39:39.063	Result			2021-09-13 12:00:00.490	F	2NA3PAC		2 person mismatching - supports non contributor														
		2021-08-31 08:15:22.283	1998	pants	Mattamyia Unit 9				2021-08-31 08:15:40.480	2021-08-31 12:39:39.063	Result			2021-09-13 12:00:00.490	F	2NAPAC		2 person mismatching - supports non contributor														
		2021-08-31 08:15:22.283	1998	pants	Mattamyia Unit 9				2021-08-31 08:15:40.480	2021-08-31 12:39:39.063	Result			2021-09-13 12:00:00.490	F	3NAPAC		3 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	1998	pants	Mattamyia Unit 9				2021-08-31 09:11:03.373	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	3NAPAC		3 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result	DNA Quantification							2021-08-31 08:15:42.535	26.828277772000000	1.099867420000000	1.213531420000000	8.606974960000000	N	N	1.826049341000000						
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result	Capillary Electrophoresis							2021-08-31 08:15:42.535	21.917195636000000	0.009914179000000	0.010871500000000	8.742406138000000	N	N	1.826049341000000						
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result	Profile Data Analysis																				
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	3NAPAC		3 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	3NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	3NP2CON		3 person mixed - support for contributor 1 3DS1Tsa														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	3NP3PAC		3 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	3NPAC		3 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	4NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	4NPAC		4 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	5NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	5NPAC		5 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	6NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	6NPAC		6 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	7NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	7NPAC		7 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	8NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	8NPAC		8 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	9NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	9NPAC		9 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	10NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	10NPAC		10 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	11NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	11NPAC		11 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	12NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	12NPAC		12 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	13NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	13NPAC		13 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	14NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	14NPAC		14 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	15NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	15NPAC		15 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	16NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	16NPAC		16 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	17NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	17NPAC		17 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	18NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	18NPAC		18 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	19NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	19NPAC		19 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	20NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	20NPAC		20 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	21NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	21NPAC		21 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	22NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	22NPAC		22 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	23NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	23NPAC		23 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	24NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	24NPAC		24 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	25NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	25NPAC		25 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	26NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	26NPAC		26 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	27NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	27NPAC		27 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	28NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	28NPAC		28 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	29NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	29NPAC		29 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	30NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	30NPAC		30 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	31NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	31NPAC		31 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	32NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	32NPAC		32 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	33NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	33NPAC		33 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	34NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	34NPAC		34 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	35NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	35NPAC		35 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	36NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	36NPAC		36 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	37NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	37NPAC		37 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	38NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	38NPAC		38 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	39NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	39NPAC		39 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	40NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	40NPAC		40 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	41NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	41NPAC		41 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	42NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	42NPAC		42 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	43NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	43NPAC		43 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	44NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	44NPAC		44 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	45NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	45NPAC		45 person mismatching - supports non contributor														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31 09:11:03.373	Result			2021-09-13 12:00:00.490	F	46NP		Submitted results pending														
		2021-08-31 08:49:40.143	EPAC	pants	Mattamyia Unit 9				2021-08-31 08:49:40.143	2021-08-31

ELVIRA 2022-2046
Study for MHRA/ISO Symposium poster
Data Source/Files obtained from participants.
Query's what_degradation indices, if quantified, reported results & trees.

Cases: mid "Training"
Exhibits Cases between 01/01/2021 - 31/12/2021
Repeated Results are Reviewed (and not marked Incorrect)
Profile Data is to Kit Based (and not marked Incorrect/replaced)

Below data is the Text and current criteria combined
- 2nd version 01/09/2022 - MVP 20190904 - Exhibit.DescriptionLicensed.DescriptionLicense contains the word "penis/penile", or Licensed.DescriptionLicense contains "DNA" and Exhibit.DescriptionLicensed.DescriptionLicense contains "DNA/Blood/Found", (and is not a non-environmental sample)
- 02/09/2022 - 30/2040 20190904 - Exhibit.DescriptionLicensed.DescriptionLicense contains the word "urethra/glans/penile/urethra/saliva", Exhibit.DescriptionLicensed.DescriptionLicense contains the word "DNA" and Exhibit.DescriptionLicensed.DescriptionLicense does not contain "vagina" (and is not a non-environmental sample)

2288 Records

Exhibit.Nbr	Parent.Barcode	Exhibit_Created.Date	Category.Code	Exhibit.Description	LicensedDescription	Blank	Result_Cyber	Result_Exhibit	Result_Cyb.Exh	Result_Photos.Date	Result_Review.Date	Process	Technique	Result.DNAQuantity	Result.DNA_Loaded	Result.DNAProfileName(s)	Result.DNA.Notes	Result.	Blank	Quant_Sample.Id	Quant_Created.Date	TAPE	TAQty	TSAQty	TSAQuantity	TSAMTC2	TSACONC2	TSQty	Blank	DNAProfile_Sample.Id	NCBIBuild%	DNAProfile_Created.Date	DNAProfile_ValidatedDate
[redacted]		2021-10-22 18:02:29	DEVC	dry urethral sw	SWA		[redacted]			2021-10-22 19:48:08	2021-10-23 09:55:13	Result					Two person mixed DNA profile															
		2021-10-22 18:02:29	DEVC	dry urethral sw	SWA					2021-10-22 19:48:08	2021-10-23 09:55:13	Result			P	2MIX	2 person mix - supports non-contributor															
		2021-10-22 18:02:29	DEVC	dry urethral sw	SWA					2021-10-24 19:04:08	2021-10-25 09:55:14	Result	Profile Data Analysis																			
		2021-10-22 20:13:59	DEVC	urethral	SWA					2021-10-22 20:28:57	2021-10-25 20:50:57	Result	DNA Quantification																			
		2021-10-22 20:13:59	DEVC	urethral	SWA					2021-10-22 20:28:57	2021-10-25 20:50:57	Result	Capillary Electrophoresis																			
		2021-10-22 20:13:59	DEVC	urethral	SWA					2021-10-24 19:04:08	2021-10-25 09:55:14	Result	Profile Data Analysis																			
		2021-10-22 20:13:59	DEVC	urethral	SWA					2021-10-22 19:48:08	2021-10-24 07:44:20	Result			P	2DNA	NCBIS upload single source DNA profile															
		2021-10-22 20:13:59	DEVC	urethral	SWA					2021-10-22 19:48:08	2021-10-24 07:44:20	Result			P	2SWA	Single Source DNA profile - assumed known contributor															
		2021-10-22 20:13:59	DEVC	urethral	SWA					2021-10-22 20:28:57	2021-10-25 20:50:57	Result	DNA Quantification		P	3MIX	DNA Insufficient for further processing															
		2021-10-22 20:13:59	DEVC	urethral	SWA					2021-10-22 20:28:57	2021-10-25 20:50:57	Result	Post-extraction		P	1TQ	Testing restarted on whole from DPS															
		2021-10-22 20:13:59	DEVC	glans dry	SWA					2021-10-22 19:48:08	2021-10-24 07:44:20	Result	DNA Quantification																			
		2021-10-22 20:13:59	DEVC	glans dry	SWA					2021-10-24 19:04:08	2021-10-25 09:55:14	Result	Capillary Electrophoresis																			
		2021-10-22 20:13:59	DEVC	glans dry	SWA					2021-10-24 20:13:36	2021-10-25 09:55:17

Ex0062 2022 3 N4
Data for NHS111 Symposium poster
Data Source/Files: obtained from parish records.
Event value_degradation Index, 1 quant.ized: exported result 0 mcs.

Cases: not "training"
Ex0062 Cases between 01/01/2023 - 31/12/2023
Reported Results are Reviewed (and not marked Incorrect)
Profile Data: is not based (and not marked Incorrect/replaced)

Below data is the Test and consent vitals combined
- 2nd version 01/01/2023 - 14:07:39.1994 - Ex0062 Description/Located Description contains the word "parish/parish", or Located Description contains "Shelf" and Ex0062 Description/Located Description contains "shelf/shoes/mould", (and is not a non-environmental sample)
- 02/09/2023 - 18:12:04.1311994 - Ex0062 Description/Located Description contains the word "washing/glass/utensil/washing machine/sink", Ex0062 Description/Located Description contains the word "dog/shirt" and Located Description contains "shelf" and Ex0062 Description/Located Description/Located Description does not contain "vegetal" (and is not an environmental sample)

2288 Records

Ex0062Title	RecordNumber	Ex0062_CreatedOnDate	CategoryCode	Ex0062DescriptionType	LocatedDescription	Blank	Result_Ident	Result_Ex0062Title	Result_Ex0062Text	Result_PhysicalDate	Result_SystemAdmin	Process	TechnicalType	ResultEXAMCreatedDate	ResultEXAM_Located	ResultEXAMFreeNarrative	ResultEXAMMethodNumber	ResultE	Blank	Quant_SampleID	Quant_CreatedDate	TVOC	TVOCQty	TVOCQty	TVOCAggregation	TVOCMCC	TVOCUNIT	TVOCQty	Blank	DNAProfile_SampleID	NCBIBioProfile	DNAProfile_CreatedDate	DNAProfile_ExtractionDate
[redacted]		2023-12-28 08:08:00.000	TANK	Shelf of pasta	Sink	[redacted]				2023-12-28 21:08:00.000	2023-12-29 14:24:46.787	Result	Profile Data Analysis	2023-12-29 14:24:46.787	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]															
		2023-12-28 08:08:00.000	TANK	Shelf of pasta	Sink					2023-12-28 21:08:00.000	2023-12-29 14:24:46.787	Result		2023-12-29 14:24:46.787	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]															
		2023-12-28 21:34:47.273	TANK	glass pieces (wet)	Sink					2023-12-28 21:34:47.273	2023-12-29 14:24:46.787	Result		2023-12-29 14:24:46.787	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]															
		2023-12-28 21:34:47.273	TANK	glass pieces (wet)	Sink					2023-12-28 22:20:02.423	2023-12-29 14:24:46.787	Result	DNA Quantification	2023-12-29 14:24:46.787	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]															
		2023-12-28 21:34:29.257	TANK	glass pieces (dry)	Sink					2023-12-28 21:34:29.257	2023-12-29 14:24:46.787	Result	DNA Quantification	2023-12-29 14:24:46.787	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]															
		2023-12-28 21:34:29.257	TANK	glass pieces (dry)	Sink					2023-12-28 21:34:46.963	2023-12-29 14:24:46.787	Result	DNA Quantification	2023-12-29 14:24:46.787	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]															
		2023-12-28 21:34:29.273	TANK	stained cutlery wet	Sink					2023-12-28 21:34:29.273	2023-12-29 14:24:46.787	Result	DNA Quantification	2023-12-29 14:24:46.787	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]															
		2023-12-28 21:34:29.273	TANK	stained cutlery wet	Sink					2023-12-28 21:34:46.787	2023-12-29 14:25:31.973	Result	DNA Quantification	2023-12-29 14:24:46.787	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]															
		2023-12-28 21:27:45.007	TANK	stained cutlery dry	Sink					2023-12-28 21:27:45.007	2023-12-29 14:25:31.987	Result	DNA Quantification	2023-12-29 14:24:46.787	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]															
		2023-12-28 21:27:45.007	TANK	stained cutlery dry	Sink					2023-12-28 21:28:26.525	2023-12-29 14:25:31.987	Result	DNA Quantification	2023-12-29 14:24:46.787	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]	[redacted]															
		2023-12-28 21:27:45.007	TANK	stained cutlery dry	Sink					2023-12-29 14:27:29.967	2023-12-29 14:28:23.263	Result	CapillaryElectrophoresis					

[redacted]
Data for MLW2025 Symposium poster
Data Source:[redacted] data extracted from parish records.
Event codes, degradation indices, & quantum[redacted] equations used.

Classes: mid "Finishing"
Birth & Christ date between 01/01/2023 - 31/12/2023
Registrars Results are Reviewed (and not marked Incorrect)
Profile Status is Verified (and not marked Incorrect/Duplicate)

Below data is ultra Fine and cannot vital to combined
- 2nd version 01/09/2022 - 14:07:39.1994 - Birth & Christ Options (Location) Description contains the word "parish/cleric", or Location) Description contains "Shell" and Birth & Christ Options (Location) Description contains "Shell/Beach/Hazel", (and is not an environmental example)
- 02/09/2022 - 18:12:04.1311994 - Birth & Christ Options (Location) Description contains the word "scattered/glass/stained/scattering/autlay", Birth & Christ Options (Location) Description contains "Shell" and Birth & Christ Options (Location) Description contains "Light/Arid" and Location) Description contains "engine" (and is not an environmental example)

2288 Records

Birth Date	Parent Records	Birth & Christ Id Value	Category of Date	Birth & Christ Location	Location Description	Silver	Result_Silver	Result_Gold	Result_Bronze	Process	Result_Process Date	Result_Review Date	Process	Technique	Result DNA Base Date	Result DNA_Loaded	Result DNA Measurements	Result DNA Weather Anomaly	Result	Silver	Quant_Sample Id	Quant_Create Date	TWCT	TuCQty	TSHQty	TSHQ mg/mLvalue	TSH MCT	TSH CMWCT	TFQty	Gold	DNA Profile_Synced Id	NCBI Buffer	DNA Profile_Create Date	DNA Profile_Validated Date
[redacted]		2023-12-08 22:23:27.553	TBHE	Library, parish (west)	SAH		[redacted]		2023-12-08 19:08:08.000	2023-12-12 19:44:53	Result	Profile Data Analysis																						
		2023-12-08 22:23:27.553	TBHE	Library, parish (west)	SAH				2023-12-08 19:08:08.000	2023-12-12 19:44:53	Result	Profile Data Analysis																						
		2023-12-08 22:23:27.817	TBHE	Library, parish (city)	SAH				2023-12-08 21:39:08.000	2023-12-12 19:44:08	Result	Profile Data Analysis																						
		2023-12-08 22:23:27.817	TBHE	Library, parish (city)	SAH				2023-12-12 22:27:39.000	2023-12-12 22:28:07	Result	DNA Quantification	2023-12-12 19:28:08.000	P	NOHAS		No DNA Detected																		
		2023-12-08 22:23:27.817	TBHE	Library, parish (city)	SAH				2023-12-12 21:34:00.000	2023-12-12 21:34:26	Result	Supernatant Tracking	2023-12-12 19:28:08.000	P	MISP		Processing could not be positive																		
		2023-12-08 22:24:39.980	TBHE	House/Enclosure of parish (city)	SAH				2023-12-08 19:08:47.000	2023-12-12 19:47:08	Result	Profile Data Analysis		P	SHP		Submitted results pending																		
		2023-12-08 22:24:39.980	TBHE	House/Enclosure of parish (city)	SAH				2023-12-12 19:37:39.000	2023-12-12 19:38:43	Result	DNA Quantification																						
		2023-12-08 22:24:39.980	TBHE	House/Enclosure of parish (city)	SAH				2023-12-12 21:34:00.000	2023-12-12 21:34:26	Result	Supernatant Tracking	2023-12-12 19:28:08.000	P	MISP		Processing could not be positive																		
		2023-12-08 22:24:39.980	TBHE	House/Enclosure of parish (city)	SAH				2023-12-12 19:37:39.000	2023-12-12 19:38:12.391	Result	Capillary Electrophoresis																						
		2023-12-08 22:24:39.980	TBHE	House/Enclosure of parish (city)	SAH				2023-12-08 21:39:08.000	2023-12-08 21:44:02	Result	Profile Data Analysis																						
		2023-12-08 22:24:39.980	TBHE	House/Enclosure of parish (city)	SAH				2023-12-12 19:37:39.000	2023-12-12 19:38:44.821

Ex1002.1022.1044
Study Ref:HA2019 Symposium poster
Data Source:Files obtained from participants.
Query:redact_degradation=false, if queried, exported results 0 rows.

Query ref: "training"
Exhibit 1 Executed between 01/01/2021 - 31/12/2021
Reported Results are Reviewed (and not marked Incorrect)
Profile Data is Verified (and not marked Incorrect/Duplicate)

Below data is the Text and second objects combined
- 2nd version 01/05/2022 - HHST 20/1994 - Exhibit Description/Executed Description contains the word "panic/panic", or assisted Description contains "EMT" and Exhibit Description/assisted Description contains "shot/Shoot/Assault", (and is not an environmental example)
- 02/05/2022 - DECEMBER 1994 - Exhibit Description/Executed Description contains the word "cardiac/glass/stomach/vomiting/autism/", Exhibit Description/Executed Description contains the word "Explicit" and assisted Description contains "EMT" and Exhibit Description/assisted Description does not contain "neglect" (and is not an environmental example)

2188 Records

Exhibit_Date	Parent_Barcode	Exhibit_Created_Date	Category_Code	Exhibit_Description	Assisted_Description	Client	Result_Client	Result_Exhibit	Result_Exhibit	Result_Photos_Date	Result_Review_Date	Process	Technique	Result_Exhibit_Location	Result_Exhibit_Location_Date	Result_Exhibit_Reference	Result_Exhibit_Manufacturer	Result	Client	Client_Sample_ID	Client_Created_Date	TAT_CT	TAT_Qty	TAT_Qty	TAT_Days_Value	TAT_Met_CT	TAT_Met_QT	TAT_Qty	Client	DNA_Profile_Sample_ID	Kit_DNA_Profile	DNA_Profile_Created_Date	DNA_Profile_Full_Created_Date
[redacted]		2021-22-08 08:38:22.223	1844	shell of penis	SAM Suspect		[redacted]			2021-22-08 09:00:00.000	2021-22-08 09:40:28	Result			2021-22-08 09:00:00.000	F	953		Possible Lock-Unlock Kit information															
		2021-22-08 08:00:00.000	1844	base of penis	SAM Suspect					2021-22-08 14:00:00.000	2021-22-08 14:53:39	Result			2021-22-08 12:00:00.000	F	859		Submitted results pending															
		2021-22-08 08:00:00.000	1844	base of penis	SAM Suspect					2021-22-07 22:00:00.000	2021-22-08 02:40:56	Result	DNA Quantification																				
		2021-22-08 08:00:00.000	1844	base of penis	SAM Suspect					2021-22-07 22:00:00.000	2021-22-08 02:43:38.000	Result	Capillary Electrophoresis																				
		2021-22-08 08:00:00.000	1844	base of penis	SAM Suspect					2021-22-08 14:00:00.000	2021-22-08 14:39:37.000	Result	Profile Data Analysis																				
		2021-22-08 08:00:00.000	1844	base of penis	SAM Suspect					2021-22-08 14:00:00.000	2021-22-08 14:39:56.750	Result	Profile Data Analysis																				
		2021-22-08 08:00:00.000	1844	base of penis	SAM Suspect					2021-22-08 14:00:00.000	2021-22-08 14:39:56.750	Result			2021-22-08 14:00:00.000	F	266		Two person mixed DNA profile															
		2021-22-08 08:00:00.000	1844	base of penis	SAM Suspect					2021-22-08 14:00:00.000	2021-22-08 14:39:56.750	Result			2021-22-08 14:00:00.000	F	266CCN		2 person mixed profile - contributor cnn															
		2021-22-08 08:00:00.000	1844	base of penis	SAM Suspect					2021-22-08 14:00:00.000	2021-22-08 14:39:56.750	Result			2021-22-08 14:00:00.000	F	266KT		2 person mix sem - suspect for contribution = KEEN Kim															
		2021-22-07 20:15:27	1942	Trace DNA	from shaft and foreskin of penis of Attendant					2021-22-08 09:00:00.000	2021-22-08 09:35:11.150	Result			2021-22-08 09:00:00.000	F	859		Submitted results pending															
		2021-22-07 20:15:27	1942	Trace DNA	from shaft and foreskin of penis of Attendant					2021-22-07 10:00:00.000	2021-22-07 20:39:39.807	Result			2021-22-08 12:00:00.000	F	SPOOA		Mixto positive for sperm. Submitted results pending															
		2021-22-07 20:15:27	1942	Trace DNA	from shaft and foreskin of penis of Attendant					2021-22-08 12:00:00.000	2021-22-08 14:39:39.797	Result	DNA Quantification		2021-22-08 14:00:00.000	F	269		DNA Insufficient for further processing	2021-22-07 22:00:00.000	2021-22-08 02:40:28.775	F	F	0.000416782000000									
		2021-22-07 20:15:27	1942	Trace DNA	from shaft and foreskin of penis of Attendant					2021-22-08 12:00:00.000	2021-22-08 12:39:51.137	Result	Supernatant Testing		2021-22-08 14:00:00.000	F	MSP		Presumptive testpositive															
		2021-22-07 20:15:27	1942	Trace DNA	from shaft and foreskin of penis of Attendant					2021-22-08 14:22:00.000	2021-22-08 14:22:48.473	Result	Polymerization		2021-22-08 14:22:00.000	F	TFCL		Testing restarted on whole from CPS															
		2021-22-07 20:15:27	1942	Trace DNA	from shaft and foreskin of penis of Attendant					2021-22-08 09:00:00.000	2021-22-08 09:39:56.742	Result	DNA Quantification								2021-22-07 20:15:27	2021-22-08 09:39:56.750	0.000	F	F	0.013788173000000									
		2021-22-07 20:15:27	1942	Trace DNA	from shaft and foreskin of penis of Attendant					2021-22-08 12:00:00.000	2021-22-08 12:40:08.820	Result	Capillary Electrophoresis																				
		2021-22-07 20:15:27	1942	Trace DNA	from shaft and foreskin of penis of Attendant					2021-22-08 09:00:00.000	2021-22-08 09:39:56.750	Result	Profile Data Analysis																				
		2021-22-07 20:15:27	1942	Trace DNA	from shaft and foreskin of penis of Attendant					2021-22-08 09:00:00.000	2021-22-08 09:39:56.750	Result			2021-22-08 14:00:00.000	F	9JAY		This sample has undergone Further processing															
		2021-22-07 20:15:27	1942	Trace DNA	from shaft and foreskin of penis of Attendant					2021-22-08 09:00:00.000	2021-22-08 09:39:56.750	Result			2021-22-08 14:00:00.000	F	2SWB		Single Source DNA profile - assumed Known contributor															
		2021-22-07 20:15:27	1942	Trace DNA	from shaft and foreskin of penis of Attendant					2021-22-08 09:00:00.000	2021-22-08 09:39:56.883	Result			2021-22-08 14:00:00.000	F	953		Possible Lock-Unlock Kit information															
		2021-22-08 07:12:17.850	1844	shaft/penis wet	SAM					2021-22-08 09:00:00.000	2021-22-08 09:40:12.190	Result			2021-22-08 12:00:00.000	F	859		Submitted results pending															
		2021-22-07 20:17:27.850	1844	shaft/penis wet	SAM					2021-22-08 12:00:00.000	2021-22-08 12:40:08.846	Result	DNA Quantification		2021-22-08 14:00:00.000	F	269		DNA Insufficient for further processing	2021-22-07 22:00:00.000	2021-22-08 02:40:28.941	F	F	0.013445454000000									
		2021-22-07 20:17:27.850	1844	shaft/penis wet	SAM					2021-22-08 09:00:00.000	2021-22-08 09:40:12.190	Result			2021-22-08 14:00:00.000	F	MSDPS		No Further work required as per advice from CPS															
		2021-22-07 20:17:27.850	1844	shaft/penis wet	SAM					2021-22-08 09:00:00.000	2021-22-08 09:40:12.190	Result			2021-22-08 14:00:00.000	F	859		Submitted results pending															
		2021-22-07 20:16:27.777	1844	shaft/penis dry	SAM					2021-22-08 12:00:00.000	2021-22-08 12:40:08.853	Result	DNA Quantification		2021-22-08 14:00:00.000	F	269		DNA Insufficient for further processing	2021-22-07 22:00:00.000	2021-22-08 02:40:28.941	F	F	0.013445454000000									
		2021-22-07 20:16:27.777	1844	shaft/penis dry	SAM					2021-22-08 09:00:00.000	2021-22-08 09:39:39.257	Result			2021-22-08 14:00:00.000	F	MSDPS		No Further work required as per advice from CPS															
		2021-22-07 13:42:43.103	1844	glans penis wet	SAM					2021-22-08 09:00:00.000	2021-22-08 09:40:08.853	Result			2021-22-08 14:00:00.000	F	859		Submitted results pending															
		2021-22-07 13:42:43.103	1844	glans penis wet	SAM					2021-22-08 12:00:00.000	2021-22-08 12:39:51.150	Result	DNA Quantification		2021-22-08 14:00:00.000	F	269		DNA Insufficient for further processing	2021-22-07 22:00:00.000	2021-22-08 02:40:28.941	F	F	0.013445454000000									
		2021-22-07 13:42:43.103	1844	glans penis dry	SAM					2021-22-08 09:00:00.000	2021-22-08 09:39:39.257	Result			2021-22-08 14:00:00.000	F	MSDPS		No Further work required as per advice from CPS															
		2021-22-07 13:42:43.103	1844	glans penis dry	SAM					2021-22-08 09:00:00.000	2021-22-08 09:40:08.853	Result			2021-22-08 14:00:00.000	F	859		Submitted results pending															
		2021-22-07 13:58:39.553	1844	stained saliva wet	SAM					2021-22-08 12:00:00.000	2021-22-08 12:39:51.153	Result	DNA Quantification		2021-22-08 14:00:00.000	F	269		DNA Insufficient for further processing	2021-22-07 22:00:00.000	2021-22-08 02:40:28.941	F	F	0.013445454000000									
		2021-22-07 13:58:39.553	1844	stained saliva wet	SAM					2021-22-08 09:00:00.000	2021-22-08 09:39:39.257	Result			2021-22-08 14:00:00.000	F	MSDPS		No Further work required as per advice from CPS															
		2021-22-07 13:58:39.553	1844	stained saliva wet	SAM					2021-22-08 09:00:00.000	2021-22-08 09:40:08.853	Result	Profile Data Analysis																				
		2021-22-07 13:58:39.553	1844	stained saliva wet	SAM					2021-22-08 09:00:00.000	2021-22-08 09:40:08.853	Result			2021-22-08 14:00:00.000	F	2SWB		Single Source DNA profile - assumed Known contributor															
		2021-22-07 13:58:39.553	1844	stained saliva wet	SAM					2021-22-08 12:00:00.000	2021-22-08 12:39:51.153	Result			2021-22-08 14:00:00.000	F	MSDPS		No Further work required as per advice from CPS															
		2021-22-07 13:42:43.103	1844	stained saliva dry	SAM					2021-22-08 12:00:00.000	2021-22-08 12:39:51.150	Result	DNA Quantification		2021-22-08 14:00:00.000	F	269		DNA Insufficient for further processing	2021-22-07 22:00:00.000	2021-22-08 02:40:28.941	F	F	0.013445454000000									
		2021-22-07 13:42:43.103	1844	stained saliva dry	SAM					2021-22-08 09:00:00.000	2021-22-08 09:39:39.257	Result			2021-22-08 14:00:00.000	F	MSDPS		No Further work required as per advice from CPS															
		2021-22-08 08:48:22	1844	Shaft/penis (wet)	SAM					2021-22-08 09:00:00.000	2021-22-08 09:40:12.190	Result			2021-22-08 12:00:00.000	F	859		Submitted results pending															
		2021-22-08 08:48:22	1844	Shaft/penis (wet)	SAM					2021-22-08 12:00:00.000	2021-22-08 12:39:51.153	Result	DNA Quantification		2021-22-08 14:00:00.000	F	269		DNA Insufficient for further processing	2021-22-07 22:00:00.000	2021-22-08 02:40:28.941	F	F	0.013445454000000									
		2021-22-08 08:48:22	1844	Shaft/penis (wet)	SAM					2021-22-08 09:00:00.000	2021-22-08 09:39:39.257	Result			2021-22-08 14:00:00.000	F	MSDPS		No Further work required as per advice from CPS															
		2021-22-07 13:58:39.553	1844	Shaft/penis (wet)	SAM					2021-22-08 09:00:00.000	2021-22-08 09:40:12.190	Result			2021-22-08 14:00:00.000	F	859		Submitted results pending															
		2021-22-07 13:58:39.553	1844	Shaft/penis (wet)	SAM					2021-22-08 12:00:00.000	2021-22-08 12:39:51.153	Result	DNA Quantification		2021-22-08 14:00:00.000	F	269		DNA Insufficient for further processing	2021-22-07 22:00:00.000	2021-22-08 02:40:28.941	F	F	0.013445454000000									
		2021-22-08 08:48:22	1844	Shaft/penis (wet)	SAM					2021-22-08 09:00:00.000	2021-22-08 09:39:39.257	Result			2021-22-08 14:00:00.000	F	MSDPS		No Further work required as per advice from CPS															
		2021-22-08 08:48:22	1844	Shaft/penis (wet)	SAM					2021-22-08 09:00:00.000	2021-22-08 09:40:12.190	Result			2021-22-08 14:00:00.000	F	859		Submitted results pending															
		2021-22-08 08:48:22	1844	Shaft/penis (wet)	SAM					2021-22-08 12:00:00.000	2021-22-08 12:39:51.153	Result	DNA Quantification		2021-22-08 14:00:00.000	F	269		DNA Insufficient for further processing	2021-22-07 22:00:00.000	2021-22-08 02:40:28.941	F	F	0.013445454000000									
		2021-22-08 08:48:22	1844	Shaft/penis (wet)	SAM					2021-22-08 09:00:00.000	2021-22-08 09:39:39.257	Result			2021-22-08 14:00:00.000	F	MSDPS		No Further work required as per advice from CPS															
		2021-22-08 07:48:22	1844	Shaft/penis (dry)	SAM					2021-22-08 09:00:00.000	2021-22-08 09:40:12.190	Result			2021-22-08 14:00:00.000	F	859		Submitted results pending															
		2021-22-08 07:48:22	1844	Shaft/penis (dry)	SAM					2021-22-08 12:00:00.000	2021-22-08 12:39:51.153	Result	DNA Quantification		2021-22-08 14:00:00.000	F	269		DNA Insufficient for further processing	2021-22-07 22:00:00.000	2021-22-08 02:40:28.941	F	F	0.013445454000000									
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		2021-22-08 08:48:22	1844	Glans penis (wet)	SAM					2021-22-08 09:00:00.000	2021-22-08 09:39:39.257	Result			2021-22-08 14:00:00.000	F	2SWB		Single Source DNA profile - assumed Known contributor															
		2021-22-08 08:48:22	1844	Glans penis (wet)	SAM					2021-22-08 12:00:00.000	2021-22-08 12:39:51.153	Result			2021-22-08 14:00:00.000	F	MSDPS		No Further work required as per advice from CPS															
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		2021-22-08 07:48:22	1844	penis	SAM					2021-22-08 09:00:00.000	2021-22-08 09:39:39.257	Result			2021-22-08 14:00:00.000	F	MSDPS		No Further work required as per advice from CPS															

Queensland Health
Forensic and Scientific Services

CA-93

Trace DNA Detection on Penile Swabs in Sexual Assault Cases, an Investigation of Queensland Data

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Abstract

Trace or touch DNA located on penile swabs of offenders can provide useful information in sexual assault cases, potentially establishing a degree of contact between an alleged victim and offender. Under ideal conditions, DNA profiles can be obtained from minimal amounts of trace DNA, however in forensic scenarios, these conditions are not always favourable. DNA can be removed, transferred or degraded and sampling success may not be uniform between samplers or sample donors. Resulting profiles may be unsuitable for either interpretation or application by statistical programs due to low-levels of cellular material available or complexity of the profile including assessment of the number of potential contributors.

This study examined data from twelve months of penile swab samples submitted to the Forensic DNA Analysis laboratory in Queensland and reports on the types of DNA results obtained. Analysis compared the quantification results of all samples and the results reported for both non-differential lysis and differential lysis extraction methods. The analysis also compared the differences or commonality between results of separately extracted wet and dry swabs from the same penile area. Case specific data was also isolated and evaluated to determine the frequency of useable profiles per case, regardless of the number of penile swabs contained within. The remainder of the study aimed to look at a breakdown of all DNA results obtained and report their variations. This included samples that resulted in no DNA being detected (no DNA detected), low-level DNA being detected which may be insufficient to result in a profile suitable for interpretation (low-level DNA detected), single source profiles, mixed profiles and profiles considered complex and unsuitable for interpretation (complex unsuitable).

This analysis showed that DNA profiles obtained from penile swabs in Queensland remain an important source of information for investigators. Results showed that the spermatozoa fraction, in differential lysis samples, had a higher prevalence of low quantification values. This increased the overall percentage of low-level results unlikely to produce interpretable profiles. It was found that only a low percentage of cases resulted in no interpretable profiles. The analysis also showed the importance of the collecting, separately processing and interpreting wet and dry swabs from the same penile area.

The analysis of these samples can be complex, and the ability to obtain DNA profiles and the assessment of informative or non-informative information is multi-layered.

Introduction

A historical data review was undertaken to investigate the frequency of obtaining DNA from penile swabs submitted in sexual assault investigation kits (SAIKs) and post-mortem samples (PM) during 2021. Depending on the case type and testing requirements requested by Queensland Police Service (QPS), swabs were submitted for routine extraction or differential lysis extraction. The investigation involved analysis of the reported results, quantification estimates, any difference or commonality in results of wet and dry swabs from the same site and an assessment of the results of swabs from the same case.

Methods

Data was extracted from the Laboratory Information Management System (LIMS) used by Forensic DNA Analysis - the Forensic Register (FR) for the period of 01/01/2021 to 31/12/2021.

Samples were located using various keywords including 'penile', 'penis', 'shaft', 'base', 'head', 'SAIK', 'urethral', 'urethra', 'glans penis', 'glans', 'coronal/glans', 'tip', 'mid' and 'coronal sulcus'.

DNA analysis of these samples was carried out using the following methods:

- Routine DNA extraction using the QIAsymphony® DNA Investigator Kit with QIAsymphony ® SP or differential lysis extraction using DNA IQ™ Casework Pro Kit with Maxwell® 16.
- DNA Quantification using the Quantifiler® Trio kit with QuantStudio™ 5 Real-Time PCR.
- DNA Amplification using the PowerPlex®21 System (PP21) with GeneAmp® PCR 9700.
- Capillary electrophoresis (CE) using AB 3130xl and 3500xL Genetic Analyzers.
- Profile analysis using the GeneMapper® ID-X software version 1.6.

Data from 281 individual samples was obtained. 215 samples underwent routine DNA extraction and 66 underwent differential lysis extraction. An epithelial fraction (EFRAC) and spermatozoa fraction (SFRAC) were created from each sample undergoing differential lysis, resulting in a total of 347 results. The 281 samples were obtained from 63 exhibits (SAIK or PM), with each exhibit containing between 1 and 8 penile swabs each.

The quantification value estimates of each sample was categorised into one of the following four reportable result categories as per standard procedures at the time of sample processing and interpretation in 2021:

- 0 to <0.001 ng/µL = No DNA was detected
- 0.001 to 0.0088 ng/µL = low-level DNA being detected which may be insufficient DNA to result in a profile suitable for interpretation
- Interpretable profiles = Single source and Mixed DNA profile
- Complex DNA profile unsuitable for interpretation

Results

Quantification results:

Quantification results of all individual samples showed no trend as can be seen in Figure 1, the values varied over a broad range. This is not unexpected due to the nature of forensic samples.



Figure 1: First run quantification values small amplicon target (SAT) only of all analysed samples.

When all of the quantification data is separated into ranges (as shown in Figure 2 below), it is evident that when the SFRAC results are removed the total number of samples within the lower quantification ranges drop considerably. However, when the SFRAC results are removed from the upper quantification ranges, minimal affect to the total number of results is observed. This result is indicative of SFRACs with nil to low spermatozoa numbers heavily contributing to the low quantification values.

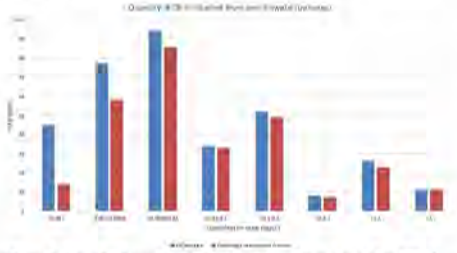

Figure 2: Quantification values of all analysed samples and excluding SFRACs.

DNA profiling outcomes:

As shown in Figure 3, of 347 total results, 31 of 66 SFRAC samples had "no DNA detected" (47.0%), 3 of 66 EFRAC samples had no DNA detected (4.5%) and 11 of 215 non-differential lysis samples had "no DNA detected" (5.1%). Of 81 samples with a "low-level DNA detected" result, 23 underwent further processing and of those, 19 yielded interpretable profiles.

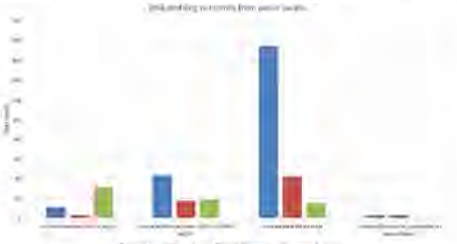

Figure 3: Profiling outcomes of non-differential lysis and differential lysis extracted samples (EFRACs and SFRACs).

Wet and dry swabs:

Of 145 paired wet and dry swabs, 109 (75.2%) obtained a result from the same result category in both swabs. Figure 4 shows that when a different result was obtained between the wet and dry swabs, generally the wet swab yielded more interpretable results. In 20 instances the wet yielded an interpretable result whilst the corresponding dry swab was "no DNA detected" or had a "low-level DNA detected" result. Conversely, there were 10 instances that the dry swab yielded an interpretable result whilst the corresponding wet swab had a "low-level DNA detected" result.

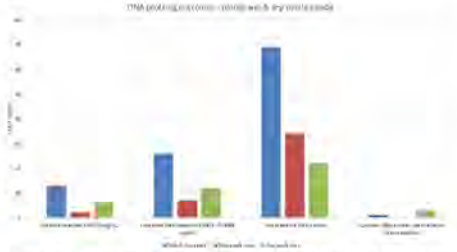

Figure 4: DNA profiling outcomes of paired wet and dry penile swabs with similar or different results.

Exhibits:

Considering the SAIK or PM in entirety (exhibit), 57 of 63 (90.5%) generated at least one interpretable result. When excluding SFRAC results, there was no change to this data. The number of exhibits without "no DNA detected" results decreased when excluding the SFRAC data. This data is shown in Figure 5.



Figure 5: DNA profiling outcomes for exhibits.

Discussion

This study aimed to investigate the frequency of detecting DNA from penile swabs, if there is an identifiable difference or commonality in results of wet and dry swabs collected from the same site and an assessment of the results of swabs from the same case. Penile swab data was extracted for samples that were submitted to Forensic DNA Analysis during 2021. A range of keywords were used to gather penile swab results from sexual assault investigation kits (SAIKs) and post-mortem samples (PM). The analysis compared reported results of no DNA being detected, low-level DNA being detected which may be insufficient DNA to result in a profile suitable for interpretation, interpretable profiles and complex profiles; which were considered unsuitable for interpretation. Results showed that DNA profiles obtained from penile swabs in Queensland remain an important source of information for investigators.

Samples that were reported as no DNA being detected were those considered to have a quantification value between 0 to <0.001 ng/µL. Samples that were considered to have low-level DNA being detected which may be insufficient DNA to result in a profile suitable for interpretation had a quantification value between 0.001 to 0.0088 ng/µL however, these samples were available for further processing. Interpretable profiles were those considered to be suitable for statistical analysis and comparison to reference samples. Complex DNA profiles were those considered to be unsuitable for interpretation or comparison.

Case context is taken into consideration when decisions are made as to whether samples with "low-level DNA detected" should undergo further testing. This may include whether probative information has been obtained from other samples or exhibits collected from the same case.

The quantification values of all the analysed samples were plotted and displayed no obvious trend. This variability could arise from differences in collection methods, the nature of the collection site, donor variations and presence of substances which may interfere with DNA collection and or preservation. Noting that this data set includes samples obtained from both living and deceased persons.

DNA was not able to be detected in 11 of 215 (5.1%) of non-differential lysis samples, 3 of 66 (4.5%) epithelial fractions and 31 of 66 (47.0%) spermatozoa fractions. The spermatozoa result is not unexpected as there are many factors that may affect the presence of spermatozoa at the time of sampling. Depending on the case circumstances, penile swabs are rarely collected for the detection of spermatozoa, rather, samples undergoing differential lysis in order to reduce DNA from spermatozoa to increase the probability of observing any non-donor DNA that may be present in an epithelial fraction. Therefore, the high percentage of SFRAC samples with little or no DNA detected is not unexpected, and tends to have little bearing on the overall profiling outcomes.

Results containing low-levels of DNA detected which may be insufficient DNA to result in a profile suitable for interpretation was seen in 44 of 215 (20.5%) non-differential lysis samples, 18 of 66 (27.3%) epithelial fractions and 19 of 66 (28.8%) spermatozoa fractions. Of the 81 samples that resulted in low-levels of DNA being detected which may be insufficient DNA to result in a profile suitable for interpretation, 23 samples underwent further processing through microcon filter concentration prior to amplification. In 19 of these samples, interpretable results were obtained.

Of the 281 non-differential lysis and epithelial fraction samples, DNA was detected in 263 (93.6%). The remaining samples were either "no DNA detected" (14) or were requested by QPS to cease testing prior to obtaining a DNA result (4). Including the samples that underwent further processing, 217 (77.2%) samples yielded interpretable profiles.

There were 145 paired wet and dry swabs, 109 (75.2%) obtained a result from the same result category in both swabs. Where a different result was obtained between the wet and dry swabs, generally the wet swab yielded more interpretable results and there were more low or no DNA detected results in the dry swabs. However, there were instances where the dry swab yielded an interpretable result and the wet did not.

There were 63 total exhibits (entire SAIK or collection of PM swabs), 6 (9.5%) of these exhibits no interpretable results were obtained from the contents of the exhibit. This count included no DNA being detected, samples considered low-levels of DNA being detected which may be insufficient DNA to result in a profile suitable for interpretation and complex profiles unsuitable for interpretation. It is noted that this result does not identify the number of swabs received within each exhibit. There were 57 (90.5%) exhibits that contained at least one interpretable DNA result from the contents of the exhibit. When excluding SFRAC results, there was no change to this data. Therefore, multiple penile swab submissions from the one individual remain an important source of information.

Conclusion

In summary, this data review highlighted the benefits of penile swab collection in from sexual assault investigation kits (SAIKs) and post mortem samples (PM). The study identified the ability to obtain a high number of interpretable results and the benefits of collecting both wet & dry and multiple swabs from the penile area. This study has a potential for further breakdown of data relating to different swab collection sites and DNA profile interpretations.

Acknowledgements

QPS Forensic Services Group
bdna and Ben Morgan for providing the raw data.

Queensland Government

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Area	Primary Metric	Rationale	Data Source	Data	Data range	Trending
In Tubes	TAT for In Tubes Receipt to Reported Result	Monitor FDNA TAT from receipt to reported result	FR: samples with technique "In-tube check", time elapsed Movement "REC" at Forensic and Scientific Services to Profile Review validated	Mean & Median TAT in days	month/quarter/annual	Compare to previous
	TAT for In Tubes Receipt to No DNA / DNA Insufficient	Monitor FDNA TAT from receipt to No DNA / DNA Insufficnet	FR: samples with technique "In-tube check", time elapsed Movement "REC" at Forensic and Scientific Services to No DNA or DNA Insufficient result line review	Mean & Median TAT in days	month/quarter/annual	Compare to previous
Cig Butts	TAT for Cig Butts Receipt to Reported Result	Monitor FDNA TAT from receipt to reported result	FR: samples with category "Cigarette Butt", time elapsed Movement "REC" at Forensic and Scientific Services to Profile Review validated	Mean & Median TAT in days	month/quarter/annual	Compare to previous
	TAT for Cig Butts Receipt to No DNA / DNA Insufficient	Monitor FDNA TAT from receipt to No DNA / DNA Insufficnet	FR: samples with category "Cigarette Butt", time elapsed Movement "REC" at Forensic and Scientific Services to No DNA or DNA Insufficient result line review	Mean & Median TAT in days	month/quarter/annual	Compare to previous
Fabrics	TAT for Fabrics Receipt to Reported Result	Monitor FDNA TAT from receipt to reported result	FR: Exhibit with category "Fabric", time elapsed Movement "REC" at Forensic and Scientific Services to Profile Review validated	Mean & Median TAT in days	month/quarter/annual	Compare to previous
	TAT for Fabrics Receipt to No DNA / DNA Insufficient	Monitor FDNA TAT from receipt to No DNA / DNA Insufficnet	FR: Exhibit with category "Fabric", time elapsed Movement "REC" at Forensic and Scientific Services to No DNA or DNA Insufficient result line review	Mean & Median TAT in days	month/quarter/annual	Compare to previous
SAWs	TAT for SAWs Receipt to Reported Result	Monitor FDNA TAT from receipt to reported result	FR: Exhibit with category "SAW", time elapsed Movement "REC" at Forensic and Scientific Services to Profile Review validated	Mean & Median TAT in days	month/quarter/annual	Compare to previous
	TAT for SAWs Receipt to No DNA / DNA Insufficient	Monitor FDNA TAT from receipt to No DNA / DNA Insufficnet	FR: Exhibit with category "SAW", time elapsed Movement "REC" at Forensic and Scientific Services to No DNA or DNA Insufficient result line review	Mean & Median TAT in days	month/quarter/annual	Compare to previous
Other Items	TAT for Other Items Receipt to Reported Result	Monitor FDNA TAT from receipt to reported result	FR: All Exhibit types other than "swab", "SAW" and "Cig butt" or samples with technique "in tube check", time elapsed Movement "REC" at Forensic and Scientific Services to Profile Review validated	Mean & Median TAT in days	month/quarter/annual	Compare to previous
	TAT for Other Items Receipt to No DNA / DNA Insufficient	Monitor FDNA TAT from receipt to No DNA / DNA Insufficnet	FR: All Exhibit types other than "swab", "SAW" and "Cig butt" or samples with technique "in tube check", time elapsed Movement "REC" at Forensic and Scientific Services to No DNA or DNA Insufficient result line review	Mean & Median TAT in days	month/quarter/annual	Compare to previous
All Items	TAT All Items from Receipt to Reported Result	Monitor FDNA TAT from receipt to reported result	FR: All Crime Scene exhibit types, time elapsed Movement "REC" at Forensic and Scientific Service to Profile Review validated	Mean & Median TAT in days	month/quarter/annual	Compare to previous
	TAT All Items Receipt to No DNA / DNA Insufficient	Monitor FDNA TAT from receipt to No DNA / DNA Insufficnet	FR: All Crime Scene exhibit types, time elapsed Movement "REC" at Forensic and Scientific Service to No DNA or DNA Insufficient result reviewed	Mean & Median TAT in days	month/quarter/annual	Compare to previous

Area	Primary Metric	Rationale	Secondary Metric	Data Source	Data Range	Trending	Measure
On Hold WL	TAT: Samples added to the On Hold worklist	Time taken for samples placed on hold to be actioned and testing re-started	On Hold - Staff Flag TAT	FR: Time elapsed samples added to On Hold worklist (Staff Flag) to added to another worklist or until result line is validated	monthly, quarterly, annual	Compare to previous period	Mean, median
			On Hold - Awaiting Advice TAT	FR: Time elapsed samples added to On Hold worklist (Staff Flag) to added to another worklist	monthly, quarterly, annual	Compare to previous period	Mean, median
			On Hold - Quality Review TAT	FR: Time elapsed samples added to On Hold worklist (Staff Flag) to added to another worklist or until result line is validated	monthly, quarterly, annual	Compare to previous period	Mean, median
Plate Reading	TAT: Plate reading	Time taken from completion of CEQ checking to plate reading commencing	TAT - plate reading CW (VFP)	FR: CW CE batches - time elapsed status "CEQ" to status "Read"	monthly, quarterly, annual	Compare to previous period	Mean, median
			TAT - plate reading FTA	FR: FTA CE batches - time elapsed status "CEQ" to status "Read"	monthly, quarterly, annual	Compare to previous period	Mean, median
			TAT - Plate Reading RPT	FR: RPT CE batches - time elapsed status "CEQ" to status "Read"	monthly, quarterly, annual	Compare to previous period	Mean, median
			TAT - Plate Reading OSD	FR: OSD CE batches - time elapsed status "CEQ" to status "Read"	monthly, quarterly, annual	Compare to previous period	Mean, median
			TAT - Plate Reading RUN	FR: RUN CE batches - time elapsed status "CEQ" to status "Read"	monthly, quarterly, annual	Compare to previous period	Mean, median
			TAT - Plate Reading EREF/REFAMP	FR: CW EREF batches - time elapsed status "CEQ" to status "Read"	monthly, quarterly, annual	Compare to previous period	Mean, median
		Time takes from plate reading commencing to plate reading completing	TAT - plate reading CW (VFP)	FR: CW CE batches - time elapsed status "Read" to status "Pass"	monthly, quarterly, annual	Compare to previous period	Mean, median
			TAT - plate reading FTA	FR: FTA CE batches - time elapsed status "Read" to status "Pass"	monthly, quarterly, annual	Compare to previous period	Mean, median
			TAT - Plate Reading RPT	FR: RPT CE batches - time elapsed status "Read" to status "Pass"	monthly, quarterly, annual	Compare to previous period	Mean, median
			TAT - Plate Reading OSD	FR: OSD CE batches - time elapsed status "Read" to status "Pass"	monthly, quarterly, annual	Compare to previous period	Mean, median
			TAT - Plate Reading RUN	FR: RUN CE batches - time elapsed status "Read" to status "Pass"	monthly, quarterly, annual	Compare to previous period	Mean, median
			TAT - Plate Reading EREF/REFAMP	FR: CW EREF batches - time elapsed status "Read" to status "Pass"	monthly, quarterly, annual	Compare to previous period	Mean, median
QFLAG	Count QFLAG	Count number of samples added to On Hold Staff Flag WL		FR: P1/P2/P3 samples - count samples added to On Hold Staff Flag WL.	monthly, quarterly, annual	Compare to previous period	Mean, median
	TAT QFLAG Identified	Monitor time taken for QPS to assess identified QFLAGs		FR: P1/P2/P3 samples - Time elapsed QFH Result line added to either Result QCFRQ or Profile Review.	monthly, quarterly, annual	Compare to previous period	Mean, median

Plate Reading Staff Level KPIs

Area	Process	Rostered Days	Metric	Measure 1	Measure 2	Measure 3	Measure 4	Measure 5	Data Range
Plate Reading	Plate reading completed	Count	Staff member changes CE batch status to Read	Count - Batches	Count - Samples	Batches / Rostered Day	Samples / Rostered Day	Mean/Median number of Batches processed by an FTE	Quarterly / 6 monthly / Annually

Area	Primary Metric	Rationale	Data Source	Metric	Data Range
FTA	FPP to FDNA	Time elapsed from delivery to FPP to delivery to FDNA	XXX - not sure this can be measured	Mean & Median time elapsed	Month, quarter, annual
	Delivery to FDNA to punching	Time elapsed from delivery to FDNA to processing in lab	FR: Sample category "FTA Cells" time elapsed from added to FTAAMP worklist to FTA batch locked.	Mean & Median time elapsed	Month, quarter, annual
RPT	RPT ord	Time elapsed from RPT test ordered to samples punched on a plate	FR: Sample category "FTA Cells" time elapsed from Method "RPT 3500xl" is added - to time sample on the RPT batch is locked	Mean & Median time elapsed	Month, quarter, annual
OSD	OSD ordered to punched and processed	Time elapsed from OSD test ordered to samples punched on a plate	FR: Sample category "FTA Cells" time elapsed from Method "OSD 3500xl" is added - to time sample on the OSD batch is locked	Mean & Median time elapsed	Month, quarter, annual
RUN	RUN ordered to punched and processed	Time elapsed from RUN test ordered to samples punched on a plate	FR: Sample category "FTA Cells" time elapsed from Method "RUN 3500xl" is added - to time sample on the RUN batch is locked	Mean & Median time elapsed	Month, quarter, annual
EREF	EREF ordered punched and processed	Time elapsed from EREF test ordered to samples punched on a plate	FR: Sample category "FTA Cells" time elapsed from added to DNAEXT worklist, method "250 FTA Preparation" to EREF batch locked.	Mean & Median time elapsed	Month, quarter, annual
Reference Summary TAT	Average time taken from receipt to Report	Average time taken for all reference samples from receipt at FPP to final result reported	FR: Sample category "FTA Cells" time elapsed from Receipt at FPP to Technique "Result" validated	Mean & Median time elapsed	Month, quarter, annual
PDF	Time taken to add PDFs to Crime Scene and Reference Samples	Time elapsed from Plate Reading complete to PDFs loaded. This is the trigger to adding samples to the PDA WL.	FR: All CE Batches, time elapsed from batch status "Pass" to all PDF loaded to the CE batch	Mean & Median time elapsed	Month, quarter, annual

Team Level **Samples and Batches**

Area	Process	Batches	Samples	Samples per Batch	Batches	Data Range	Trending
FTA	Count number of FTA batches and samples per FTA batch	Count number of FTA Batches with batch Status changed to Complete	Count number of samples on FTA batches with batch status changed to Complete	Mean & Median number of samples per batch	Total batches per period. Mean and Median batches per period	week/month/quarter/year	Compare to previous periods
RPT	Count number of RPT batches and samples per RPT batch	Count number of RPT Batches with batch Status changed to Complete	Count number of samples on RPT batches with batch status changed to Complete	Mean & Median number of samples per batch	Total batches per period. Mean and Median batches per period	week/month/quarter/year	Compare to previous periods
OSD	Count number of OSD batches and samples per OSD batch	Count number of OSD Batches with batch Status changed to Complete	Count number of samples on OSD batches with batch status changed to Complete	Mean & Median number of samples per batch	Total batches per period. Mean and Median batches per period	week/month/quarter/year	Compare to previous periods
RUN	Count number of RUN batches and samples per RUN batch	Count number of RUN batches with batch Status changed to CEQ	Count number of samples on RUN batches with batch status changed to Complete	Mean & Median number of samples per batch	Total batches per period. Mean and Median batches per period	week/month/quarter/year	Compare to previous periods
EREF	Count number of EREF batches and samples per EREF batch	Count number of EREF batches with batch Status changed to Complete	Count number of samples on EREF batches with batch status changed to Complete	Mean & Median number of samples per batch	Total batches per period. Mean and Median batches per period	week/month/quarter/year	Compare to previous periods

Area	Pirmary Metric	Rationale	Data Source	Secondary Metrics	Data range
In tubes	FPP Receipt to delivery to DNA	Time taken from delivery to FSS to availability for ER to examine. This is an area out of FDNA control but included in end to end TAT.	FR: samples with technique "In-tube check", time elapsed Movement "REC" at Forensic and Scientific Services to Movement "In tubes Box"	Mean & Median time elapsed	Month, quarter, annual
	Delivery-FDNA to In Tube Check	Time from delivery to FDNA to examination completed	FR: Samples with technique "In-tube check", time elapsed Movement "In_Tubes Box" to "In-tube Check" technique entered	Mean & Median time elapsed	Month, quarter, annual
	Examination to Examination Review	Time taken from examination to examination review and addition to Extraction WL	FR: Samples with technique "In-tube check", time elapsed "In-tube check" technique entered to reviewed	Mean & Median time elapsed	Month, quarter, annual
	Number Manual Interventions	Number of manual interventions required for intube samples. Manual interventions	FR: Samples with result lines HOIS, MIES, MISSTL, MITRI,SRMI	Number of Manual Interventions for each result line category as a total and also proportion of total in tube samples	
Cig Butts	FPP Receipt to delivery to DNA	Time taken from delivery to FSS to availability for ER to examine. This is an area out of FDNA control but included in end to end TAT.	Unsure if this can be collected.	Mean & Median time elapsed	Month, quarter, annual
	Delivery-FDNA to Item Exam	Time taken from delivery to FDNA to examination completed	FR: Sample with category "Cigarette Butt", time elapsed from Movement "In-Tubes Box" to Item Examination ordered	Mean & Median time elapsed	Month, quarter, annual
	Examination to Examination Review	Time taken from examination to examination review and addition to Extraction WL	FR: Samples with category "Cigarette Butt", time elapsed from Item Examination ordered to Reviewed.	Mean & Median time elapsed	Month, quarter, annual
Fabrics	FPP Receipt to delivery to DNA	Time taken from delivery to FSS to availability for ER to examine. This is an area out of FDNA control but included in the end to end TAT	FR: Exhibit with category "Fabric", time elapsed from Movement "REC" at Forensic and Scientific Services to Movement "FSS Forensic DNA Analysis FDNA-EREB-XXXX".	Mean & Median time elapsed	Month, quarter, annual
	Delivery-FDNA to Examination	Time taken from delivery to examination completed	FR: Exhibit with category "Fabric", time elapsed from Movement "FSS Forensic DNA Analysis FDNA-EREB-XXXX" to Item Examination ordered	Mean & Median time elapsed	Month, quarter, annual
	Examination to Examination Review	Time taken from examination to examination review and addition to Extraction WL	FR: Exhibit with category "Fabric", time elapsed from Item Examination ordered to reviewed.	Mean & Median time elapsed	Month, quarter, annual
Other Small Items	FPP Receipt to Deliver to DNA	Time taken fom delivery to FSS to availability for ER to examine. This is an area out of FDNA control but included in end to end TAT.	FR: All Exhibit types other than "swab", "SAIK" and "Cig butt" or samples with technique "in tube check", time elapsed from Movement "REC" to XXXXX	Mean & Median time elapsed	Month, quarter, annual
	Delivery-FDNA to Examination	Time taken frim delivery to FDNA to examination completed	FR: All Exhibit types other than "swab", "SAIK" and "Cig butt" or samples with technique "in tube check", Movement XXXX to Item Examination ordered	Mean & Median time elapsed	Month, quarter, annual
	Examination to Examination Review	Time taken from examination to examination review and addition to Extraction WL	FR: All Exhibit types other than "swab", "SAIK" and "Cig butt" or samples with technique "in tube check", Item Examination ordered to reviewed	Mean & Median time elapsed	Month, quarter, annual
SAIKs	FPP SAIK receipt to delivery to DNA	Time taken from delivery to FSS to availability for ER to examine. This is an area out of FDNA control but included in end to end TAT.	FR: Exhibit "SAIK Kit", time elapsed from Movement "REC" at Forensic and Scientific Services to Movememnt "FDNA-EXFZ-XXXX"	Mean & Median time elapsed	Month, quarter, annual
	Delivery-FDNA to Exam Strategy written	Time taken from SAIK delivery to FDNA to Exam Strategy written.	FR: Exhibit "SAIK Kit", time elapsed from Movement "FDNA-EXFZ-XXXX" to Notation "Examination Strategy"	Mean & Median time elapsed	Month, quarter, annual
	Exam strategy written to reviewed	Time taken from SAIK strategy writing to review.	FR: Exhibit "SAIK Kit", time elapsed from Notation "Examination Strategy" creation to added to Examination WL	Mean & Median time elapsed	Month, quarter, annual
	Exam strategy reviewed to Examination	Time taken from Examination strategy review to Examination	FR: exhibit category "SAIK Kit", time elapsed from added to Examination WL to Examination technique ordered	Mean & Median time elapsed	Month, quarter, annual
	Examination to Examination Complete	Time taken to review Examination and validate	FR: Exhibit category "SAIK Kit", time elapsed from "Examination" technique to Result "Item has been examined/subsampled".	Mean & Median time elapsed	Month, quarter, annual
Micro	DNA Extraction Complete to Microscopy	Time taken from DNA Extraction complete to Microscopy Read	FR: sample with technique "DNA Extraction" and Method "Differential Lysis DNA IQ" or Method "Diff Lysis Retain Supernatant", time elapsed from DNA Extraction batch "Complete" batch status to "Microscope" Technique ordered.	Mean & Median time elapsed	Month, quarter, annual
	Microscopy to Micro Review	Time taken from Microscopy read to Microscopy results validated	FR: sample with technique "DNA Extraction" and Method "Differential Lysis DNA IQ" or Method "Diff Lysis Retain Supernatant", time elapsed from "Microscope" technique ordered to validated.	Mean & Median time elapsed	Month, quarter, annual
Phadebas	DNA Extraction Complete to Phadebas test	Time taken from supernatant availability to supernatant testing	FR: Sample added to SNTTST worklist to Result entry "Presumptive saliva test positive" or "Presumptive saliva test negative"	Mean & Median time elapsed	Month, quarter, annual
	Phadebas test to Review	Time taken from supernatant result entry to validation	FR: Sample Result entry "Presumptive saliva test positive" or "Presumptive saliva test negative" to result validated	Mean & Median time elapsed	Month, quarter, annual
ER TAT	ER average TAT	Average TAT for all items submitted to ER for testing	FR: All samples average elapsed time from delivery to FDNA to added Examination Review	Mean & Median time elapsed	Month, quarter, annual
On Hold	Measure TAT samples placed on hold awaiting advice from QPS	Time taken from placing on hold to reactivation decision made based on QPS advice	FR: TAT from SOHAA Result line validated to SRP line validated or No Further Work or exhibit returned.	Mean & Median time elapsed	Month, quarter, annual

Area	Process	Rostered Days	Metric	Measure 1	Measure 2	Measure 3	Data Range
In Tube	In tube check	Count	FR: Sample with Technique "In Tube Check", count number ordered	Count - total	Mean & Median count per rostered day - by staff member	Mean & Median count per rostered day - team level	quarter, annual
	Examination review		Fr: Sample with Technique "In Tube Check", count number reviewed		Mean & Median count per rostered day - by staff member	Mean & Median count per rostered day - team level	quarter, annual
Cig butt	Examination	Count	FR: Sample category "Cigarette Butt", count number of Item Examinations ordered	Count - total	Mean & Median count per rostered day - by staff member	Mean & Median count per rostered day - team level	quarter, annual
	Examination review		FR: Sample category "Cigarette Butt", count number of Item Examinations reviewed		Mean & Median count per rostered day - by staff member	Mean & Median count per rostered day - team level	quarter, annual
Fabrics	Examination	Count	FR: Sample category "Fabric", count nunmer of Item Examinations ordered	Count - total	Mean & Median count per rostered day - by staff member	Mean & Median count per rostered day - team level	quarter, annual
	Examination review		FR: Sample category "Fabric", count nunmer of Item Examinations reviewed		Mean & Median count per rostered day - by staff member	Mean & Median count per rostered day - team level	quarter, annual
SAIKs	Examination strategy write	Count	FR: Sample category "SAIK Kit", count number of Examination Strategies ordered	Count - total	Mean & Median count per rostered day - by staff member	Mean & Median count per rostered day - team level	quarter, annual
	Examination strategy review		FR: Sample category "SAIK Kit", count number of Examination Strategies reviewed		Mean & Median count per rostered day - by staff member	Mean & Median count per rostered day - team level	quarter, annual
	Examination	Count	FR: Sample category "SAIK Kit", count number of "Examination" techniques ordered		Mean & Median count per rostered day - by staff member	Mean & Median count per rostered day - team level	quarter, annual
	Examination review		FR: Sample category "SAIK Kit", count number of "Examination" techniques reviewed		Mean & Median count per rostered day - by staff member	Mean & Median count per rostered day - team level	quarter, annual
Other Items	Examination	Count	FR: Sample All Others, count number of Item Examinations ordered	Count - total	Mean & Median count per rostered day - by staff member	Mean & Median count per rostered day - team level	quarter, annual
	Examination review		FR: Sample All Others, count number of Item Examinations reviewed		Mean & Median count per rostered day - by staff member	Mean & Median count per rostered day - team level	quarter, annual
Microscopy	Microscopy Read	Count	FR: Sample with "Microscope" Technique, count number ordered	Count - total	Mean & Median count per rostered day - by staff member	Mean & Median count per rostered day - team level	quarter, annual
	Microscopy Review		FR: Sample with "Microscope" Technique, count number reviewed		Mean & Median count per rostered day - by staff member	Mean & Median count per rostered day - team level	quarter, annual
Phadebas	Examination	Count	FR: Sample, count Result entry "Presumptive saliva test positive" or "Presumptive saliva test negative"	Count - total	Mean & Median count per rostered day - by staff member	Mean & Median count per rostered day - team level	quarter, annual
	Examination review		FR: Sample, count Result review "Presumptive saliva test positive" or "Presumptive saliva test negative"		Mean & Median count per rostered day - by staff member	Mean & Median count per rostered day - team level	quarter, annual

Team Level: TAT's

Area	Primary Metric	Rationale	Secondary Metric	Data Source	Data range	Measure	Trending
Extraction	Time elapsed: Added to Extraction WL to Batch Located	Time elapsed between extraction ordered and batch located and ready for processing.	TAT: Added to Extraction WL - Batch Located - PreLysis	FR - Mean & Median time elapsed: Sample added to Extraction WL - Sample on Pre-Lysis Batch status Locked	week/month/quarter/year	Time:	Compare to previous periods
			TAT: Added to Extraction WL - Batch Located - Ref Maxwell	FR - Mean & Median time elapsed: Sample added to Extraction WL - Sample on Ref Maxwell Batch status Located	week/month/quarter/year	Time:	Compare to previous periods
			TAT: Added to Extraction WL - Batch Located - DLYS	FR - Mean & Median time elapsed: Sample added to Extraction WL - Sample on DLYS Batch status Located	week/month/quarter/year	Time:	Compare to previous periods
			TAT: Added to Extraction WL - Batch Located - Retain SN	FR - Mean & Median time elapsed: Sample added to Extraction WL - Sample on Retain SN Batch status Located	week/month/quarter/year	Time:	Compare to previous periods
	Time elapsed: Extraction Batch Located to Prepared	Time elapsed between extraction batch ready for processing to processing commencing.	TAT: Pre-Lysis batch located to batch prepared	FR: Mean & Median time elapsed: Pre Lysis batch status Located - batch status Prepared	week/month/quarter/year	Time:	Compare to previous periods
			TAT: Ref Maxwell batch located to batch prepared	FR: Mean & Median time elapsed: Ref Maxwell batch status Located - batch status Prepared	week/month/quarter/year	Time:	Compare to previous periods
			TAT: DLYS batch located to batch prepared	FR: Mean & Median time elapsed: DLYS batch status Located - batch status Prepared	week/month/quarter/year	Time:	Compare to previous periods
			TAT: Retain SN batch located to batch prepared	FR: Mean & Median time elapsed: Retain SN batch status Located - batch status Prepared	week/month/quarter/year	Time:	Compare to previous periods
			TAT: CBA-SP batch located to batch prepared	FR: Mean & Median time elapsed: CBA-SP batch status Located - batch status Prepared	week/month/quarter/year	Time:	Compare to previous periods
			TAT: CBA-Integrated batch located to batch prepared	FR: Mean & Median time elapsed: CBA-Integrated batch status located - batch status Prepared	week/month/quarter/year	Time:	Compare to previous periods
	Time elapsed: Extraction Batch started to completed	Time take to perform each of the different extraction batches. This can be monitored for variations over time to detect issues with instruments, protocols or workflows.	TAT: Pre-lysis batch	FR: Mean & Median time elapsed: Pre-Lysis batch status Prepared - batch status Completed	week/month/quarter/year	Time:	Compare to previous periods
			TAT: Ref Maxwell Batch	FR: Mean & Median time elapsed: Ref Maxwell batch status Prepared - batch status Completed	week/month/quarter/year	Time:	Compare to previous periods
			TAT: DLYS batch	FR: Mean & Median time elapsed: DLYS batch status Prepared - batch status Completed	week/month/quarter/year	Time:	Compare to previous periods
			TAT: Retain SN batch	FR: Mean & Median time elapsed: Retain SN batch status Prepared - batch status Completed	week/month/quarter/year	Time:	Compare to previous periods
			TAT: CBA-SP	FR: Mean & Median time elapsed: CBA batch status Prepared - batch status Completed	week/month/quarter/year	Time:	Compare to previous periods
			TAT: CBA-Integrated	FR: Mean & Median time elapsed: CBA batch status Prepared - batch status Completed	week/month/quarter/year	Time:	Compare to previous periods
Quant	Time elapsed: Added to Quant WL to batch located	Time taken from extraction batch completion and transition to the Quant WL until the Quant batch has been created and samples located by LIAs.	NA	FR: Mean & Median time elapsed: Sample added to Quant WL - Sample on Quant batch status Located	week/month/quarter/year	Time:	Compare to previous periods
	Time taken to process Quant Batches	Time taken to run a Quant batch.	NA	FR: Mean & Median time elapsed: Quant batch status Prepared - Quant batch status Completed	week/month/quarter/year	Time:	Compare to previous periods
Amp	Time elapsed: added to Amp WL to batch located	Time taken from Quant batch completion and transition to the Amp WL until the Amp batch has been created and located by LIAs.	NA	FR: Mean & Median time elapsed: Sample added to Amp WL - Sample on Amp batch status Located	week/month/quarter/year	Time:	Compare to previous periods
	Time taken to process Amp Batches	Time taken to run an Amp batch. This can be monitored to detect issues with instruments, protocols or workflows.	NA	FR: Mean & Median time elapsed: Amp batch status Located - Amp Batch status Completed	week/month/quarter/year	Time:	Compare to previous periods
CE	Time elapsed: Amp batch complete to CE complete	Time taken elapsed between completing an Amp batch and completing running on CE instrument. CW/REF/Direct Batches may be impacted by different factors and will be measured seperately.	TAT: CW amp batch	FR: Mean & Median time elapsed: CW amp batch status Completed - CW CE batch status Completed	week/month/quarter/year	Time:	Compare to previous periods
			TAT: REF amp batch	FR: Mean & Median time elapsed: REF amp batch status Completed - REF CE batch status Completed	week/month/quarter/year	Time:	Compare to previous periods
			TAT: Direct amp batch	FR: Mean & Median time elapsed: Direct amp batch status Completed - Direct CE batch status Completed	week/month/quarter/year	Time:	Compare to previous periods
			TAT: DSD amp batch	FR: Mean & Median time elapsed: DSD amp batch status Completed - DSD CE batch status Completed	week/month/quarter/year	Time:	Compare to previous periods
			TAT: RUN amp batch	FR: Mean & Median time elapsed: RUN amp batch status Completed - RUN CE batch status Completed	week/month/quarter/year	Time:	Compare to previous periods
	Time elapsed: CE batch complete to CEQ complete	Time taken to complete CEQ checking, including time for investigations.CW/REF/Direct Batches may be impacted by different factors and will be measured seperately	TAT: CEQ CW CE batch	FR: Mean & Median time elapsed: CW CE batch status Completed - batch status CEQ	week/month/quarter/year	Time:	Compare to previous periods
			TAT: CEQ REF CE batch	FR: Mean & Median time elapsed: REF CE batch status Completed - batch status CEQ	week/month/quarter/year	Time:	Compare to previous periods
			TAT: CEQ Direct CE batch	FR: Mean & Median time elapsed: Direct CE batch status Completed - batch status CEQ	week/month/quarter/year	Time:	Compare to previous periods
			TAT: CEQ DSD CE batch	FR: Mean & Median time elapsed: DSD CE batch status Completed - batch status CEQ	week/month/quarter/year	Time:	Compare to previous periods
			TAT: CEQ RUN CE batch	FR: Mean & Median time elapsed: RUN CE batch status Completed - batch status CEQ	week/month/quarter/year	Time:	Compare to previous periods
Post Extraction	Time elapsed: added to Post Extraction WL to batch located	Time taken from assigning Post Extraction test to batch creation and samples being located.	TAT: added to Microbiom WL - Microbiom batch located	FR: Mean & Median time elapsed: Sample added to Microbiom WL - Sample on Microbiom batch status Located.	week/month/quarter/year	Time:	Compare to previous periods
			TAT: added to NGRN WL - NGRN batch located	FR: Mean & Median time elapsed: Sample added to Nigair WL - Sample on Nigair batch status Located	week/month/quarter/year	Time:	Compare to previous periods
			TAT: added to Dilution WL - Dilution batch located	FR: Mean & Median time elapsed: Sample added to Dilution WL - Sample on Dilution batch status located.	week/month/quarter/year	Time:	Compare to previous periods
	Time taken to process Post Extraction Batches.	Time taken to process Post Extraction batches.	TAT: Mbiom batch Locked - Mbiom batch Completed	FR: Mean & Median time elapsed: Mbiom batch status Locked - Mbiom batch status Completed	week/month/quarter/year	Time:	Compare to previous periods
			TAT: Ngair batch Locked - Ngair batch Completed	FR: Mean & Median time elapsed: Ngair batch status Locked - Ngair batch status Completed	week/month/quarter/year	Time:	Compare to previous periods
			TAT: Dilution batch Locked - Dilution batch Completed	FR: Mean & Median time elapsed: Dilution batch status Locked - Dilution batch status Completed	week/month/quarter/year	Time:	Compare to previous periods
Re DNA	Time elapsed: from Quant Batch complete to Re DNA/DNA insufficient results entered.	Time taken to upload quant results and enter Re DNA/DNA insufficient result lines.	TAT: Quant batch status Complete - Sample quant result (ITSA) entered	FR: Mean & Median time elapsed: Quant batch status Complete - Sample quant result (ITSA) entered	week/month/quarter/year	Time:	Compare to previous periods
	Time elapsed: from result entry and addition to Re DNA WL to result reviewed	Time taken to review and release Re DNA/DNA insufficient results.	TAT: Re DNA/DNA insufficient result line entry to result review	FR: Mean & Median time elapsed: Re DNA/DNA insufficient result line entry - Re DNA/DNA insufficient result line review.	week/month/quarter/year	Time:	Compare to previous periods
Overall Time:	Analytical total TAT	Total time for samples to be processed through the Analytical Team (first extraction to first CEQ check completed)	NA	FR: Mean & Median time elapsed: Sample addition to DNA Extraction WL - Sample on CE batch with CEQ status	week/month/quarter/year	Time:	Compare to previous periods

Team Level: Throughput

Area	Process	Batches	Samples	Samples per Batch	Data Range	Trending
DNA-Extraction	Pre-Lysis	[Count number of Batches with Batch Status changed to Complete]	[Count number of Samples on Batches with Batch status changed to Complete]	[Mean & Median number of samples per batch]	week/month/quarter/year	[Compare to previous periods]
	Ref Maxwell					
	DLYS					
	QIA-SP					
	QIA-Integrated					
	Mbiom					

Team Level: TATs

Area	Primary Metric	Rationale	Secondary Metric	Data Source	Data range	Measure	Trending
Post Extraction	Nipar	Count number of Batches with batch status changed to Complete	Count number of samples on Batches with batch status changed to Complete	Mean & Median number of samples per batch	week/month/quarter/year	Compare to previous periods	
	Dilution						
Quant	Quant CW/REF preparation in Pre-PCR	Count number of Batches with batch status changed to Complete	Count number of samples on batches with batch status changed to Complete	Mean & Median number of samples per batch	week/month/quarter/year	Compare to previous periods	
Amp	Amp CW/Ref preparation in Pre-PCR	Count number of Batches with batch status changed to Complete	Count number of samples on batches with batch status changed to Complete	Mean & Median number of samples per batch	week/month/quarter/year	Compare to previous periods	
CE	CE plates prepared	Count number of Batches with batch status changed to Complete	Count number of samples on batches with batch status changed to Complete	Mean & Median number of samples per batch	week/month/quarter/year	Compare to previous periods	
CEQ	CEQ checks completed	Count number of Batches with batch status changed to CEQ	Count number of samples on batches with batch status changed to CEQ	Mean & Median number of samples per batch	week/month/quarter/year	Compare to previous periods	

Team Level: Controls

Controls	Primary Metric	Rationale	Secondary Metric	Data Source	Data range	Trending
Amp Pos (007) CW and REF	Monitor peak height - D3 (blue small)	Monitor small and large loci for each dye to identify trends/changes over time which may indicate instrument or kit changes	NA	CW and REF Amp Pos 007 - Mean & Median peak height D3	month/quarter/year	Compare to previous periods
	Monitor peak height - D6 (blue large)		NA	CW and REF Amp Pos 007 - Mean & Median peak height D6	month/quarter/year	Compare to previous periods
	Monitor peak height - D8 (green small)		NA	CW and REF Amp Pos 007 - Mean & Median peak height D8	month/quarter/year	Compare to previous periods
	Monitor peak height - D5 (green large)		NA	CW and REF Amp Pos 007 - Mean & Median peak height D5	month/quarter/year	Compare to previous periods
	Monitor peak height - D2 (yellow small)		NA	CW and REF Amp Pos 007 - Mean & Median peak height D2	month/quarter/year	Compare to previous periods
	Monitor peak height - D10 (yellow large)		NA	CW and REF Amp Pos 007 - Mean & Median peak height D10	month/quarter/year	Compare to previous periods
	Monitor peak height - D22 (red small)		NA	CW and REF Amp Pos 007 - Mean & Median peak height D22	month/quarter/year	Compare to previous periods
	Monitor peak height - Penta E (red large)		NA	CW and REF Amp Pos 007 - Mean & Median peak height Penta E	month/quarter/year	Compare to previous periods
	Monitor peak height - Penta D (purple small)		NA	CW and REF Amp Pos 007 - Mean & Median peak height Penta D	month/quarter/year	Compare to previous periods
	Monitor peak height - TPOX (purple small)		NA	CW and REF Amp Pos 007 - Mean & Median peak height TPOX	month/quarter/year	Compare to previous periods
EXTP Blood	Monitor peak height - D3 (blue small)	Monitor small and large loci for each dye to identify trends/changes over time which may indicate instrument or kit changes	NA	EXTP Blood - Mean & Median peak height D3	month/quarter/year	Compare to previous periods
	Monitor peak height - D6 (blue large)		NA	EXTP Blood - Mean & Median peak height D6	month/quarter/year	Compare to previous periods
	Monitor peak height - D8 (green small)		NA	EXTP Blood - Mean & Median peak height D8	month/quarter/year	Compare to previous periods
	Monitor peak height - D5 (green large)		NA	EXTP Blood - Mean & Median peak height D5	month/quarter/year	Compare to previous periods
	Monitor peak height - D2 (yellow small)		NA	EXTP Blood - Mean & Median peak height D2	month/quarter/year	Compare to previous periods
	Monitor peak height - D10 (yellow large)		NA	EXTP Blood - Mean & Median peak height D10	month/quarter/year	Compare to previous periods
	Monitor peak height - D22 (red small)		NA	EXTP Blood - Mean & Median peak height D22	month/quarter/year	Compare to previous periods
	Monitor peak height - Penta E (red large)		NA	EXTP Blood - Mean & Median peak height Penta E	month/quarter/year	Compare to previous periods
	Monitor peak height - Penta D (purple small)		NA	EXTP Blood - Mean & Median peak height Penta D	month/quarter/year	Compare to previous periods
	Monitor peak height - TPOX (purple small)		NA	EXTP Blood - Mean & Median peak height TPOX	month/quarter/year	Compare to previous periods
EXTP SERAC	Monitor peak height - D3 (blue small)	Monitor small and large loci for each dye to identify trends/changes over time which may indicate instrument or kit changes	NA	EXTP SERAC - Mean & Median peak height D3	month/quarter/year	Compare to previous periods
	Monitor peak height - D6 (blue large)		NA	EXTP SERAC - Mean & Median peak height D6	month/quarter/year	Compare to previous periods
	Monitor peak height - D8 (green small)		NA	EXTP SERAC - Mean & Median peak height D8	month/quarter/year	Compare to previous periods
	Monitor peak height - D5 (green large)		NA	EXTP SERAC - Mean & Median peak height D5	month/quarter/year	Compare to previous periods
	Monitor peak height - D2 (yellow small)		NA	EXTP SERAC - Mean & Median peak height D2	month/quarter/year	Compare to previous periods
	Monitor peak height - D10 (yellow large)		NA	EXTP SERAC - Mean & Median peak height D10	month/quarter/year	Compare to previous periods
	Monitor peak height - D22 (red small)		NA	EXTP SERAC - Mean & Median peak height D22	month/quarter/year	Compare to previous periods
	Monitor peak height - Penta E (red large)		NA	EXTP SERAC - Mean & Median peak height Penta E	month/quarter/year	Compare to previous periods
	Monitor peak height - Penta D (purple small)		NA	EXTP SERAC - Mean & Median peak height Penta D	month/quarter/year	Compare to previous periods
	Monitor peak height - TPOX (purple small)		NA	EXTP SERAC - Mean & Median peak height TPOX	month/quarter/year	Compare to previous periods
EXTP EERAC	Monitor peak height - D3 (blue small)	Monitor small and large loci for each dye to identify trends/changes over time which may indicate instrument or kit changes	NA	EXTP SERAC - Mean & Median peak height D3	month/quarter/year	Compare to previous periods
	Monitor peak height - D6 (blue large)		NA	EXTP SERAC - Mean & Median peak height D6	month/quarter/year	Compare to previous periods
	Monitor peak height - D8 (green small)		NA	EXTP SERAC - Mean & Median peak height D8	month/quarter/year	Compare to previous periods
	Monitor peak height - D5 (green large)		NA	EXTP SERAC - Mean & Median peak height D5	month/quarter/year	Compare to previous periods
	Monitor peak height - D2 (yellow small)		NA	EXTP SERAC - Mean & Median peak height D2	month/quarter/year	Compare to previous periods
	Monitor peak height - D10 (yellow large)		NA	EXTP SERAC - Mean & Median peak height D10	month/quarter/year	Compare to previous periods
	Monitor peak height - D22 (red small)		NA	EXTP SERAC - Mean & Median peak height D22	month/quarter/year	Compare to previous periods
	Monitor peak height - Penta E (red large)		NA	EXTP SERAC - Mean & Median peak height Penta E	month/quarter/year	Compare to previous periods
	Monitor peak height - Penta D (purple small)		NA	EXTP SERAC - Mean & Median peak height Penta D	month/quarter/year	Compare to previous periods
	Monitor peak height - TPOX (purple small)		NA	EXTP SERAC - Mean & Median peak height TPOX	month/quarter/year	Compare to previous periods
EXTP Blood	Monitor quant results	Monitor quant results for EXTP to detect sample, extraction and quantitation variation over time	NA	EXTP Blood - Mean & Median quant result	month/quarter/year	Compare to previous periods
EXTP SERAC	Monitor quant results	Monitor quant results for EXTP to detect sample, extraction and quantitation variation over time	NA	EXTP SERAC - Mean & Median quant result	month/quarter/year	Compare to previous periods
EXTP EERAC	Monitor quant results	Monitor quant results for EXTP to detect sample, extraction and quantitation variation over time	NA	EXTP EERAC - Mean & Median quant result	month/quarter/year	Compare to previous periods
EXTN	Monitor CW and REF EXTN quant results	Monitor quant results for EXTNs to identify trends over time	NA	CW and Ref EXTNs - Mean & Median quant results	month/quarter/year	Compare to previous periods
	CW and REF EXTNS - 1 peak present	Monitor number of peaks present in EXTNs to identify trends over time	NA	CW and Ref EXTNs with 1 peak present at any locus	month/quarter/year	Compare to previous periods
	CW and REF EXTNS - 2 peaks present		NA	CW and Ref EXTNs with 2 peaks present at any locus	month/quarter/year	Compare to previous periods
	CW and REF EXTNS - 3 peaks present		NA	CW and Ref EXTNs with 3 peaks present at any locus	month/quarter/year	Compare to previous periods
	CW and REF EXTNS - >3 peaks present		NA	CW and Ref EXTNs with >3 peaks present at any locus	month/quarter/year	Compare to previous periods

Individual Level These KPIs are measured for each staff member individually

Area	Process	Rostered Days	Metric	Measure 1	Measure 2	Measure 3	Measure 4	Measure 5	Data Range
DNA Extraction	Pre-Lysis Ref Maxwell DLYS QIA-SP QIA-Integrated	Count	FR: Staff member changes extraction batch status to Prepared	Count - Batches	Count - Samples	Batches / Rostered Day	Samples / Rostered Day	Mean & Median number of Batches processed by an FTE	Quarterly / 6 monthly / Annualy
Post Extraction	Mcon Nspin Dilution	Count	Staff member changes post extraction batch	Count - Batches	Count - Samples	Batches / Rostered Day	Samples / Rostered Day	Mean & Median number of Batches processed by an FTE	Quarterly / 6 monthly / Annualy
Quant	Quant CW/REF preparation in Pre-PCR	Count	Staff member changes quant batch status to Prepared	Count - Batches	Count - Samples	Batches / Rostered Day	Samples / Rostered Day	Mean & Median number of Batches processed by an FTE	Quarterly / 6 monthly / Annualy
Amp	Amp CW/Ref preparation in Pre-PCR	Count	Staff member changes amp batch status to Prepared	Count - Batches	Count - Samples	Batches / Rostered Day	Samples / Rostered Day	Mean & Median number of Batches processed by an FTE	Quarterly / 6 monthly / Annualy
CE	CE plates prepared	Count	Staff member changes CE batch status to Prepared	Count - Batches	Count - Samples	Batches / Rostered Day	Samples / Rostered Day	Mean & Median number of Batches processed by an FTE	Quarterly / 6 monthly / Annualy
CEQ	CEQ checks completed	Count	Staff member changes CE batch status to CEQ	Count - Batches	Count - Samples	Batches / Rostered Day	Samples / Rostered Day	Mean & Median number of Batches processed by an FTE	Quarterly / 6 monthly / Annualy

Team Level TATs

Area	Primary Metric	Rationale	Secondary Metric	Data Source	Analyses	Data range	Measure	Trending
PDA - P1/P2/P3	TAT: Results available to PDA commence	Time between results being available on the PDA worklist and PDA commencing by a scientist.	NA	FR: P1/P2/P3 samples separately - time elapsed between added to PDA worklist - Allocate to scientist	Mean & Median	week/month/quarter/year	time	Compare to previous periods
	TAT: Results available to PDA complete (Reporting TAT Overall)	Time between results being available on the PDA worklist and results being reviewed and Profile Review validated.	NA	FR: P1/P2/P3 samples separately - time elapsed between added to PDA worklist - Profile Review Ordered	Mean & Median	week/month/quarter/year	time	Compare to previous periods
	TAT: PDA commence to PDA Complete	Time between a scientist "Allocate" from the PDA worklist to the scientist completing PDA and ordering a Profile Review.	NA	FR: P1/P2/P3 samples separately: time elapsed between Allocate to scientist to first Profile Review ordered.	Mean & Median	week/month/quarter/year	time	Compare to previous periods
	Reworks at PDA stage	Total number and proportion of reworks ordered at the PDA stage by the PDA scientist.	Collate separately for extraction, microcon, nucleospin, quantification, amplification and capillary electrophoresis.	FR: P1/P2/P3 samples separately: collate separately number of additions to extraction worklist, quantification worklist, microcon worklist, nucleospin worklist, amplification worklist and capillary electrophoresis worklist after the PDA scientist has "Allocate".	Total, Mean & Median	week/month/quarter/year	time	Compare to previous periods
	Volume of PDA conducted	Measure the number of samples which have undergone PDA and compare to previous periods and to TAT Measure the number of results lines entered over a period - this can be used to monitor the complexity of results/review required and also changes to result line (addition/removal).	NA NA	FR: P1/P2/P3 samples separately: count samples added to PDA worklist FR: P1/P2/P3 samples separately: count number of Result Lines added to samples added to PDA worklist	Mean & Median Mean & Median	week/month/quarter/year week/month/quarter/year	time time	Compare to previous periods Compare to previous periods
Review - P1/P2/P3	TAT: PDA complete to Results Released	Time between PDA completed by the PDA scientist and adding to the PDA Review worklist and the Profile Review being validated.	NA	FR: P1/P2/P3 samples separately: time elapsed between Profile Review ordered and Profile Review validated	Mean & Median	week/month/quarter/year	time	Compare to previous periods
	Number and proportion of reworks required at Profile Review Stage	Total number and proportion of reworks ordered once PDA has been completed, following feedback from the reviewer.	Collate separately for extraction, microcon, nucleospin, quantification, amplification and capillary electrophoresis.	FR: P1/P2/P3 samples separately: collate separately number of additions to extraction worklist, quantification worklist, microcon worklist, nucleospin worklist, amplification worklist and capillary electrophoresis worklist after the first Profile Review is ordered.	Total, Mean & Median	week/month/quarter/year	time	Compare to previous periods
	Amount of Reviews Conducted	Measure the number of samples which have undergone PDA review and compare to TAT and previous period volumes	NA	FR: P1/P2/P3 samples separately: Count number of samples with Profile Review validated	Total, Mean & Median	week/month/quarter/year	time	Compare to previous periods
		Measure the number of result lines which have been reviewed and compare to TAT and previous period volumes	NA	FR: P1/P2/P3 samples separately: Count number of Result Lines reviewed	Total, Mean & Median	week/month/quarter/year	time	Compare to previous periods
Ref PDA	Number of Ref PDA conducted	Monitor number of Ref PDA conducted	NA	FR: Count all priorities and samples types: Number of samples added to the Ref PDA worklist.	Total, Mean & Median	week/month/quarter/year	time	Compare to previous periods
	Ref PDA Comparisons - pre/post C5 delivery - P2 Cases only	Monitor number of EVID comparisons done where Ref sample is delivered prior to C5 profile review		FR: Count Reference sample comparisons to C5 sample where Reference sample delivery date is before Profile Review date	Total,Mean & Median, proportion	quarterly/year	Count	Compare to previous periods
		Monitor number of EVID comparisons done where Ref sample is delivered after first C5 profile review		FR: Count Reference sample comparisons to C5 sample where Reference sample delivery date is after Profile Review date	Total,Mean & Median, proportion	quarterly/year	Count	Compare to previous periods
	TAT: Result available to result reviewed	Monitor REF PDA TAT to identify trends.	NA	FR: P1/P2/P3 samples separately: time elapsed between added to Ref PDA worklist to result reviewed/PDA complete.	Mean & Median	week/month/quarter/year	time	Compare to previous periods
NCIDD	Number of NCIDD uploads	Monitor number of NCIDD uploads	NA	FR: count number of NCIDD upload batches completed	Total, Mean & Median	week/month/quarter/year	time	Compare to previous periods
	TAT: PDA complete to NCIDD Uploaded	Monitor time elapsed between PDA Review and NCIDD upload complete	NA	FR: For samples with NCIDD Upload, time elapsed between Profile Review validated and NCIDD Upload validated	Mean & Median	week/month/quarter/year	time	Compare to previous periods
	Link Reporting	Monitor number of NCIDD new link lines		FR: Number of new Link Lines reported	Count	week/month/quarter/year	Count	Compare to previous periods
		Monitor TAT from link creation to review	NA	FR: Time elapsed - NCIDD upload file loaded to Link Report reviewed	Time	week/month/quarter/year	Count	Compare to previous periods
Statements	Number of Statements written	Monitor the total number of statements written	NA	FR: Cases with Statement request task	Count	Month/quarter/year	Count	Compare to previous periods
	TAT: Statement request to Allocated	Monitor time elapsed between a statement request being received and the statement being allocated to a scientist	NA	FR: Cases with Statement request task - time elapsed between request task creation and allocation to scientist.	Mean & Median Time	Month/quarter/year	Time	Compare to previous periods
	TAT: Statement allocated to statement draft complete	Monitor time elapsed between statement being allocated and a draft complete	NA	FR: Cases with Statement request task - time elapsed between allocated to scientist and check Draft Complete	Mean & Median Time	Month/quarter/year	Time	Compare to previous periods
	TAT: Statement draft complete to reviewed	Monitor time elapsed between statement draft completion and statement review	NA	FR: Cases with Statement Request Task - time elapsed between check Draft Complete and check Review Complete	Mean & Median Time	Month/quarter/year	Time	Compare to previous periods
	Statement Request time frames	Monitor statement request time frames for all priority cases	Tally of statement request period by week (i.e. number of statement requests with 1 week TAT, 2 week TAT, 3 week TAT etc...)	FR: Statement Request Date to Statement Due Date	Count - TAT weeks	quarter/year	Count	Compare to previous periods
	Meeting Statement Date required	Monitor the time differential between Statement Required date and Statement Published date	NA	FR: Cases with Statement Request Task - time differential between Required Date and Statement Published date	Mean & Median Time	Month/quarter/year	Time	Compare to previous periods
Court and Case Conferences	Court Attendance	Monitor amount of court attendance	Collate number of instances of court attendance as a total. Also collate total hours of court attendance. Collate average hours per each instance of court attendance.	FR: Cases with Case Report - Court Attendance (count, duration total, average duration per instance)	Count instances, duration total, average duration per instance, method (in person/phone).	Quarter/year	Count, time, average time per instance	Compare to previous periods
	Court appearance per Statement Issued	Monitor number of court appearances against number of statements issued		FR: Proportion of cases with Statements Published with a Court Report	Proportion	Quarter/year	Proportion	Compare to previous periods
	Case Conference	Monitor amount of case conferences	Collate number of case conferences as a total but also time spent in case conferences	FR: Cases with Case Report - Case Conference (Count, duration total, average duration per instance)	Count instances, duration total, averages duration per instance	Quarter/year	Count, time, average time per instance	Compare to previous periods
Cold Cases	Count Cases	Monitor number of cold cases						
	Count Samples Started retesting	Monitor number of samples where testing has been started						
	Count Samples No DNA/DNA Insuff							
	Count Samples Final Result (DNA Profile)	Monitor number of samples testing started with final DNA result						
	Count Case Conferences	Monitor number of cold cases case conferences						
	Count Casefile Review	Monitor number/time for casefile review by scientist						
	Count Statements	Monitor number of cold cases statements						
	Count Court Appearances	Monitor number of cold cases court appearances						
Paternity	Count Cases	Monitor number of paternity cases reported		FR: the following result lines and count the number of unique FR numbers: NEABF Not excluded as biological father EABF Excluded as biological father CNBM Consistent with being biological mother NCNBM Not consistent with being biological mother CNBC Consistent with being child of NCNBC Not consistent with being child of	Count unique FR numbers with paternity result lines	Quarter/year	Count	Compare to previous

KPI Data Available for each staff member

Area	Rostered Days	Rostering	Process	Data source	Measure 1	Measure 2	Measure 3	Measure 4	Data Range	Trend
PDA	Count - PDA Rostered Days (Preparate PE and P5 rostered days?)	Rostered days as proprtion of total rostered days for FDNA	PDA P2 SS	FR: Sample allocated to scientist, Priority 2, SS result line	Count	Mean & Median TAT from Allocate to Profile Review ordered	Proportion of total P2 SS by FDNA	P2 SS proportion of total PDA by scientist	Month/Quarter & Month/Annual	Compare to previous period
			PDA P2 SS NCOD	FR: Sample allocated to scientist, Priority 2, SSNCD result line			Proportion of total P2 SS NCOD by FDNA	P2 SS NCOD proportion of total PDA by scientist	Month/Quarter & Month/Annual	Compare to previous period
			PDA P2 MIX	FR: Sample allocated to scientist, Priority 2, *comple result lines			Proportion of total P2 Mix by FDNA	P2 MIX proportion of total PDA by scientist	Month/Quarter & Month/Annual	Compare to previous period
			PDA P2 MIX NCOD	FR: Sample allocated to scientist, Priority 2, MIXNCOD* result lines			Proportion of total PDA P2 SS completed by FDNA	P2 MIX NCOD proportion of total PDA by scientist	Month/Quarter & Month/Annual	Compare to previous period
			PDA P2 Complex	FR: Sample allocated to scientist, Priority 2, CMPLI result line			Proportion of total P2 Complex completed by FDNA	P2 Complex proportion of total PDA by scientist	Month/Quarter & Month/Annual	Compare to previous period
			PDA P2 Plus Reference	FR: Sample allocated to scientist, Priority 2, Reference sample comparison after first Profile Review			Proportion of total P2 Plus Reference completed by FDNA	P2 Plus Reference proportion of total PDA by scientist	Month/Quarter & Month/Annual	Compare to previous period
			PDA P2 Total	**FR: Sample allocated to scientist, Priority 2, Profile Review result line ordered**			Proportion of total P2 PDA completed by FDNA	Proportion of P2 P5 PDA	Month/Quarter & Month/Annual	Compare to previous period
			PDA P5 SS	FR: Sample allocated to scientist, Priority 3, SS result line	Count	Mean & Median TAT from Allocate to Profile Review ordered	Proportion of total P3 SS by FDNA	P3 SS proportion of total PDA by scientist	Month/Quarter & Month/Annual	Compare to previous period
			PDA P5 SS NCOD	FR: Sample allocated to scientist, Priority 3, SSNCD result line			Proportion of total P2 SS NCOD by FDNA	P3 SS NCOD proportion of total PDA by scientist	Month/Quarter & Month/Annual	Compare to previous period
			PDA P5 MIX	FR: Sample allocated to scientist, Priority 3, *comple result lines			Proportion of total P3 Mix by FDNA	P3 MIX proportion of total PDA by scientist	Month/Quarter & Month/Annual	Compare to previous period
			PDA P5 MIX NCOD	FR: Sample allocated to scientist, Priority 3, MIXNCOD* result lines			Proportion of total PDA P3 SS completed by FDNA	P3 MIX NCOD proportion of total PDA by scientist	Month/Quarter & Month/Annual	Compare to previous period
			PDA P5 Complex	FR: Sample allocated to scientist, Priority 3, CMPLI result line			Proportion of total P3 Complex completed by FDNA	P3 Complex proportion of total PDA by scientist	Month/Quarter & Month/Annual	Compare to previous period
			PDA P5 Plus Reference	FR: Sample allocated to scientist, Priority 3, Reference sample comparison after first Profile Review			Proportion of total P3 Plus Reference completed by FDNA	P3 Plus Reference proportion of total PDA by scientist	Month/Quarter & Month/Annual	Compare to previous period
			PDA P5 Total	**Fc: Sample allocated to scientist, Priority 3, Profile Review result line ordered**			Proportion of total P3 PDA completed by FDNA			
Review	Count - Review Rostered Days (Preparate PE and P5 rostered days?)	Rostered days as proprtion of total rostered days for FDNA	Review P2 SS	FR: Sample reviewed by scientist, Priority 2, SS result line	Count	Mean & Median TAT from Allocate to Profile Review	Proportion of total P2 SS review - total FDNA	P2 SS proportion of total Review by scientist	Month/Quarter & Month/Annual	Compare to previous period
			Review P2 SS NCOD	FR: Sample reviewed by scientist, Priority 2, SSNCD result line			Proportion of total P2 SS NCOD review - total FDNA	P2 SS NCOD proportion of total Review by scientist	Month/Quarter & Month/Annual	Compare to previous period
			Review P2 MIX	FR: Sample reviewed by scientist, Priority 2, *comple result lines			Proportion of total P2 MIX review - total FDNA	P2 MIX proportion of total Review by scientist	Month/Quarter & Month/Annual	Compare to previous period
			Review P2 MIX NCOD	FR: Sample reviewed by scientist, Priority 2, MIXNCOD * result lines			Proportion of total P2 MIX NCOD review - total FDNA	P2 MIX NCOD proportion of total Review by scientist	Month/Quarter & Month/Annual	Compare to previous period
			Review P2 Complex	FR: Sample reviewed by scientist, Priority 2, CMPLI result line			Proportion of total P2 Complex review - total FDNA	P2 Complex proportion of total Review by scientist	Month/Quarter & Month/Annual	Compare to previous period
			Review P2 Plus Reference	FR: Sample reviewed by scientist, Priority 2, Reference sample comparison after first Profile Review			Proportion of total P2 Plus Reference Review - total FDNA	P2 Plus Reference proportion of total Review by scientist	Month/Quarter & Month/Annual	Compare to previous period
			Review P2 Total	**FR: Sample reviewed by scientist, Priority 2, Profile Review line validated**			Proportion of total P2 Review completed by FDNA	Proportion of P2 P5 PDA	Month/Quarter & Month/Annual	Compare to previous period
			Review P5 SS	FR: Sample reviewed by scientist, Priority 3, SS result line	Count	Mean & Median TAT from Allocate to Profile Review	Proportion of total P3 SS review - total FDNA	P3 SS proportion of total Review by scientist	Month/Quarter & Month/Annual	Compare to previous period
			Review P5 SS NCOD	FR: Sample reviewed by scientist, Priority 3, SSNCD result line			Proportion of total P3 SS NCOD review - total FDNA	P3 SS NCOD proportion of total Review by scientist	Month/Quarter & Month/Annual	Compare to previous period
			Review P5 MIX	FR: Sample reviewed by scientist, Priority 3, *comple result lines			Proportion of total P3 MIX review - total FDNA	P3 MIX proportion of total Review by scientist	Month/Quarter & Month/Annual	Compare to previous period
			Review P5 MIX NCOD	FR: Sample reviewed by scientist, Priority 3, MIXNCOD * result lines			Proportion of total P3 MIX NCOD review - total FDNA	P3 MIX NCOD proportion of total Review by scientist	Month/Quarter & Month/Annual	Compare to previous period
			Review P5 Complex	FR: Sample reviewed by scientist, Priority 3, CMPLI result line			Proportion of total P3 Complex review - total FDNA	P3 Complex proportion of total Review by scientist	Month/Quarter & Month/Annual	Compare to previous period
			Review P2 Plus Reference	FR: Sample reviewed by scientist, Priority 3, Reference sample comparison after first Profile Review			Proportion of total P3 Plus Reference Review - total FDNA	P3 Plus Reference proportion of total Review by scientist	Month/Quarter & Month/Annual	Compare to previous period
			Review P3 Total	**FR: Sample reviewed by scientist, Priority 3, Profile Review line validated**			Proportion of total P3 Review completed by FDNA	Proportion of P3 P5 PDA	Month/Quarter & Month/Annual	Compare to previous period
Incorrect	Count of incorrect (error) ly scientist - PDA		Incorrects when scientist performs PDA	FR: Sample allocated to scientist, Result line incorrected	Count - number of samples with incorrected result line	Staff Error rate: Samples with incorrected result lines as a proportion of total samples PDA'd by a scientist	Team Error rate: total samples with incorrected result lines as a proportion of total samples PDA'd by all scientists		Quarter & month/annual	Compare to previous period
	Count of incorrect (error) ly scientist - Review		Incorrects when scientist performs Review	FR: Sample reviewed by scientist, Result line incorrected	Count - number of samples with incorrected result line	Staff Error rate: Samples with incorrected result lines as a proportion of total samples reviewed by a scientist	Team Error rate: total samples with incorrected result lines as a proportion of total samples reviewed by all scientists		Quarter & month/annual	Compare to previous period
Court Attendance / Case Conference	Count number court attendance and case conferences	NA	Court Attendance	FR: Case reports - Court Attendance entered by an individual Case Scientist	Count	Number of hours total	Number of hours per instance of court attendance		6 month/annual	Compare to previous period
			Case Conferences	FR: Case reports - Case Conference entered by an individual Case Scientist	Count	Number of hours total	Number of hours per Case Conference instance		6 month/annual	Compare to previous period
Statements	Count - Rostered Days	Rostered day as a proportion of total rostered days	Number of statements written	FR: Cases with Statement Request Task - Published status - Allocated to scientist	Count	Proportion of statements written - total FDNA	Proportion of Statements written by Priority P1, P2 and P3		Quarter & Month/Annual	Compare to previous period
			Statement writing - allocate to commence draft	FR: Case with Statement Request Task - scientist allocates to click Statement Technical Report	TAT	Mean & Median TAT from allocate to commence draft	TAT by case priority		Quarter & Month/Annual	Compare to previous period
			Statement writing - commence draft to review	FR: Case with Statement Request Task - scientist clicks Statement Technical Report to click Draft Complete	TAT	Mean & Median TAT from allocate to commence draft	TAT by case priority		Quarter & Month/Annual	Compare to previous period
			Statement review	FR: Case with Statement Request Task - scientist checks Review Complete	Count	Proportion of statements reviewed - total FDNA	Proportion of Statements reviewed by Priority P1, P2 and P3		Quarter & Month/Annual	Compare to previous period
	NA	NA	Statement - Date Required	FR: Cases with Statement Request Task - Time differential between Date Required and Results Published	Difference	Mean & Median time differential for scientist	Compare to data for all Scientists		Quarter & Month/Annual	Compare to previous period
Ref PDA	NA	NA	RFF PDA conducted	FR: Reference samples PDA'd by a scientist (Final result copied down)	Count	Mean & Median per collection period (week/month etc)	Proportion of total Ref PDA conducted		Month/Quarter & Month/Annual	Compare to previous period
NCOD	Count - Rostered Days	Rostered day as a proportion of total	Link Creation	FR: Link Reports which a scientist has created	Count	Mean & Median per rostered day			Month/Quarter & Month/Annual	Compare to previous period
			Link Review	FR: Link Reports which a scientist has reviewed	Count	Mean & Median per rostered day			Month/Quarter & Month/Annual	Compare to previous period

Team Level TATs

Area	Primary Metric	Rationale	Secondary Metric	Data Source	Data range	Measure	Trending
Admin Team	**Case creation**	A measure of the number of casefiles created by each admin team member. Number of files being created assists with rostering, capacity of staff	TAT: From Added to *Statement / Unallocated Statement List* - to registration of barcode for casefile (NOTE: currently not created until all green dots present, or as directed to create by FRIT officers)	FR - Mean & Median time elapsed: Sample add to Statement / Unallocated Statement List - Barcode registered	week/month/quarter/year	time	Compare to previous periods
	Case creation - Time elapsed: Storage of file from *FDNA Analysis* to *FRIT In-tray - Case Files for Reporting*	A measure of the time elapsed between file created *FDNA Analysis* and being placed in the *FRIT In-tray - Case Files for Reporting* for the Statement process to be undertaken	TAT: *FDNA Analysis* to *FRIT In-tray - Case files for Reporting*	FR: Mean & Median time elapsed: created in FDNA Analysis and tracked to FRIT In-tray - Case files for Reporting	week/month/quarter/year	time	Compare to previous periods
	Issuing Statement / Evid Cert. Time elapsed: Storage of file from *Scientist In-Tray* to *Admin In-tray - Statements* / then from *Admin In-tray - Statements* to *Admin In-tray After Statements*	A measure of the time elapsed between file being placed in the *Admin In-tray - Statements* to the *Admin In-tray - After Statement* process being undertaken	TAT: *Admin In-tray - Statements* to the *Admin In-tray - After Statement tray*	FR: Mean & Median time elapsed: tracked Admin In-tray - Statements to the Admin In-tray - After Statement tray	week/month/quarter/year	time	Compare to previous periods
	Issuing Statement / Evid Cert. Time elapsed: Storage of file from *Admin In-tray After Statements* to *Admin In-tray - Case file Finish*	A measure of the time elapsed between file being placed in the *Admin In-tray After Statements* to *Admin In-tray - Case file Finish* process being undertaken	TAT: *Admin In-tray After Statements* to *Admin In-tray - Case file Finish*	FR: Mean & Median time elapsed: tracked Admin In-tray After Statements to Admin In-tray - Case file Finish	week/month/quarter/year	time	Compare to previous periods
	Case File Finish - Time elapsed: Storage of file from *Admin In-tray - Case file Finish* to Shelf / Bench location	A measure of the time elapsed between file being placed in the *Admin In-tray - Case file Finish* to the Shelf / Bench location being undertaken	TAT: *Admin In-tray - Case file Finish* to the Shelf / Bench location	FR: Mean & Median time elapsed: tracked to Admin In-tray - Case file Finish to the Shelf / Bench location	week/month/quarter/year	time	Compare to previous periods

Individual Level

Primary Metric	Rostered Days	Metric	Measure 1	Measure 2	Measure 3	Data Range
Case creation	Count	Staff member registers the barcode for the new case file	Count - Files	Files / Rostered Day	Mean & Median number of Files	Monthly / Quarterly / 6 Monthly / Annually
Pre - Statement Creation	Count	Staff member tracks file to *FRIT In-Tray - Case Files for Reporting.*	Count - Files	Files / Rostered Day	Mean & Median number of Files	Monthly / Quarterly / 6 Monthly / Annually
Files after Statements	Count	Staff member tracks file to *Admin In - Tray - After Statements*	Count - Files	Files / Rostered Day	Mean & Median number of Files	Monthly / Quarterly / 6 Monthly / Annually
Completed files ready for storage	Count	Staff member tracks file to *Admin In - Tray - Casefile Finish*	Count - Files	Files / Rostered Day	Mean & Median number of Files	Monthly / Quarterly / 6 Monthly / Annually
Storage of Files	Count	Staff member tracks file to Shelf / Bench	Count - Files	Files / Rostered Day	Mean & Median number of Files	Monthly / Quarterly / 6 Monthly / Annually

CA-95

Report for QIS OQI as of 29/07/2022 11:34:15 AM

Report for QIS OQI -

[redacted] QPS accessing Forensic DNA Analysis Information

OQI Details

Status	Closed Approved
Subject	New OQI opened to include further information. Information from OQI 52987 has been copied in here: On 30 January, 2020 it was observed in the Forensic Register that a QPS Officer attached to the Homicide Cold Case Investigation Team (CCIT) had accessed information thought to be only available to Forensic DNA Analysis for [redacted] This includes information that may not be peer reviewed. On 11 February, 2020 it was verbally confirmed to Justin Howes that a QPS Management Section Research Officer had access to the same information. On the same date, the aforementioned officer from CCIT confirmed in an email to Team Leader Justin Howes what they could see in the Forensic Register. On 30 January, 2020 it was observed in the Forensic Register that a QPS Officer attached to the Homicide Cold Case Investigation Team (CCIT) had accessed information thought to be only available to Forensic DNA Analysis for [redacted] This includes information that may not be peer reviewed. On 11 February, 2020 it was verbally confirmed to Justin Howes that a QPS Management Section Research Officer had access to the same information. On the same date, the aforementioned officer from CCIT confirmed in an email to Team Leader Justin Howes what they could see in the Forensic Register.
Source of OQI	Other
Date Identified	05/06/2020

OQI Creator Contact Details

Creator	Justin HOWES
Organisational Unit/s	Forensic Reporting and Intelligence
Service/s	Forensic and Scientific Service
Site Location/s	Coopers Plains

Investigator/Actioner Contact Details

Actioner	Cathie ALLEN
Organisational Unit/s	Police Services
Service/s	Forensic and Scientific Service
Site Location/s	Coopers Plains

Investigation Details

Investigation Completed 17/02/2020 **Root Cause Type** | OtherInformation from OQI #[redacted] has been copied here:

Investigation Details

After email advice from Justin Howes, Team Leader for Forensic Reporting & Intelligence Team, I advised John Doherty, Executive Director of possible inappropriate access of the Forensic Register to FSS data prior to peer review. I provided the screenshot of the Forensic DNA Analysis profile determination analysis page from the FR which highlighted [redacted] as the last staff member to access this page. No staff member in Police Services Stream (or SSLU or FPP) that access the FR has the surname of[redacted]. However there is a Sgt Dale Fletcher that works in the QPS Cold Case Unit.

Further to this, on the 12th of Feb 2020 (10.40am), I was provided with email advice from Justin Howes regarding a screenshot of the access view of the FR from Sgt Dale Fletcher. Sgt Fletcher advised that whilst using his 'Results Management Access' in the FR, he was able to view the Exhibit Testing table (as an example) which showed all results (presumptive and final) for an item. This access also enabled staff with this access to view (and possibly) edit both non-peer reviewed and peer reviewed DNA and Chemistry results. Whilst at a meeting with the QPS on the 11th of Feb 2020, Dr Matt Krosch, QPS Research Officer, also confirmed to Justin that he could view those results under his access of the FR.

I sought advice from Helen Gregg regarding NATA accreditation and it appeared that this could be against NATA accreditation guidelines.

At 2pm on Wednesday, 12th of Feb 2020, a teleconference was held between John Doherty, Supt Bruce McNab, Insp David Neville and myself. I explained that Sgt Fletcher's name had been noted on the bottom of a Forensic DNA Analysis only page of the FR and it could be seen an against NATA accreditation guidelines. I also advised that Sgt Fletcher appeared to be using his 'Results Management' access, however the 'Quality' access also gave the same view of Forensic DNA Analysis pages (as confirmed by Dr Matt Krosch). Supt McNab advised that the access had been amended for QPS Forensic Officers and that the access had now been reverted back to the original by bdna that day. bdna is an external company that is currently providing support and maintenance of the FR to the QPS. I advised that due to our NATA accreditation requirements we would need additional information so that this change could be documented. The Supt advised that I should put that in writing and that he would look at it and run it past the QPS lawyers to see if the information could be provided to FSS.

At 2.13pm on the 12th of Feb 2020, I followed up with the below email request to Supt McNab (with a cc to John Doherty):

Hi Supt McNab, Thank you for your time today on the teleconference regarding access by QPS staff members to Forensic DNA Analysis results that may have not been through the peer review process (via Exhibit Testing Table and Profile Data Analysis page). Forensic DNA Analysis are accredited through NATA, under ISO17025. Under Section 7.11 – Control and data and information management, there appears to have been a breach ('…changes need to be authorised, documented and validated before implementation.' And 'LIMS must be: be protected from unauthorised access; LIMS must be maintained in a manner which ensures the integrity of the data and information'). An investigation, including corrective actions, regarding this will need to be conducted to advise NATA. This is normal for a breakdown in accreditation requirements and is not intended to be adversarial. Documenting an investigation and addressing the root cause is a requirement under any quality system. To assist us to address this corrective action report, can you please provide either John or myself with the following information:

- How did it occur that QPS staff who have Results Management or Quality access were also provided with access to Forensic DNA Analysis Exhibit Testing and Profile Data assessment information?

• When did this change occur? (noting the removal of access was on Wednesday, 12th of Feb, prior to or at 2pm).

• What did the QPS staff do with the information that they had available to them?

• Who authorised the change to occur?

• Why was FSS not advised of this change prior to it occurring?

This will inform a risk-based assessment of the issue and allow us to demonstrate to NATA that we took appropriate action to address the issue and the root cause. Cheers Cathie

On the 17th of Feb 2020, Supt McNab responded to my email (with a cc to John Doherty and Insp David Neville):

Hi Cathie,

We've had a look at this issue from our end. In short, it was changed from our end unintentionally, as such, much of FSG we were unaware until advised by your team. Those who located it, did so whilst performing their normal duties of scanning the FR to either see the progress, or the results of your examinations. No action was taken with any of the information that could be seen, as soon as you advised us, we changed it back so no one could see. I am confident with the departure of Tim, and the movement of all work over to BDNA till the commercialisation process is completed that such an issue will not arise again. We accept that his unintentional change took place at our end. In conclusion it shows that they greater degree of cooperation and information sharing between our departments is ensuring that the people of Queensland are being well served. Have a great weekend.

Bruce McNab BM Superintendent [redacted]
Operations Commander Forensic Services Group
OPERATIONS SUPPORT COMMAND Queensland Police Service [redacted]

Preformed By Cathie ALLEN

Action Details

Action Complete 05/06/2020 **Action Fix Type** OtherFurther enquiries made with the QPS

Title

Action Description

Information below copied from previous OQI [redacted]

Further enquiries made with the QPS.

Numerous enquiries have been made with the QPS for more specific information to address the dot points originally requested:

•

How did it occur that QPS staff who have Results Management or Quality access were also provided with access to Forensic DNA Analysis Exhibit Testing and Profile Data assessment information?

•

When did this change occur? (noting the removal of access was on Wednesday, 12th of Feb, prior to or at 2pm).

•

What did the QPS staff do with the information that they had available to them?

•

Who authorised the change to occur?

•

Why was FSS not advised of this change prior to it occurring?

New information for this OQI:
Email correspondence between John Doherty and Supt Bruce McNab from 29 May 2020:

Key questions put to the QPS

- When did this change occur?
- When was it rectified (noting that I discussed with you on 12th Feb and you informed me that it had been remedied at around 2pm that day).
- What caused the issue?
- What did the QPS staff do with the information that they had available to them? (we may not know this, but we might be able to determine who accessed data that they shouldn't have had access to via the audit trail)
- Who authorised the change to occur?

- If this change was intentional, why was FSS not advised of this change prior to it occurring?
- What is in place to prevent this from happening again?

Email response from Supt McNab:

- When did this change occur? I'm not sure when the change occurred, due to our recent pressures I haven't been able to progress that, but I can look again after we finishing commercialising the register.
- When was it rectified (noting that I discussed with you on 12th Feb and you informed me that it had been remedied at around 2pm that day). It was rectified as soon as you drew my attention to it.
- What caused the issue? We suspect that in an attempt to improve efficiencies one of our civilian employees made a change without approval, or misunderstood a request that had been made of him.
- What did the QPS staff do with the information that they had available to them? (we may not know this, but we might be able to determine who accessed data that they shouldn't have had access to via the audit trail) Nothing was done with the information.
- Who authorised the change to occur? It would appear it was changed by a civilian employee, there is no trail of any authorisation.
- If this change was intentional, why was FSS not advised of this change prior to it occurring? It does not appear to be intentional.
- What is in place to prevent this from happening again? Apart from the civilian leaving our employ, we made sure through communication prior to his departure that no such changes would be made without proper authorisations.

Task Details

No Tasks found

Follow-up And Approval

Follow-up Status	Accepted
Follow-up Status Comment	5/06/2020 2:28:46 PM Justin HOWES: Accepted actions.
Approver	John DOHERTY
Approval/Rejection Date	05/06/2020
Approval/Rejection Comment	5/06/2020 3:08:51 PM John DOHERTY: Clearly documenting what the correct 'authorisation procedure' is for future changes is required 5/06/2020 3:05:56 PM John DOHERTY: Further information received from QPS Hi John in relation to your questions; - When did this change occur? I'm not sure when the change occurred, due to our recent pressures I haven't been able to progress that, but I can look again after we finishing commercialising the register. - When was it rectified (noting that I discussed with you on 12th Feb and you informed me that it had been remedied at around 2pm that day). It was rectified as soon as you drew my attention to it. - What caused the issue? We suspect that in an attempt to improve efficiencies one of our civilian employees made a change without approval, or misunderstood a request that had been made of him.

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- What is in place to prevent this from happening again? Apart from the civilian leaving our employ, we made sure through communication prior to his departure that no such changes would be made without proper authorisations.

I hope this assists in your enquiries, if you require anything else please let me know, and please accept my apologies for not replying earlier, I have simply been swamped with other duties, and then COVID related issues.

Thanks for your patience.

Bruce McNab BM
Superintendent [redacted]
Operations Commander
Forensic Services Group
OPERATIONS SUPPORT COMMAND
Queensland Police Service
[redacted]

Associations

No Associations found

Records

No Records found

[redacted] QPS accessing Forensic DNA Analysis Information

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CA-96

Report for QIS OQI as of 29/06/2022 10:48:03 AM

Report for QIS OQI -

[redacted] QPS accessing Forensic DNA Analysis information

OQI Details

Status	Closed Approved
Subject	On 30 January, 2020 it was observed in the Forensic Register that a QPS Officer attached to the Homicide Cold Case Investigation Team (CCIT) had accessed information thought to be only available to Forensic DNA Analysis for [redacted]. This includes information that may not be peer reviewed. On 11 February, 2020 it was verbally confirmed to Justin Howes that a QPS Management Section Research Officer had access to the same information. On the same date, the aforementioned officer from CCIT confirmed in an email to Team Leader Justin Howes what they could see in the Forensic Register.
Source of OQI	Other
Date Identified	06/05/2020

OQI Creator Contact Details

Creator	Justin HOWES
Organisational Unit/ s	Forensic Reporting and Intelligence
Service/ s	Forensic and Scientific Service
Site Location/ s	Coopers Plains

Investigator/ Actioner Contact Details

Actioner	Cathie ALLEN
Organisational Unit/ s	Police Services
Service/ s	Forensic and Scientific Service
Site Location/ s	Coopers Plains

Investigation Details

Investigation Completed	13/05/2020	**Root Cause Type**	Other
Investigation Details	After email advice from Justin Howes, Team Leader for Forensic Reporting & Intelligence Team, I advised John Doherty, Executive Director of possible inappropriate access of the Forensic Register to FSS data prior to peer review. I provided the screenshot of the Forensic DNA Analysis profile determination analysis page from the FR which highlighted [redacted] as the last staff member to access this page. No staff member in Police Services Stream (or SSLU or FPP) that access the FR has the surname of [redacted] However there is a Sgt Dale Fletcher that works in the QPS Cold Case Unit. Further to this, on the 12th of Feb 2020 (10.40am), I was provided with email advice from Justin Howes regarding a screenshot of the		

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Cheers Cathie

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We accept that his unintentional change took place at our end.

In conclusion it shows that they greater degree of cooperation and information sharing between our departments is ensuring that the people of Queensland are being well served.

Have a great weekend.

Bruce McNab BM

Superintendent [redacted]

Operations Commander

Forensic Services Group

OPERATIONS SUPPORT COMMAND

Queensland Police Service

[redacted]

Preformed By Cathie ALLEN

Action Details

Action Complete 13/05/2020 **Action Fix Type** No Action PossibleFurther equiries

Title made with the QPS

Action Description Numerous enquiries have been made with the QPS for more specific information to address the dot points originally requested:

- How did it occur that QPS staff who have Results Management or Quality access were also provided with access to Forensic DNA Analysis Exhibit Testing and Profile Data assessment information?
- When did this change occur? (noting the removal of access was on Wednesday, 12th of Feb, prior to or at 2pm).
- What did the QPS staff do with the information that they had available to them?
- Who authorised the change to occur?
- Why was FSS not advised of this change prior to it occurring?

To date, no further information has been provided to FSS regarding this.

Task Details

No Tasks found

Follow-up And Approval

Follow-up Status Accepted

Follow-up Status Comment 15/05/2020 4:11:32 PM Justin HOWES:

It appears specific questions remain unanswered for now. Should answers be received, it is highly recommended that these are retained/linked to this OQI.

Approver Andrea NORTON

Approval/ Rejection Date 21/05/2020

Approval/ Rejection Comment 21/05/2020 8:43:08 AM Andrea NORTON:

Nothing further to add

Associations

No Associations found

Records

No Records found

[redacted]QPS accessing Forensic DNA Analysis Information

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Queensland Health

Forensic and Scientific Services

Procedure for the Release of Results using the Forensic Register

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1 Purpose

The purpose of this document is to describe the procedure for release of results using the Forensic Register to our clients for the following formats:

- Exhibit Report results/Profile Data Analysis results
- Reports
  - Statements
  - Evidentiary Certificates
  - Intelligence Reports

2 Scope

This procedure applies to all reports and results within the FR issued by Profile Analysts and Reporting Officers to clients.

3 Definitions

Result line(s) – also referred to as Profile Data Analysis Results are electronic results sent directly to the Queensland Police Service (QPS).
Statement of Witness – report containing a summary of results and other relevant information relating to a case for use in court.
DNA Evidentiary Certificate – report issued in accordance with s 95A Evidence Act 1977 (Qld).
Intelligence Report – a report containing information that may not be included in a statement for evidentiary purposes.
Case Officer – Officer allocated to or conducted a task within the Forensic Register; eg, profile analysis, review, statement drafting/issuing, case communication
Personal Work List (PWL) – list which highlights activities allocated to an individual staff member
Reporting Officer/Scientist – Staff member who performs profile data analysis and issues evidentiary statements
Profile Data Analyst / Profile Analyst – Staff member involved in profile data analysis
Sample Management – interpretation and management of a single sample
Case Management – management of the entire case; view of all samples

CPT – Case Profile table
DRMU – DNA Results Management Unit (QPS)
EB – Extraction Batch
FSS – Forensic and Scientific Services
Forensic Register (FR) – Forensic DNA Analysis LIMS
LIMS – Laboratory Information Management System
LR – Likelihood Ratio
P+ – ProfilerPlus® DNA amplification kit
PP21 – PowerPlex® 21 DNA amplification kit
PDA – Profile Data Analysis
PSD – Police Services DNA
QIS2 – Quality Information System version 2
QPS – Queensland Police Service
SMU – Sample Management Unit (QPS)
SSLU – Scientific Services Liaison Unit (FSS)
STRmix™ – Software used to assist profile interpretation and Likelihood Ratio generation

4 Exhibit Report Result Release

This section focusses on the review of a DNA profile interpretation completed by a Profile Analyst and the release/transfer of said DNA information to the client.

The following information will cover:

- Review Worklists and navigation to these worklists,
- Worklist information display,
- Order of samples displayed in these worklists, and
- Reviewing a profile data analysis record and release of results to the client

4.1 Profile Review Worklists

A DNA profile is ready for review when it populates an appropriate 'Profile Data Analysis Review Worklist'. A Profile Analyst will work from one of four profile data analysis review worklists, as discussed in section 4.1.1:

As the titles suggest, the review worklist for PP21 are for DNA profiles processed using the PowerPlex® 21 amplification system. The 'UK' worklist, refers to 'Unknown' and is used to capture DNA profiles where the amplification chemistry has not been identified; rare event.

4.1.1 Navigating to Profile Review Worklists

The PP21 and P+ samples can be located by following these steps:

- From the Main Menu click the 'Unit Work List' tab
- Click on the 'Unit Work List' again to reveal a dropdown list
- Navigate to 'Sample Management' and select
- Navigate to the tab 'Worklist' and select to reveal a drop down list
- Move the cursor to 'Profile Review' which will display a set of five lists (see **Figure 1**)
    - 'Case Work PP21'
    - 'Case Work PP21 (P3)'
    - 'Case Work Unknown'
    - 'Case Work +Ref'

The above first three steps can be by-passed by adding 'sm' in the search bar on the main menu and entering; this will navigate to the screen displayed in ***Figure 1***

The Review Worklists are described in section 4.2.

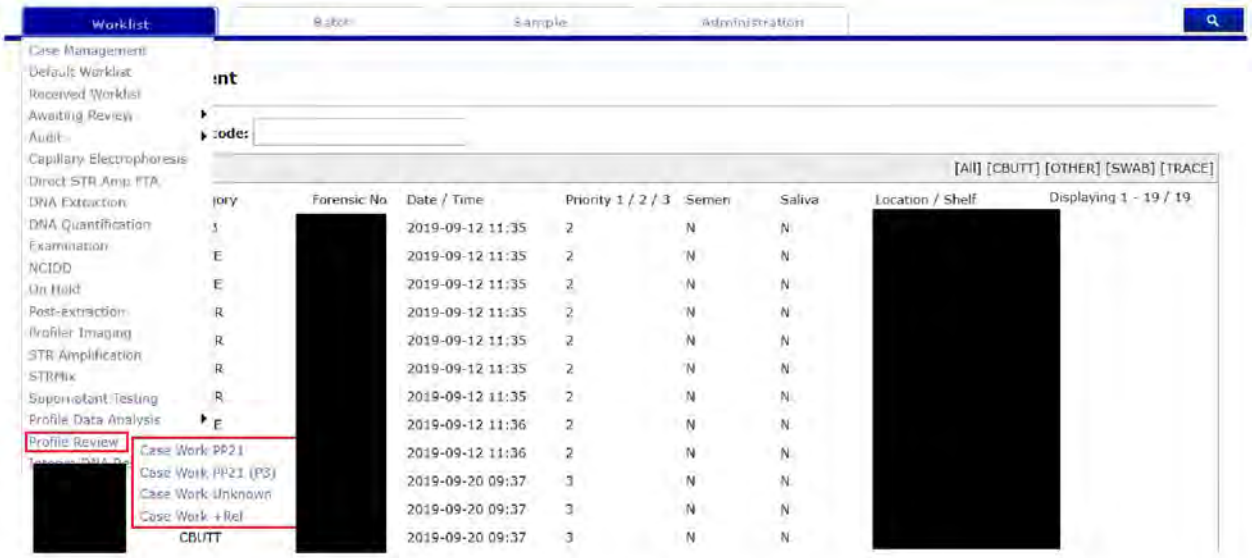
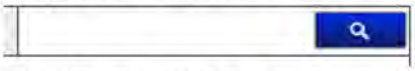


Figure 1 – Navigating to Profile Review Worklists

A specific sample can be located by entering the barcode into the search bar



located on a number of screens within the FR; eg, '*Main Menu*', and '*Worklist*' tab.

The sample will open on either the case management or sample management side of the FR depending on whether the search bar utilised was on the case management or sample management tab.

Figure 2a displays the result of a sample search opened on the case management side (note, image is a portion of the full page) and **Figure 2b** shows the result of a sample search opened on the sample management side.

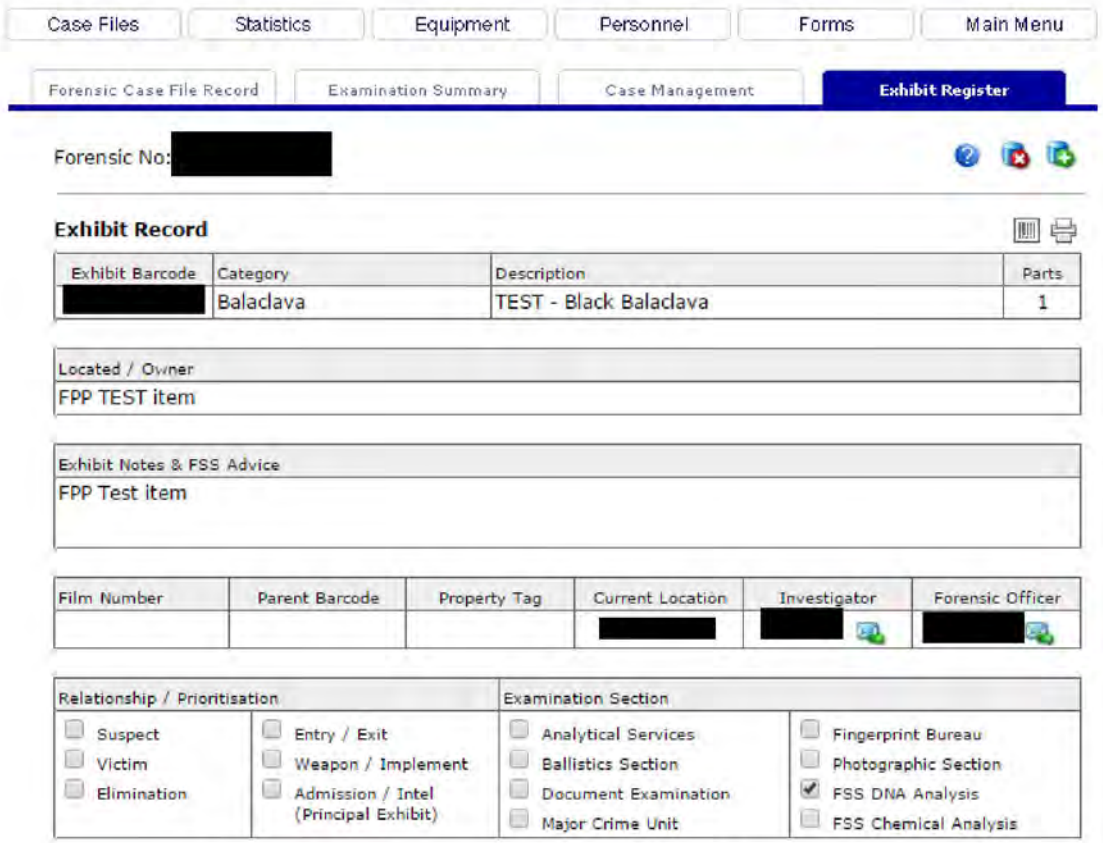


Figure 2a – Sample Search via Search Bar (Case Management side)

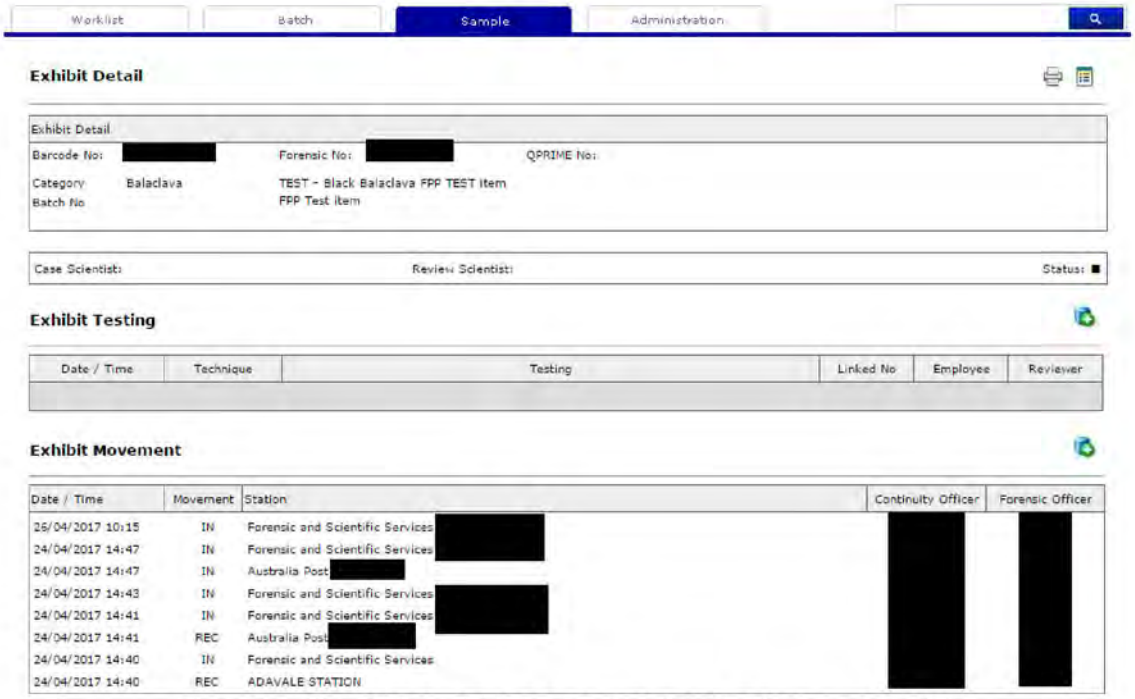


Figure 2b - Sample Search via Search Bar (Sample Management side)

Alternatively, a barcode search aid

▼ **Barcode:** [ ] is located on the upper left hand side of all sample management and review worklists. Entering a specific barcode and pressing *enter* will navigate to the page on which the sample is located. This function will take the scientist to the specific page but will not highlight the sample amongst the list. Where multiple pages exist in the review worklist, a specific page can be navigated to by clicking on the downward facing triangle to the left of the above barcode search field.

4.2 Profile Review Worklist Displays

The profile review worklists are configured to display information about the sample to enable ease of review. **Figure 3** defines this information.

Note - PP21 and the Unknown review worklists have been developed in the same format with the same business rules.

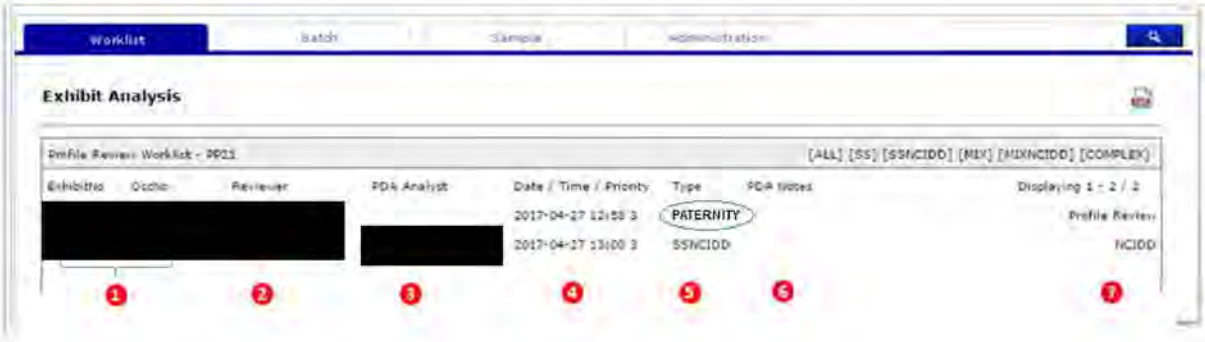


Figure 3 - Review Worklist Displayed Information

- 1 Identification information of the sample
- 2 Allocated reviewer for an entire case – if a Profile Analyst has not been allocated to complete the review of all samples, this field will be blank
- 3 Profile Analyst who performed the profile data analysis
- 4 Information used to prioritise the sample on the worklist. The date and time is the date and time of the first Exhibit Report entry added against the sample. For the majority of instances this will coincide with the exhibit report entered by an Evidence Recovery staff member.
- 5 Summary of the DNA profile interpretation as a function of the result in the 'Contributors' field in the '*Profile Interpretation*' table on the profile data analysis screen, combined with NCIDD upload information – **Table 1** shows the possible entries.
    - Samples in the form of reference samples received for Paternity evaluation, will be highlighted with 'PATERNITY' in the 'Type' field (see green circle in **Figure 3**). Product of Conception (POC) samples will not display on a PDA worklist with this 'Type'

'Contributors'	+ '+NCIDD'	= Profile Type
1	No tick	SS
NP	No tick	SS
PU	No tick	SS
1	Tick	SSNCIDD
2 or 3	No tick	MIX
2 or 3	Tick	MIXNCIDD
CX	No tick	COMPLEX

Table 1 – 'Type' Information

- 6 Information within the 'Notes' section on the PDA page added by the Profile Analyst will be viewed in this field. Example; '15' pk @ D16 considered as high stutter' or 'CMPU – sub thresh info @ D21'
- 7 Information regarding the progress of the sample through sample management is captured from the 'Exhibit Testing' table on the case management side of the FR

4.3 Sample Order, Filtering Results and Populating and Removal from a Worklist

The worklists are configured to display samples in the following order:

- Samples that you are the nominated reviewer followed by;
- Priority – priority 1, priority 2, and 3 in a descending order, followed by;
- Date and time to further separate those samples of the same priority, in descending order
    - The date and time is the date and time of the first entry added to the "*Exhibit Testing/Examination*" table; eg, 'In-tube check', 'Result', 'Notation'

4.3.1 Filtering Samples on the Review Worklists

The PDA review worklists are able to be filtered so that only DNA profiles of a specific category are viewed.

This is achieved with a few simple tile selections as described in the following:

- Navigate to the tiles in the top righthand corner of the table (See **Figure 4**)



Figure 4 - Tiles for Filtering

- Select one of the tiles, eg, the [SSNCIDD] tile = this will filter the worklist and only display those DNA profiles which have been assessed as a single source profile allocated to be uploaded to NCIDD (see **Figure 5**). This can be completed for all types of profiles listed in **Table 1** of this document.



Figure 5 - Filtered Worklist = SSNCIDD

- To display all DNA profiles again, select the [ALL] tile

4.3.2 Population and Removal of Samples from a Review Worklist

A sample will populate a review worklist when a 'Profile Review' process is ordered by the Profile Analyst. This process will also trigger the removal of the sample from the PDA worklist.

Samples will be removed from the review worklists by one of the following rules:

1. Validating the 'Profile Review' in the *Exhibit Testing* table
2. Clicking on the '[CLICK TO REWORK]' field in the 'Profile Review' result when ordering further processing, see **Figure 36**
3. Incorrecting the 'Profile Review'

4.4 Exhibit Report Review

The review and validation of results transfers evidentiary information to the clients via the validation of report line(s) for an exhibit. This process involves the review of various aspects of profile interpretation which include:

- External notes/information
- Exhibit image(s)
- Exhibit descriptions
- Examination/processing
- DNA profile interpretation
- Report line(s)

4.4.1 Notes and Information

External notes/information such as [redacted] and Government Medical Officer (GMO) notes will be stored against a 'Case File Notation' usually created by a Property Point staff member. This information can be located by selecting the 'Case Management' tab and searching for a 'Note' that is linked to the specific exhibit you are reviewing. The following steps outline this process:

<u>SAIK – GMO notes</u>

- Select the 'Case Management' tab,
- Navigate to the entry with 'Report Type' *NOTE* and the comment 'SAIK medical notes' or equivalent (see **Figure 6**).
- Click on the 'Forensic Officer' ID associated to the record to reveal a 'Case Report' page with the GMO notes as a '.pdf' file (see **Figure 7**)

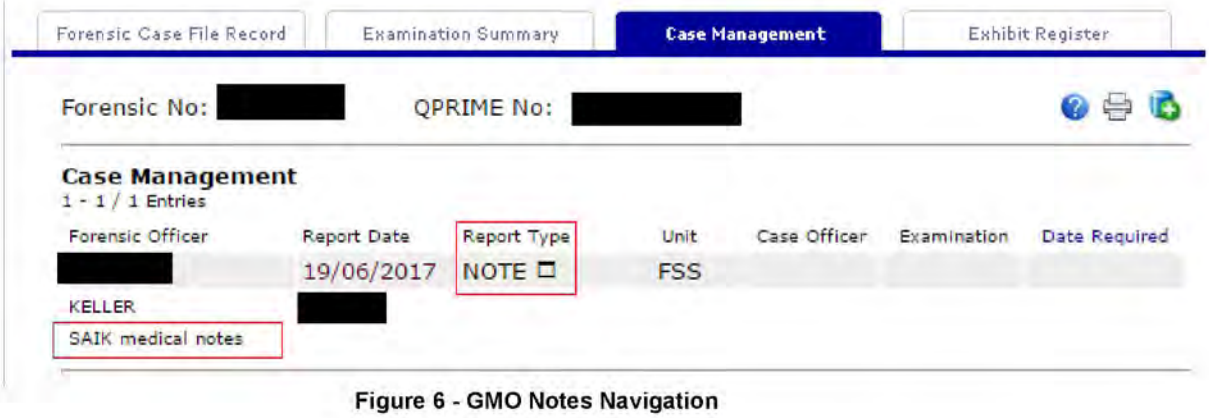


Figure 6 - GMO Notes Navigation

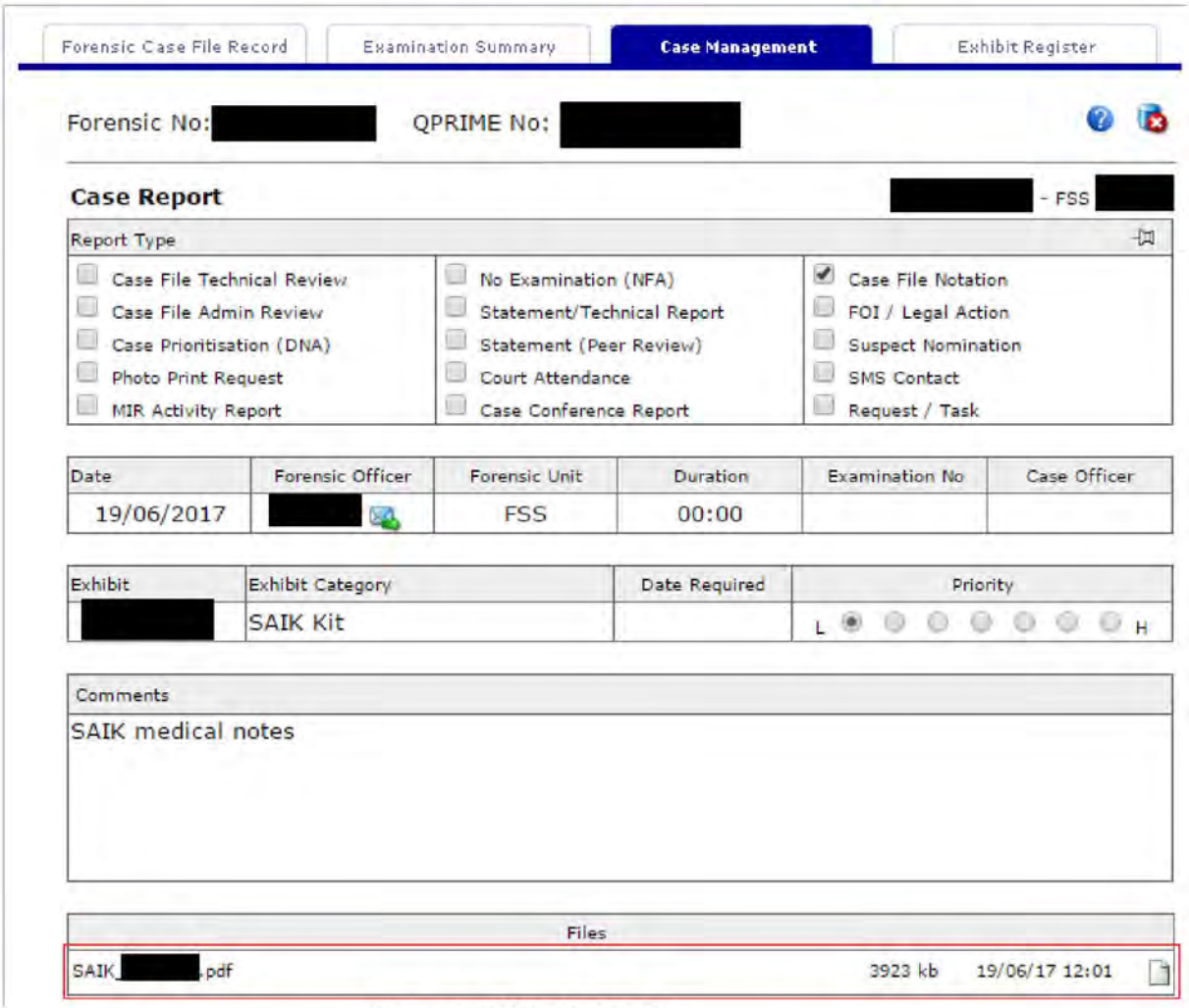


Figure 7 - GMO Notes '.pdf'

- Click on the '.pdf' to open the GMO notes

4.4.2 Image(s)

The review of exhibit images/photos is completed by Evidence Recovery staff, where any discrepancy is investigated and resolved (see section 4.4 of QIS: 33771 'Examination of in-tube sample (Forensic Register)'. However, it is good practice for the Reviewing Scientist and the Profile Analyst to check this information as well.

All exhibits received within the laboratory will have images loaded to the FR by the QPS officers of the packaging and where applicable the exhibit. The images will be located in the 'Exhibit Images' table, on the 'Exhibit Record' page of an exhibit (see **Figure 8**). These images should be assessed to ensure they meet the requirements of the laboratory; image quality, correct image attached to the record and the description matches that registered in FR.



Figure 8 - Exhibit Images

Where additional images are required for quality aspects or as part of an examination they will be added to the FR in a number of ways dependent on the sample type.

In-tube Samples

For in-tube samples, additional photos will be added against a 'Notation' by an Evidence Recovery staff member. If a 'Notation' has been added it will be located in the 'Exhibit Testing' table, see **Figure 9.**

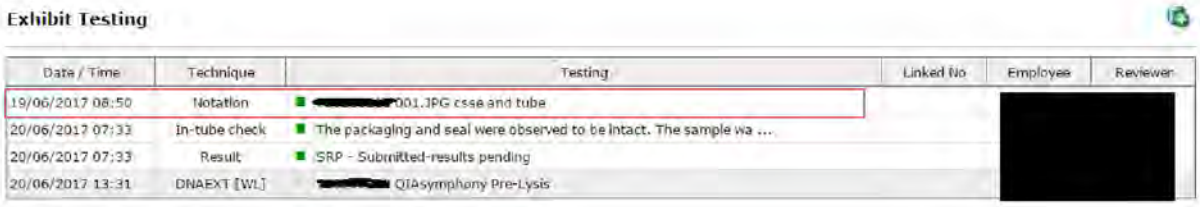


Figure 9 - Further Images

The image can be viewed by clicking on the 'JPG' in the 'Testing' column against the 'Notation' or by following the steps listed below.

- Click on the Date/Time stamp
- Click on the JPG attachment to view the additional image; see **Figure 10**
- The 'Notes' table will detail the reasoning for an extra image; see **Figure 10**

Forensic No: [redacted] QPRIME No: [redacted]

Exhibit Record

Exhibit Barcode	Category	Description	Parts
[redacted]	Swab - Blood	G, dry stain, ceramic	1

Located / Owner
tile floor in master bedroom en-suite

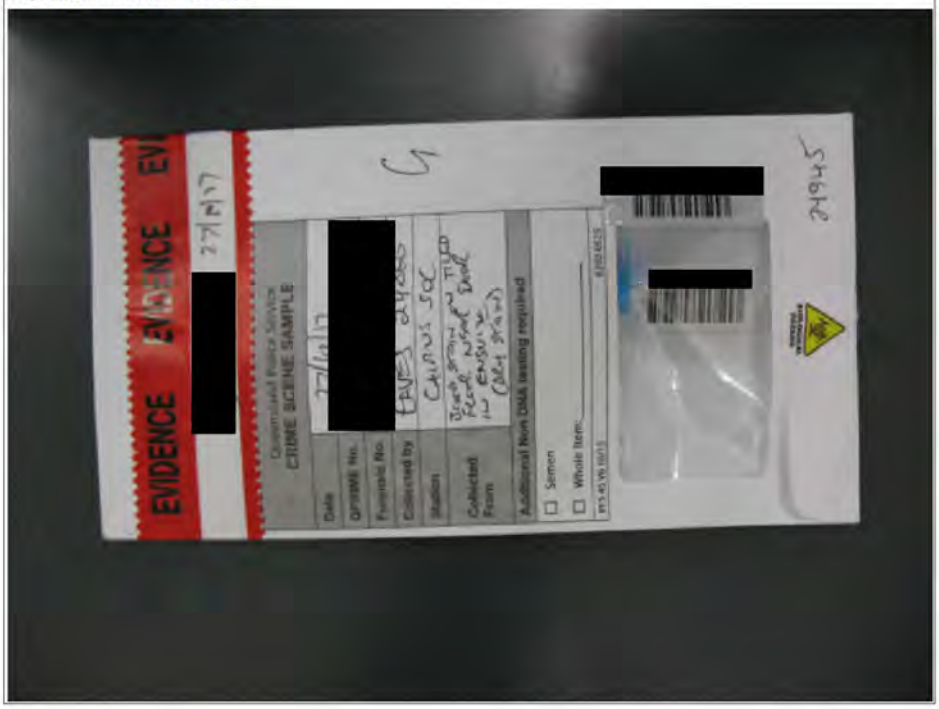
Exhibit Notes & FSS Advice
victim reported to have been assaulted in en-suite

Testing / Analysis [redacted] SB.DATAFTCU[OSC], PSD FSS

Date	Process	SubID	SubType	Equipment No
04/12/2017 08:04	Notation			

Notes
Csse and tube

Attachment: 791739132 001.JPG



Storage Rack ID	Position	Tube Lot No	Volume (µL)	Priority
				1 2 3

Change Log			
2017-12-04 08:05	CURRENT	[redacted]	SYSTEM

Figure 10 - Additional Image

Whole Items

Whole items include, but are not limited to, a Sexual Assault Investigation Kit (SAIK), a package containing multiple cigarette butts, or a piece of fabric required for semen analysis. Where additional images are required these will be added in the following ways:

Extra photos of packaging, or general images taken of the exhibit will be stored in the 'Exam Images' table within the Examination List table on the case management side of the FR. The following steps detail how to locate this information:

- Click on the 'Forensic Officer' ID of an entry (see **Figure 11**)
- Navigate to the 'Exam Images' table (see **Figure 12**)
    - Click on an image to open the image



Figure 11 - Stored Image(s)



Figure 12 - Exam Images

Alternatively, the same entry can be listed under the 'Examination Summary' tab, along with all other 'Examination/Reports associated to the case. To view these images complete the following steps:

- Select the 'Examination Summary' tab to display 'Examination/Reports' table (see **Figure 13**)
- Where multiple entries exist against an Occurrence Number, locate the item of interest (see red box)
- The icon (green circle) indicates that images exist under this entry
- Click on the employee ID associated to the entry to display the image(s)
- Images will be located in the 'Exam Images' table (see **Figure 12**)

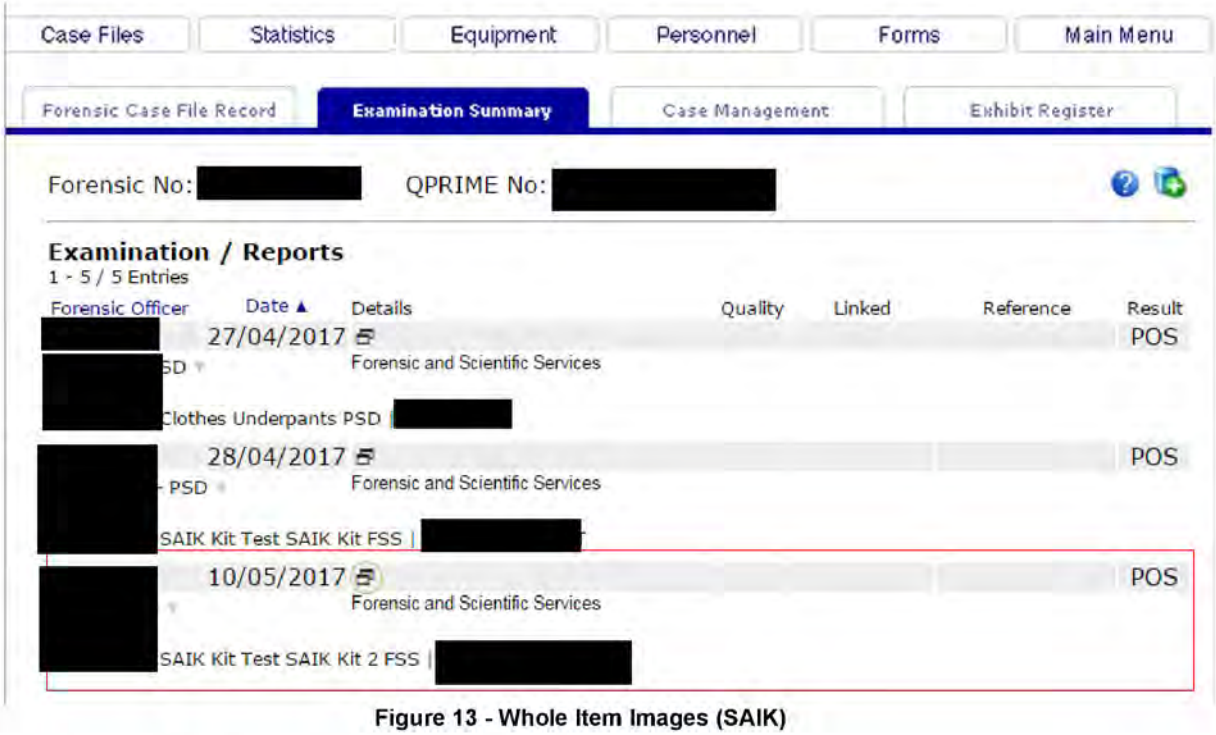


Figure 13 - Whole Item Images (SAIK)

Images detailing screening results will be added against a 'Notation' or a specific 'Technique/Result', both of which can be located in the 'Exhibit Testing' table.

In general, a photo displaying an AP positive area on a fabric will be added against a 'Notation' whereas an image displaying microscopic information will be added against the 'Microscopic' technique. The following example using a High Vaginal swab details how to locate and view an image associated to a 'Microscopic' examination:

- Navigate to the 'Exhibit Testing' table (see **Figure 14**)
- Click on the 'Date/Time' stamp against the 'Microscopic' technique or result
  - This will open the microscopic result
- Navigate to the 'JPG' attachment (see **Figure 15**)
- Click on the 'JPG' to open the image



Figure 14 - Microscopic Result Image



Figure 15 - Microscopic Result 'JPG'

Note, the same steps will be used to view an image associated to a 'Notation' – simply look for a 'Notation' in the Exhibit Testing table.

4.4.3 Descriptions

Labelling information can be cross referenced, by comparing the information contained on the exhibit package from an image(s) to the information located on the *'Exhibit Record'* or *'Exhibit Detail'* tables.

Packaging photos containing labelling or an adhesive label with the item description can be found as per information in section 4.4.1 and 4.4.2 of this document.

Where discrepancies exist, which have not been highlighted, follow the process detailed in section 4.4.15.

4.4.4 Review of Examination

Although a review of the examination will have been completed by Evidence Recovery, it is important to assess the examinations performed on each exhibit/sample in conjunction with examination strategies, where applicable, formulated from the history of the case.

This section will describe where to find examination information, strategies and records for exhibits. The following sections will focus on a whole exhibit with sub-samples such as a Sexual Assault Investigation Kit (SAIK), and a simpler exhibit, an in-tube.

SAIK

A SAIK consists of multiple components which if required for DNA profiling will be registered into a stand-alone exhibit for reporting purposes. Each of these components will have their own examination records with the SAIK containing information/records such as notes, packaging details, additional images and an examination strategy, discussed in section 4.4.1.

The review of a SAIK, from a paperless perspective, will usually commence from a sub-sample which has populated a review list. The following will explore the review of a SAIK starting with the High Vaginal swab, progressing to navigating through the FR to gain information about the SAIK and the individual components.

- High Vaginal swab (HVS)

Entering the HVS from the 'Profile Review Worklist – PP21' will display the HVS summary screen (see **Figure 16**).

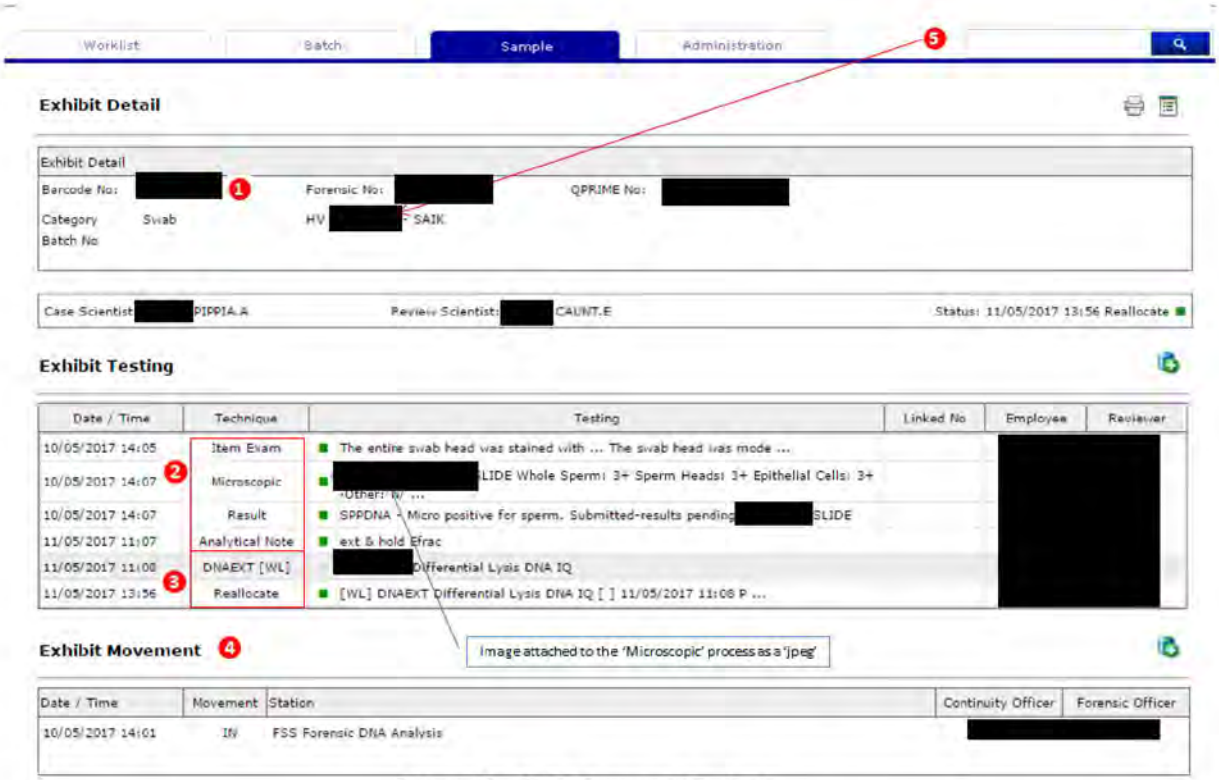


Figure 16 – HVS Summary Screen

From this screen the reviewer can access examination information about the sample:

- 1 click on the barcode to get to the 'Exhibit Record', which contains information such as:
    - 'Exhibit Movement' – storage information
    - 'Examination List' – details of the examination; date, time, duration, forensic officer, etc
    - 'Link Chart' - shows all associations to original exhibit, eg, SAIK barcode, other sub-samples and barcodes generated during the evidence recovery and analytical processes – **Figure 17**). Navigate to the SAIK or associated sub-samples by hovering over the barcode and clicking
    - 'Exhibit Testing' table – discussed below

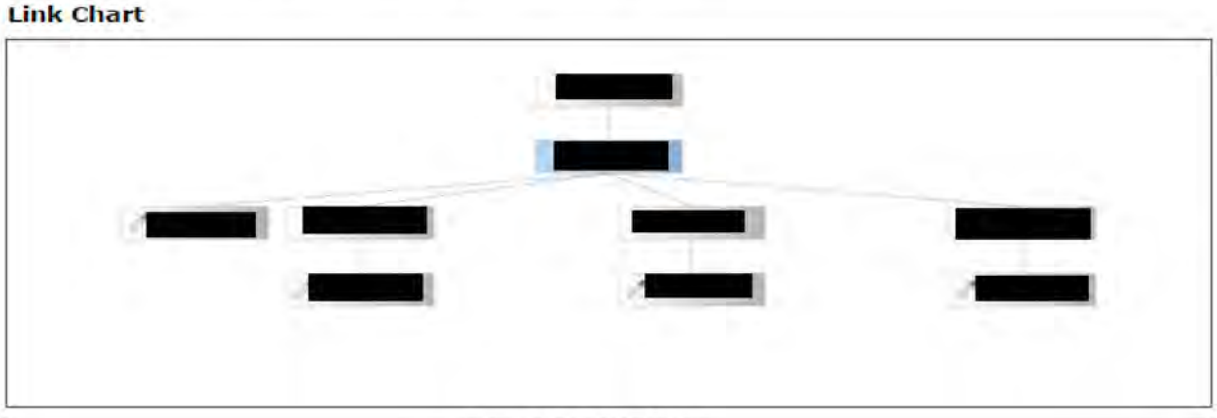


Figure 17 - Link Chart

- 2 Evidence Recovery testing and results can be viewed by clicking on the 'Date/Time' stamp associated to the specific technique. The procedure under QIS: 34298 'Validation of Examinations (Forensic Register)' discusses how the exhibit examination validation process occurs and lists all relevant standard operation procedures in the 'Associated Documentation' section
    - 'Item Exam' process will display information about the examination conducted on the HVS, including a physical description of the item, consumable 'Lot No', sample priority, examining scientist ('Change Log') and the reviewing scientist (see **Figure 18**)
    - 'Microscopic' process will display information about the microscopic examination performed (see **Figure 19**)
        - A 'JPG' file may be attached as displayed by the information circled in blue
    - 'Result' will display result line information for the item (see **Figure 20**)
    - 'Analytical Note' process will display notes entered by Evidence Recovery for downstream Analytical processing (see **Figure 21**)

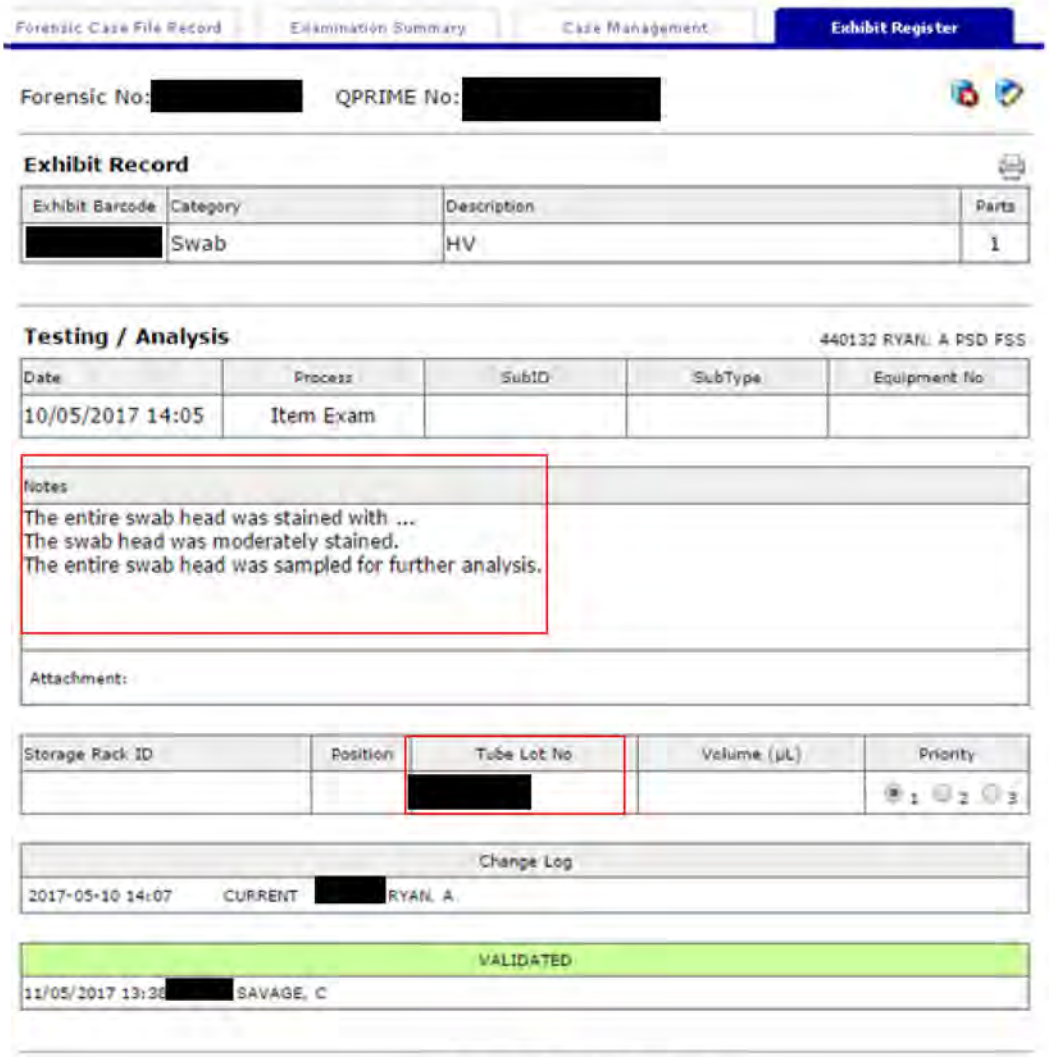


Figure 18 - Item Exam

Testing / Analysis

440132 RYAN, A PSD FSS

Date	Process	SubID	SubType	Equipment No
10/05/2017 14:07	Microscopic	[redacted]	SLIDE	[redacted]

Results of Microscopy Examination		
(•) Spermatozoa were detected.	( ) No spermatozoa were detected.	( ) No result.

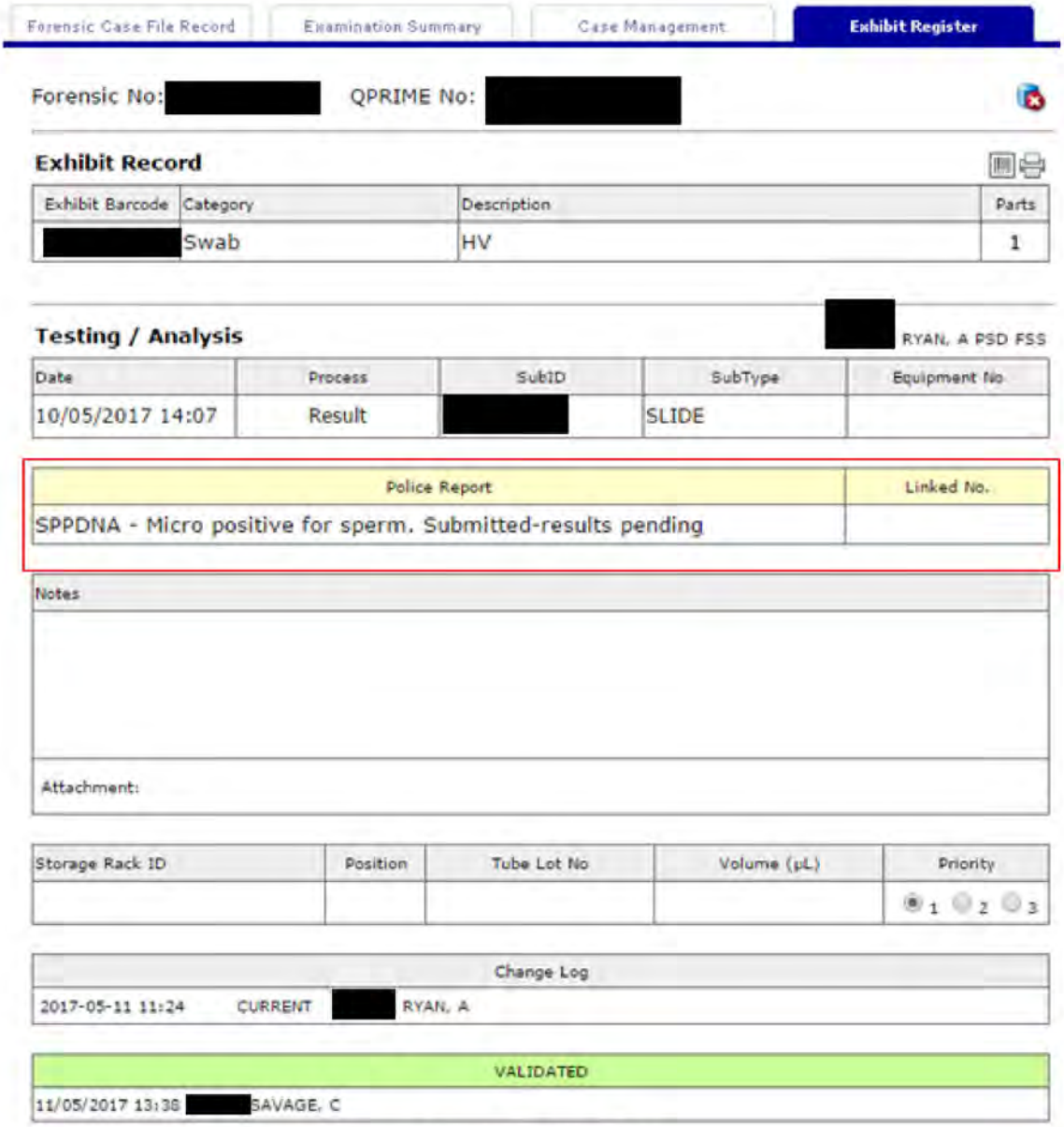
Reagents				
[redacted]				
HE Stain				

Notes
Whole Sperm: 3+ Sperm Heads: 3+ Epithelial Cells: 3+ Other: N/A Magnification: x400
Attachment: 001.JPG

Attached Image

Storage Rack ID	Position	Tube Lot No	Volume (µL)	Priority
			175	(•) 1 ( ) 2 ( ) 3

Figure 19 – Microscopic Process Records



Forensic Case File Record | Examination Summary | Case Management | **Exhibit Register**

Forensic No: [redacted] QPRIME No: [redacted]

Exhibit Record

Exhibit Barcode	Category	Description	Parts
[redacted]	Swab	HV	1

Testing / Analysis [redacted] RYAN, A PSD FSS

Date	Process	SubID	SubType	Equipment No
10/05/2017 14:07	Result	[redacted]	SLIDE	

Police Report	Linked No.
SPPDNA - Micro positive for sperm. Submitted-results pending	

Notes

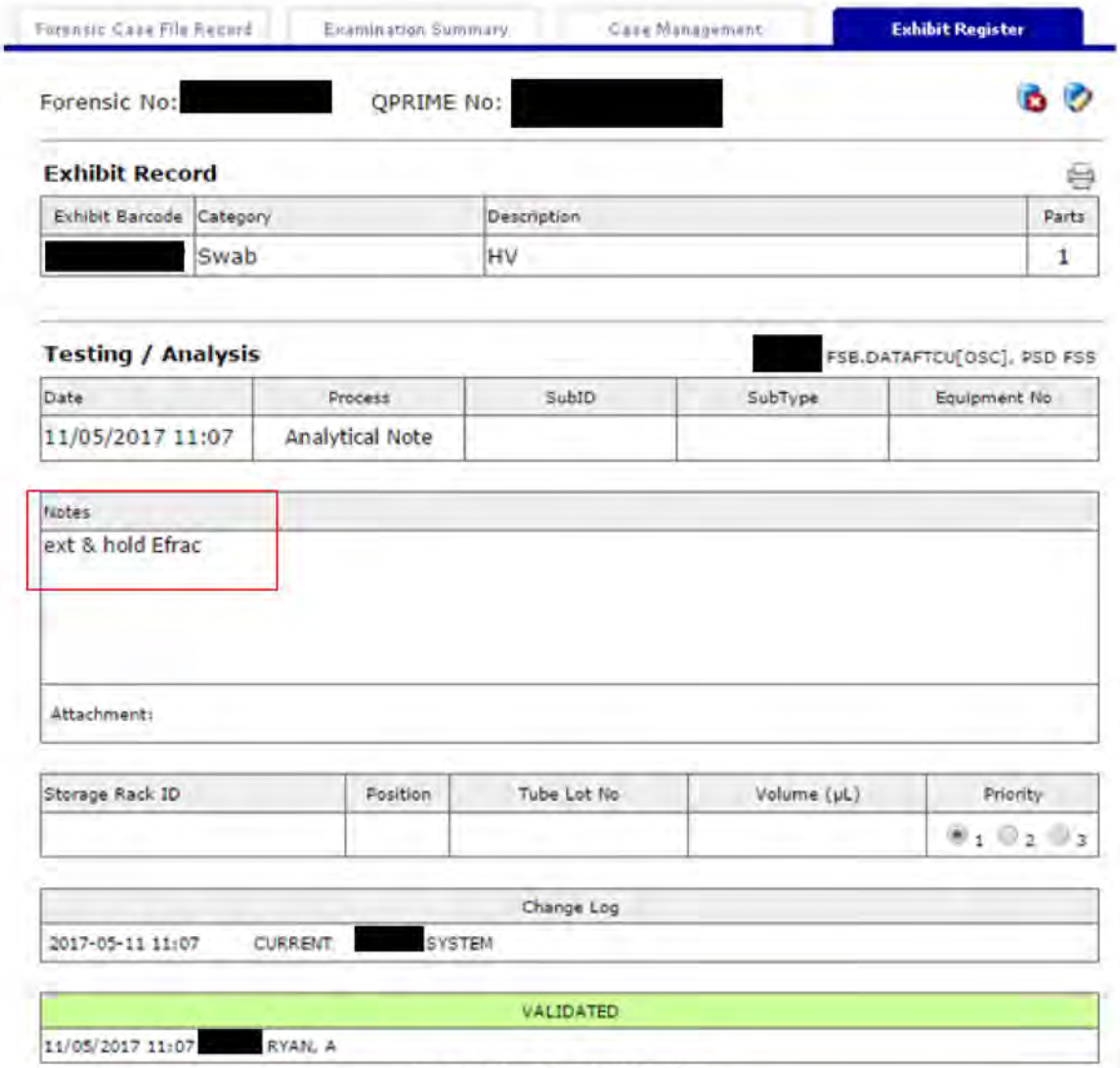
Attachment:

Storage Rack ID	Position	Tube Lot No	Volume (µL)	Priority
				1 2 3

Change Log
2017-05-11 11:24 CURRENT [redacted] RYAN, A

VALIDATED
11/05/2017 13:38 [redacted] SAVAGE, C

Figure 20 – Result Line



Forensic Case File Record | Examination Summary | Case Management | **Exhibit Register**

Forensic No: [redacted] QPRIME No: [redacted]

Exhibit Record

Exhibit Barcode	Category	Description	Parts
[redacted]	Swab	HV	1

Testing / Analysis [redacted] FSB.DATAFTCU[OSC], PSD FSS

Date	Process	SubID	SubType	Equipment No
11/05/2017 11:07	Analytical Note			

Notes
ext & hold Efrac

Attachment:

Storage Rack ID	Position	Tube Lot No	Volume (µL)	Priority
				1 2 3

Change Log

2017-05-11 11:07 CURRENT [redacted] SYSTEM

VALIDATED

11/05/2017 11:07 [redacted] RYAN, A

Figure 21 - Analytical Notes

- ❸ Analytical processes undertaken on the sample will be recorded in the 'Exhibit Testing' table. The process along with the batch ID will be displayed
    - The individual batch can be selected to open the batch to reveal information about the sample position, operator, batch status, and consumables
- ❹ The 'Exhibit Movement' table shows the storage of the HVS sample within the laboratory

- SAIK (whole exhibit)

Information pertaining to the SAIK can be viewed by navigating to the SAIK barcode via one of the following steps:

- ❺ cut and paste the parent barcode into the search field; top righthand corner of page **OR**

- Click barcode of HVS 1 which displays the 'Exhibit Record' page and from here
  - navigate to the 'Link Chart' and click on the SAIK barcode
  - click on the '*Exhibit Register*' tab and search for the SAIK barcode and select

Once on the SAIK page, testing/results can be viewed by clicking on the 'Date/Time' stamp associated to the specific information required within the 'Exhibit Testing' table (see **Figure 22**):

Exhibit Testing

Date / Time	Technique	Testing	Employee	Reviewer
10/05/2017 13:32	Notation	[redacted] MISC SAIK exam strategy - examine s ...	[redacted]	[redacted]
10/05/2017 13:35	Examination [WL]	[redacted] In-tube Manipulation		
10/05/2017 13:42	Item Exam	The packaging and seal were ob ...		

Figure 22 – Exhibit Testing table

- SAIK examination strategy by clicking the 'Notation' technique (see **Figure 23**)

Forensic Case File Record | Examination Summary | Case Management | **Exhibit Register**

Forensic No: [redacted] QPRIME No: [redacted]

Exhibit Record

Exhibit Barcode	Category	Description	Parts
[redacted]	SAIK Kit	Test SAIK Kit 2	1

Testing / Analysis

[redacted] FSB.DATAFTCU[OSC], PSD FSS

Date	Process	SubID	SubType	Equipment No
10/05/2017 13:32	Notation	[redacted]	MISC	

Notes

SAIK exam strategy - examine swabs for semen
AR - agree with SAIK strategy

Attachment: 20170510-690636371.pdf

Storage Rack ID	Position	Tube Lot No	Volume (µL)	Priority
[redacted]				1 2 3

Figure 23 – SAIK Exam Notes

- Packaging and seal information by clicking on the 'Item Exam' technique/process (see **Figure 24**)

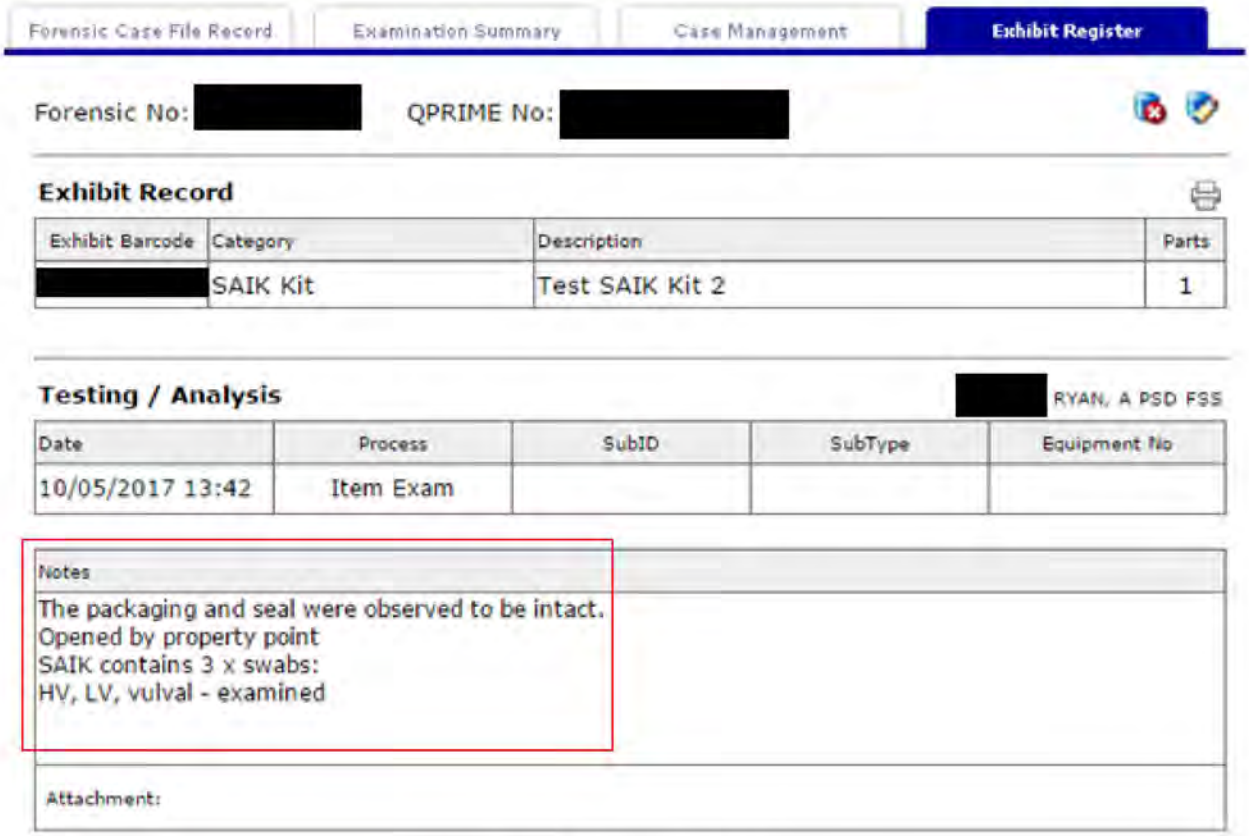


Figure 24 - SAIK Packaging Details

- Examination summary by clicking on the *'Forensic Officer'* ID in the 'Examination List' table (see **Figure 25**)

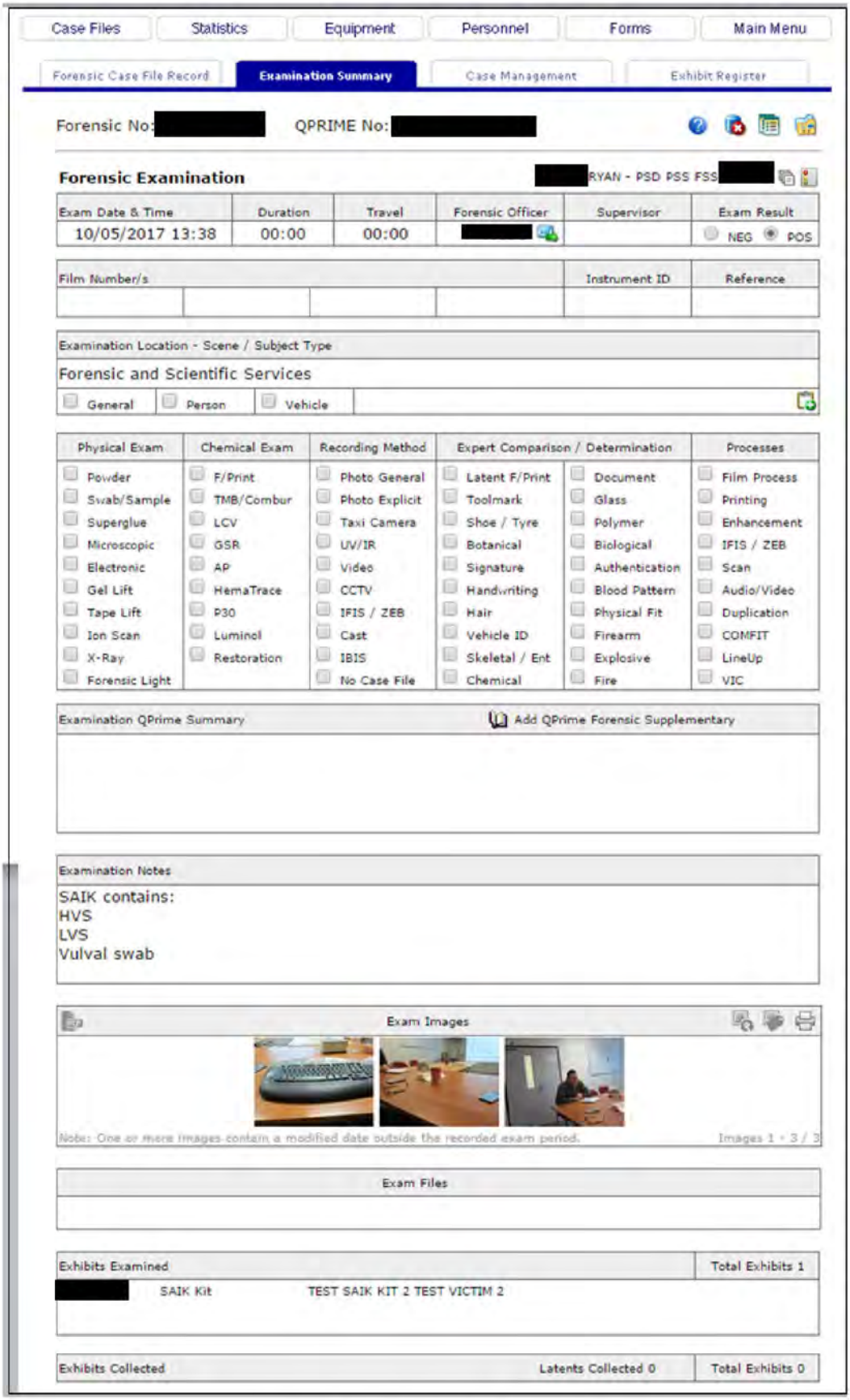


Figure 25 - Examination Summary (SAIK)

4.4.5 Exhibit Overview of the Case

An overview of all exhibits and samples associated to the case can be displayed in a number of ways. This information is located on the case management side of the FR from the 'Exhibit Register' tab.

Clicking on the 'Exhibit Register' tab will display an exhibit list of all exhibits (scene samples and reference samples) for the case regardless of whether that item has been received at the laboratory or not. See **Figure 26**; note that the information has been taken from a training case and will not display items collected by QPS not transferred to the laboratory.

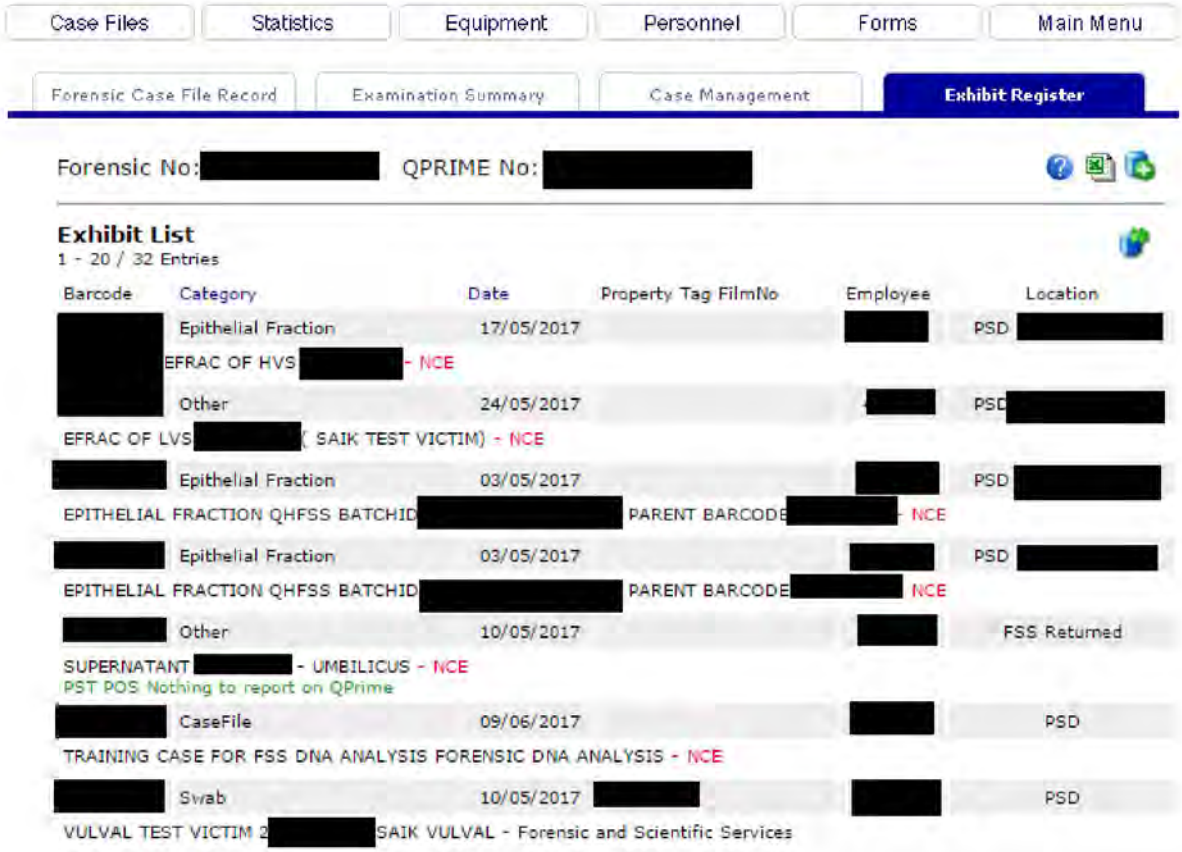


Figure 26 - Exhibit List

Information specific to Forensic DNA Analysis processing can be viewed by the following steps:

- Click onto the 'Exhibit Register' tab to enable the dropdown menu
- Navigate to 'DNA Analysis' which will open another dropdown menu
- Select one of the following options (See **Figure 27**)
    - 'All Exhibits' – displays all exhibits, sub-samples (spin basket, slide, supernatant and epithelial fractions where applicable)

- 'Single Source' – filters list to display DNA profiles nominated as a single source at the GMIDx plate reading phase
- 'Mixed Source' – filters list to display DNA profiles nominated as a mixture at the GMIDx plate reading phase
- 'Undefined' – filters to display DNA profiles with no or incorrect GMIDx comments
- 'Reference' – filters list to display reference samples associated to the case
- 'Evidence Cert – Profiles' and 'Evidence Cert – Analysis' are discussed in section 8
- 'Case File – Preview' – generates a combined pdf of all DNA profiles within the case
- 'Image Report' – displays all images taken and stored by FSS staff

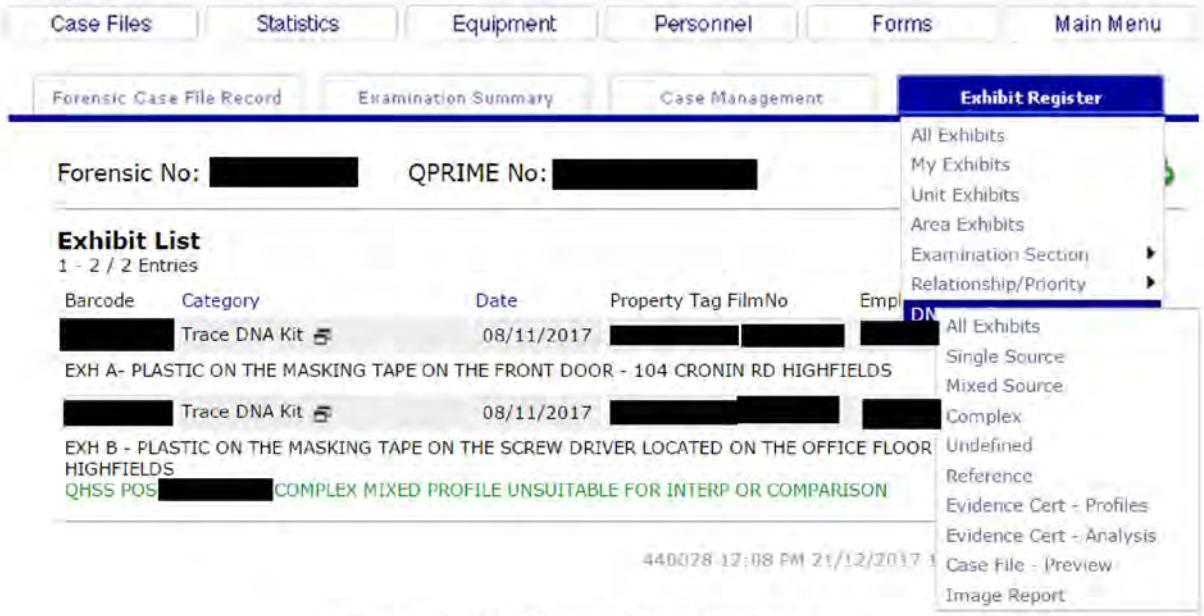


Figure 27 - DNA Specific Item Information

Alternatively, the FR displays a web of information titled 'Link Chart'. This can be opened by clicking on the icon (see **Figure 28**) on all exhibits received for testing on the following pages:

- Exhibit Testing page on the sample management side
- Exhibit Testing page on the case management side

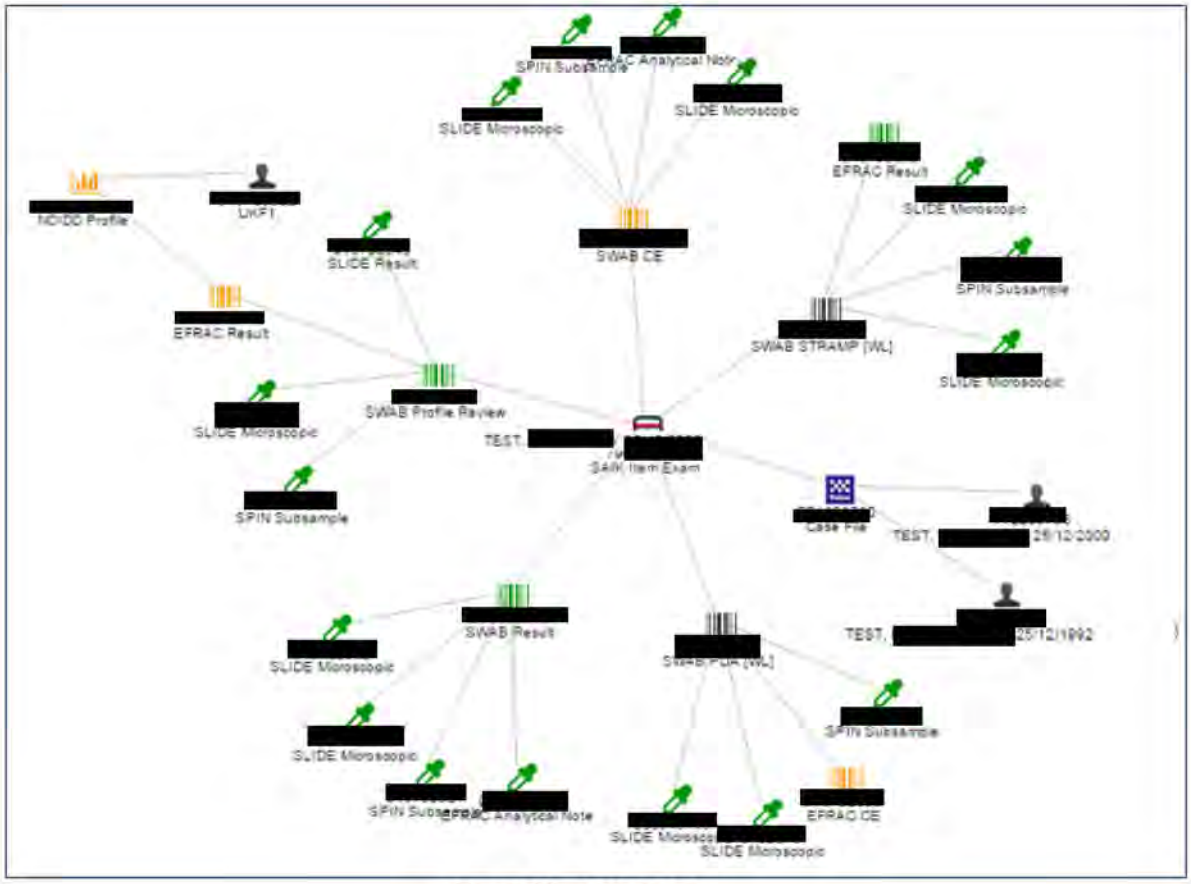


Figure 28 – Link Chart

4.4.6 Interpretation of the DNA Profile

It is important to perform an independent assessment of the DNA profile prior to reviewing the result obtained by the Profile Analyst. Procedures for the interpretation of a DNA profile are not included in this document, however, guidelines for the scientific interpretation of DNA profiling results can be found in QIS: 17117 'Procedure for Case Management'.

Information required to perform DNA profile interpretation within the FR is located within QIS: 33773 'Procedure for profile data analysis using the Forensic Register'. This document will highlight the functions and areas within the FR to gather the information to perform DNA profile interpretation and review.

Table 2 is a list of areas and functions within the FR used to complete DNA profile interpretation and the corresponding section within document QIS: 33773.

Function	Information	Section
Basic PDA function	# of Contributors; DNA profile resolution and upload; Reference comparison;	5
Quality control	Analytical batches; status indicators	6.1
GeneMapper ® Record	Profile PDF; GeneMapper information; amendments to the Genemapper file	6.2

Table 2 - PDA Information Repository

4.4.7 Further Processing of the DNA Profile

During the assessment of a DNA profile the reviewer may consider that further processing/reworking is required to either gain more information from the sample, check a specific component of a DNA profile or update the profile interpretation based on the receipt of a reference sample, conditioned mixture interpretation. If this is a consideration, then a discussion between the Profile Analyst and the Reviewer will follow. If it is decided that no further testing is required and the reasons are clear then the review is to continue without a note.

A note can be added to the 'Notes' or 'Sample Notes' field on the PDA page if there is a specific piece of information about the profile that will aid in future interpretation/reporting of the DNA profile.

Where it is decided that further processing is required, the Profile Analyst will order the appropriate rework as per section 11.2 within QIS: 33773. An accompanying note can be added to the 'Notes' field on the PDA page if desired.
In order to remove the sample from the review list the Profile Analyst will click on the '[CLICK TO REWORK]' (see **Figure 36**) button in the Profile Review process located on the Exhibit Testing table.

Reporting results after the completion of further processing or an interpretation update, specifically conditioned mixture interpretation, ensure the first result line is "Sample Undergone Further Testing" or applicable as per QIS: 34229 'Explanation of Exhibit Results for FR'. In this situation, the original result has been superseded and it is a requirement that the full complement of result lines describing the updated result are to be added.

4.4.8 Calculations and Notations

4.4.8.1 Calculations

A calculation will be entered at plate reading stage where a VAR/OLA/ULP/XOVER is calculated. This information will be located as a 'Calculation' in the 'Exhibit Testing' table, see section 11.7 in QIS: 33773. In most situations, this result will be validated however on occasion the original calculation may have been edited by the Profile Analyst and will require validation – details of which can be found in section 11.7, QIS: 33773.

For a DNA profile which has been determined to be 'Complex Unsuitable' and has a 'Calculation', the Profile Analyst is to add a comment such as "Complex profile, calculation review not performed" against the 'Calculation record. This comment is to be inserted at the top of the 'Comments' field so it is easily seen by the Reviewer.

4.4.8.2 Notations

A 'Notation' can be used to record notes against a sample and should be checked by the Reviewer for extra information about the sample being reviewed. This information will be located as a 'Notation' in the 'Exhibit Testing' table, see section 11.8 in QIS: 33773. Note, a 'Notation' will self-validate.

4.4.9 Profile Data Analysis Page Information

Once an independent interpretation of the DNA profile has been completed, the Reviewing Scientist will compare the information entered on the PDA page by the Profile Analyst.

Any information within the PDA page highlighted as being potentially incorrect needs to be discussed with the Profile Analyst. If the Profile Analyst is unavailable at the time the Reviewing Scientist can add a note to the 'Notes' field within the PDA page to highlight to other reviewers that this sample is being managed. This information will be visible in the 'PDA Notes' field within the review worklists (see 6 **Figure 3)**.

This information is summarised in **Table 3** and shows links to the associated sections within QIS: 33773.

Profile Interpretation – PDA page	Information	Section
Profile Analysis	All batches visible; All batches have a green square or a red square with appropriate batch acknowledgements * PDFs available Edits to GMIDx file accompanied with notes	
Profile Interpretation Table	Number of contributors; STRmix decon available (if applicable); Resolved Profiles match decon output information	7
Profile Record Table	Profile Interpretation; FR Database matching; Nomination of upload; Suffix added to all copied down profiles	8
Case Profiles Table	Reference samples associated to case (indicators ■ or ■ ▲ displays when DNA profile available and validated and if a crime scene sample has been nominated for upload that matches the reference sample; Unknown profiles nominated uploaded to NCIDD (■ ▲); Associations between Unknown profiles and Reference Samples completed where applicable; Matching DNA Intel samples added to CPT where applicable	9
Sample Notes	Details about the DNA profile and DB search information	
Notes	Information about DNA profile; eg, 'Complex – D18'	

Table 3 - PDA information

* Where a batch comment has not been reviewed by the Profile Analyst, the Review Scientist is to acknowledge the batch comment. If there is a critical element that could have affected the sample processing or interpretation strategy and there is no note from the Profile Analyst, the Reviewing Scientist needs to discuss this with the Profile Analyst to ensure the point is covered. A batch acknowledgement should then be added prior to the results being validated.

4.4.9.1 Profile Interpretation and Profile Record Information Difference – PP21 vs P+

As of January 2018 all Priority 3 samples were amplified using the PowerPlex® 21 DNA amplification kit due to ProfilerPlus® DNA amplification reagents no longer being manufactured. Information specific to Profiler® Plus processing has been retained in this

document as this information may still be required for sample management and or reporting purposes.

When reviewing a P+ sample vs a PP21 sample there are some inclusions and absences of information the reviewer should be aware of, particularly when moving from P+ to PP21 sample review and vice versa.

The major difference in sample management between PP21 and P+ samples is the use of STRmix for PP21 and the translation of this information to the 'Profile Interpretation' table, the 'Profile Record' table and the 'Case Profile table'. The following information highlights these differences.

'Profile Interpretation' and 'Profile Record' tables

The difference in information contained within the P+ and PP21 pages is listed below as well as displayed in **Figure 29** (P+) and **Figure 30** (PP21).

- Extra tile, 'MiU', in the P+ page
- Use of STRmix pdf field in the PP21 page
- Resolved/deconvoluted contribution information in PP21 page
- Mixture ratio between major and minor contributions in the P+ page
- Different suffixes



Figure 29 – P+ PDA Information



Figure 30 - PP21 PDA Information

Case Profile table

The difference in information contained within the P+ and PP21 CPT can be seen within **Figure 31** (P+) and **Figure 32** (PP21):

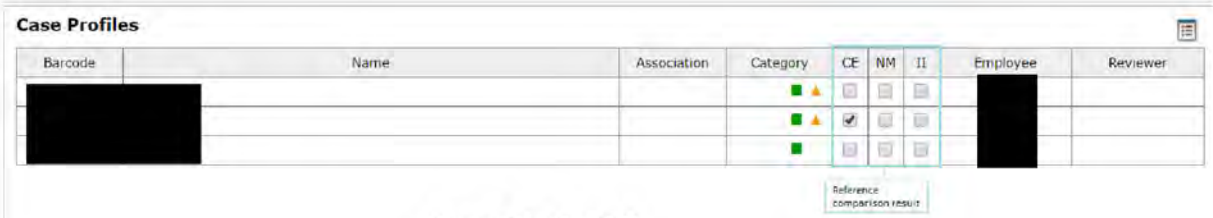


Figure 31 - P+ CPT



Figure 32 - PP21 CPT

4.4.10 Review of Result Line Information

Result lines are a reflection of the interpretation of the DNA profile (discussed in 4.4.6 and 4.4.9) and it is the responsibility of the reviewer to check that all the information in the PDA page has been translated into the appropriate exhibit results in the 'Exhibit Testing' table (see **Figure 33**) prior to release.

The following key 'Records' will serve as a check list for the reviewer to ensure all aspects of a DNA interpretation have been captured and ultimately communicated to the clients:

- Result (1) = Information from the 'Profile Record' table (automatically entered by the FR)
- Result(s) (2) = number of exhibit result lines to describe the DNA profile
- NCIDD (3) = upload information (barcode with suffix)
    - The NCIDD line is important as validation of this line will drive the profile to the NCIDD worklist
- Profile Review (4) = validation triggers the sample to be removed from the profile review worklist

A list of the accepted result lines (Exhibit Results) and their expanded comments are located in QIS: 34229 'Explanation of Exhibit Results for FR'. Section 18 within QIS: 33773 explains how to enter a result line. **Figure 33** is an example of expected result lines for a given DNA profile interpretation.

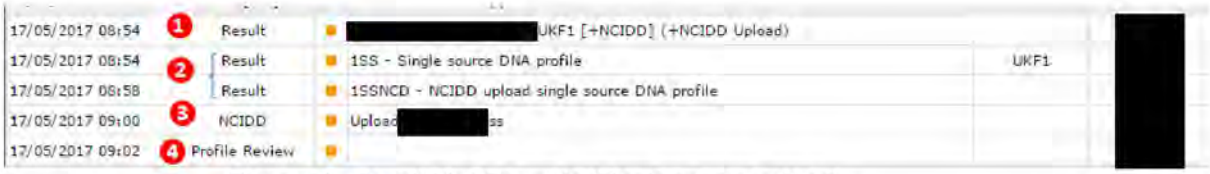


Figure 33 - Result Line Example (Single source upload)

Likewise, the FR has a built in *Review Robot* which can be utilised to check that the appropriate result lines have been entered. The *Review Robot* icon  is situated at the top righthand corner of the PDA page and Exhibit Report page and when clicked, will open a table titled "Exhibit Profile Result Mnemonics Check", see **Figure 34**.

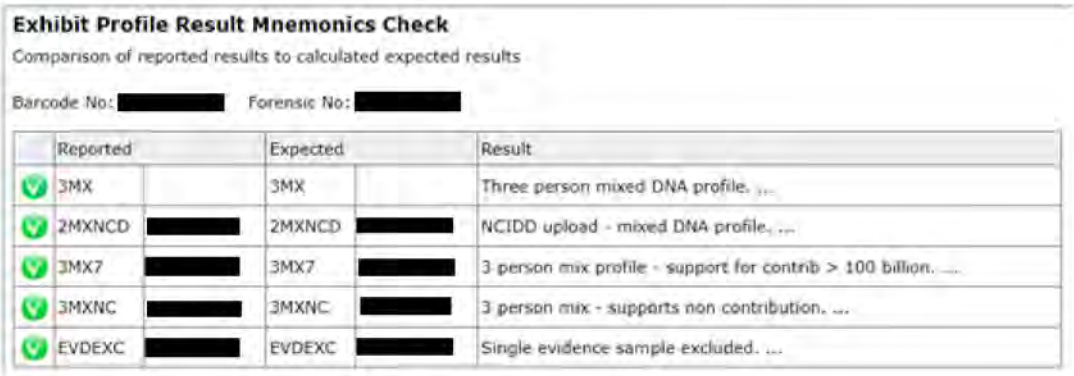


Exhibit Profile Result Mnemonics Check

Comparison of reported results to calculated expected results

Barcode No: [redacted] Forensic No: [redacted]

	Reported		Expected		Result
✓	3MX		3MX		Three person mixed DNA profile. ...
✓	2MXNCD	[redacted]	2MXNCD	[redacted]	NCIDD upload - mixed DNA profile. ...
✓	3MX7	[redacted]	3MX7	[redacted]	3 person mix profile - support for contrib > 100 billion. ...
✓	3MXNC	[redacted]	3MXNC	[redacted]	3 person mix - supports non contribution. ...
✓	EVDEXC	[redacted]	EVDEXC	[redacted]	Single evidence sample excluded. ...

Figure 34 - Review Robot table

A green tick associated to a result line, as displayed in **Figure 34,** indicates that the correct result line has been added for the DNA profile interpretation. A red cross against a line indicates that the incorrect result line has been added and that reassessment of that result is required. An example can be seen in **Figure 35.**

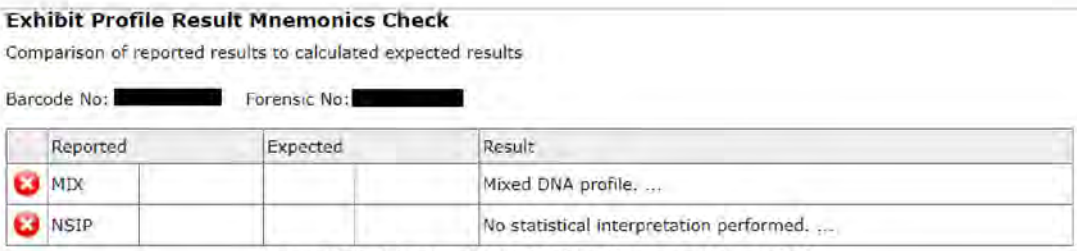


Exhibit Profile Result Mnemonics Check

Comparison of reported results to calculated expected results

Barcode No: [redacted] Forensic No: [redacted]

	Reported		Expected		Result
✖	MIX				Mixed DNA profile. ...
✖	NSIP				No statistical interpretation performed. ...

Figure 35 - Review Robot table (Incorrect Results)

Once the Reviewer confirms the DNA profile assessment and is satisfied all result lines have been entered are correct, the result can be validated. Review of the results is completed by the following process:

- Click on the 'Date and Time' stamp associated to the 'Profile Review' record.
- This will display a 'Testing/Analysis' table with two validation bars (red) and one rework bar (grey) (see **Figure 36**)
    - Clicking the '[CLICK TO VALIDATE ALL]' will allow the reviewer to validate all results in one go, including NCIDD records
    - '[CLICK TO VALIDATE]' will validate the line that has been entered on.
- Once the appropriate red validation tab has been clicked the [CLICK TO VALIDATE] bar will change to green and display [VALIDATED] (see **Figure 37**)
    - 'Date/Time' stamp along with the identification of the reviewer will appear underneath the [VALIDATED] bar (see **Figure 37**)
- In turn the previous orange square against the result(s) will change green to signify that the result(s) has been validated (see **Figure 38**)

Upon validation of the 'Profile Review' result the sample/DNA profile will be removed from the profile review worklist.

Note – When reviewing an NCIDD delete result line, ensure the "Linked No" field is left blank. Information within this field will not allow the result line to be sent to QPS and prevents all other DNA profiling result lines from transferring to QPS.



Police Report	Linked No.
PRNCID - DNA profile removed from NCIDD ▼	

Testing / Analysis [redacted]AMES, C PSD FSS

Date	Process	SubID	SubType	Equipment No
23/10/2017 11:42	Profile Review			

Notes
Attachment:

Storage Rack ID	Position	Tube Lot No	Volume (µL)	Priority
				1 2 3

Change Log
2017-10-23 11:42 CURRENT [redacted]AMES, C

[CLICK TO REWORK]	[CLICK TO VALIDATE]	[CLICK TO VALIDATE ALL]

Figure 36 - Testing/Analysis table

VALIDATED
17/05/2017 15:1[redacted]IPPIA, A

Figure 37 - Validated Result Line (Validated Bar)

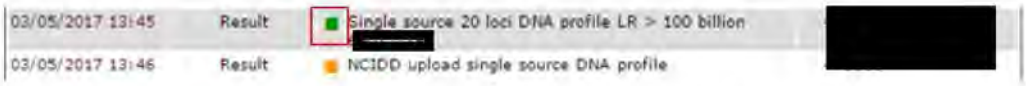


Figure 38 - Validated Result Line (Square Indicator)

Acknowledgement of Result by DRMU

DNA results released to the QPS are reviewed by DRMU as part of the QPS quality assurance. A statement can only be released when all results associated to the case have gone through this external review. A result will be shaded green once this quality control has been complete, as per **Figure 39**.



Figure 39 - Acknowledged Result Lines

A result line will only ever show the date and time the line was added, even after the result line has been validated. Information regarding the Peer Review date can be found by completing the following steps:

- Click on the barcode at the top left corner of either the PDA page or the Exhibit Testing (page displaying the result lines) page which will open a separate page
- Scroll down to the table "FSS DNA Analysis" which has the validated result lines incorporating the review date, no time will be displayed, see **Figure 40**

FSS DNA Analysis

	Lab No	Result / Status	Linked No	Peer Review	
31		Submitted-results pending		REV	10-Sep-18
32		Two person mixed DNA profile		REV	28-Nov-18
33		2 person mix profile - support for contrib > 100 billion	[redacted]	REV	28-Nov-18
34		2 person mix profile - support for contrib > 100 billion	[redacted]	REV	28-Nov-18
35		Single evidence sample excluded	[redacted]	REV	28-Nov-18
36		Single evidence sample excluded	[redacted]	REV	28-Nov-18
37		Single evidence sample excluded	[redacted]	REV	28-Nov-18

Figure 40 - Result Line Review Date

4.4.11 Urgent (Priority 1) Requests

Routine Urgent Requests

The requests for urgent processing will come via Inspector of DNA Management Unit (or higher) and are forwarded to the Managing Scientist and Team Leaders. A phone call may accompany these requests. Details regarding the urgent request (eg. Number of samples, estimated arrival time, status of reference samples) should be forwarded to all Forensic DNA Analysis Management Team staff and Forensic Property Point supervisor where appropriate. The case will be allocated by the Reporting Supervising Scientists and appropriate Request/Tasks created in the FR.

Urgent requests are for a 5-day turnaround time (TAT); however, Forensic DNA Analysis will attempt to release results within a 3-day TAT (ie. by 4pm on the third day of processing); however, this is dependent on the types of samples and examinations required, the time of receipt and the availability of other information eg. Item ownership information. The interval is until the time the initial result is reported. If the sample requires a rework, an appropriate result can be used to explain the preliminary result. These reworked samples should be reported as soon as they become available.

If the urgent items are not in the possession of Forensic DNA Analysis, then Forensic Property Point staff must be alerted to the likely time of arrival and should communicate with Forensic DNA Analysis staff when the exhibits arrive.

If a reference sample is received for the case, these should have the DNA priority elevated to enable a profile to be obtained before, or soon after the crime scene profile.

NB. Priority 1 is used for client requested and internally-raised urgent processing. If internally-raised, approval from Supervising Scientist/Team Leader is required.

Urgent Result Communication on Friday (only)

If priority 1 urgent sample results are likely to be available on a Friday, email DNA Management Unit ([redacted]) in the morning with the relevant barcodes and expected time of release. Aim to release prior to the 3pm and call DNA Management if the results are likely to be released later than 3pm.

When results are reviewed, email DNA Management that results have been released and alert them whether there are actionable results, or not. Suggested wording is *'the electronic transfer includes actionable results'* or *'the electronic transfer includes non-actionable results'* depending on whether there are results for comparison or not.

Streamlining to Reporting Urgent Samples

A streamlining strategy may be employed in consultation with a line manager. It is useful when a large number of urgent samples are being processed at the same time.

If we receive a number of urgent samples for a case and the results are all indicative of the same unknown profile, select the most suitable and probative profile for interpretation and loading to NCIDD and any matches will be reported on this sample within the urgent timeframe. Liaise with the QPS to determine if these remaining results can be downgraded to High Priority (Priority 2) status. This will enable the reporting scientists to allocate their time to interpreting and reporting other urgent samples. The allocated scientist will ensure the results for all downgraded samples are reported in a timely manner.

A reference sample from the complainant, for example from a sexual assault, as well as ownership of the item is critical for the interpretation of any DNA results obtained. Without these, interpretation of the resulting DNA profiles is limited and may not provide information that can be loaded to NCIDD. If urgent samples are all indicative of the same unknown profile/s, and the reference sample of the complainant has not been received or is still undergoing processing, only the most suitable DNA profile will be chosen for interpretation in order to obtain a DNA profile loadable to NCIDD. This will enable critical information to be sent back to the QPS for the urgent case, and the reporting scientist to allocate their time to interpreting and reporting other urgent P1 samples. The result interpreted in the absence of the reference sample or ownership information will be re-interpreted and reported along with the remaining results once the reference sample is completed.

These strategies will only be implemented on a case by case basis AFTER communication with Inspector DNA Management Unit, or S/Sgt DNA Results Management Unit.

4.4.12 Incorrect Result/Record

A 'Result', such as a result line, which has been ordered in error is unable to be deleted from the 'Exhibit Testing' table and can be dealt with in one of two ways. If the 'Result' has not been validated it can be reused, ie, another result line entered. If however the 'Result' has been validated it is to be incorrected which will be highlighted by a strike through rendering the line unable to be accessed.

The same applies to a 'Record' such as an NCIDD record; it can be reused if not validated however if it is validated it will need to be incorrected.

An incorrect can be performed by the Reviewer or Profile Analyst only if the result has not been validated. Where the result has been validated then the incorrect process has been restricted to staff at a HP5 level and above.

The correction process is described in section 13 within QIS: 33773.

4.4.13 Suspect Checks

Review and validation of a suspect check follows the same process as described in sections 4.4.4 and 4.4.9. The differences are listed below:

- The use of specific 'Suspect Check' result lines, listed in QIS: 34229
- The Suspect check reference profile will not be displayed in the CPT
- The STRmix file(s) is added to the FR under a 'Notation' or added to the result line, the latter is preferable

4.4.14 Review of Exhibits Highlighted as Requiring No Further Testing

Queensland Police may decide at any stage of DNA processing that testing is no longer required. QPS will update the 'Forensic Triage' field to 'No Testing Required' which will automatically enter the 'No further work required as per advice from QPS' (NWQPS) result line against the exhibit.

The process on how to action an exhibit that is no longer required for testing is described in **Appendix 7**.

4.4.15 Request for Further Information

If a discrepancy has been found not previously noted, this will need to be investigated prior to releasing the result. Most discrepancies can be actioned by communicating with the relevant QPS Forensic Officer or a QPS Officer within the DNA Management Team via a "Request/Task" (see **Figure 41** and **Figure 42**) or email - a Request/Task is the preferred method of communication. A Request/Task is completed by the following:

- From within a Forensic Case File Record (CM side) select the *Case Management* tab
- Select *Add Record* 
- Select 'Request/Task'
- Add the QPS Officer's ID into the 'Case Officer' field
- Select 'Review' from the 'Request Type'
- Add notes to the 'Comments' section describing clarification being sought
- Save the record 

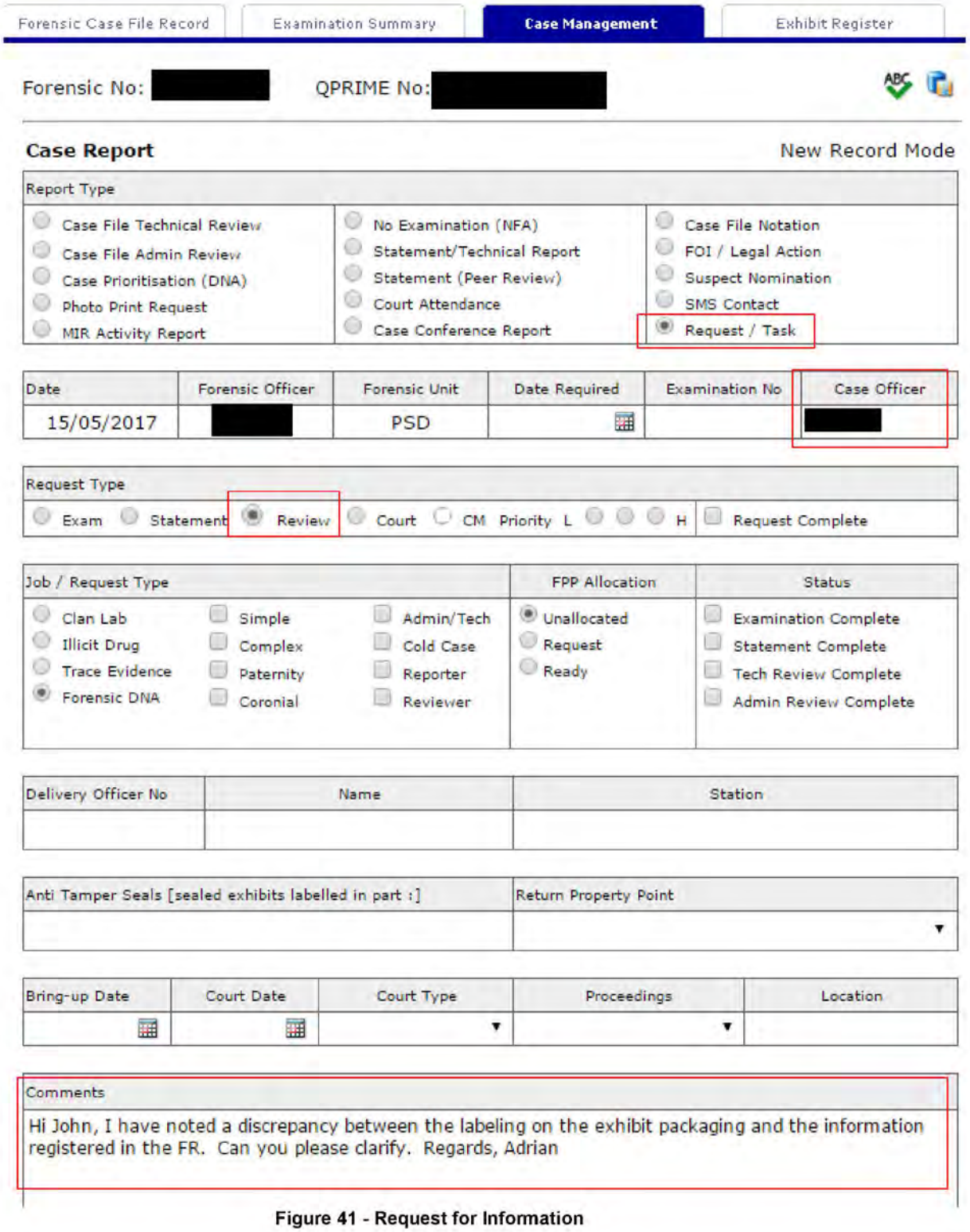


Figure 41 - Request for Information

- Once saved the 'Exhibit /Item' table will appear
- Associate the exhibit by selecting the icon within the 'Exhibit/Items' table and add the exhibit(s) barcode to the table

- Save the record (see **Figure 42**)

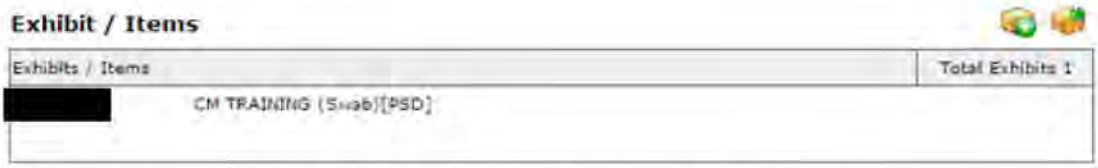


Figure 42 - Adding Exhibit to Request for Information

This request will be sent to the nominated QPS Officer for actioning, possibly via the same record. This will add a flag to the Profile Analyst/Reviewers 'Personal Work List'.

Request via 'Email correspondence'

- This action can be completed from the 'Exhibit Record' of the sample in question within the Case Management side of the FR if corresponding with the Forensic Officer
- Simply click on the email icon associated to the QPS Forensic Officer in the 'Forensic Officer' field
- This will open up 'Outlook' and correspondence can be completed via the Queensland Health email system – write a short, concise description of the query and send
- Await return correspondance and document this within the FR

Save the email as a pdf via the 'Microsoft Print to PDF' printing option and upload as a 'Notation' against the case (ensure to add information to the 'Comments' section).

4.4.16 Quantification Initiated Result Release

Samples with no DNA detected, quantitation values <0.001ng/uL, will be released with the result line "No DNA Detected" and will be actioned as per process described in section 9.1 of document QIS: 34064 'Miscellaneous Analytical Procedures and Tasks'. All other samples with quantitation values >0.001ng/uL will be amplified.

4.4.17 Miscellaneous Information Release

Release of Quantitation Results – Quant and Hold Data

Samples may be elected by QPS to be held after quantification, the results of which are used to assess other DNA processing techniques offered outside of the laboratory – most commonly utilised for cold case investigation where the samples are old.

The process is initiated by a 'Request/Task' to either the Team Leader for Cold Cases if unallocated, or the case scientist. The 'Request/Task' will list the samples that the "Quant & Hold" strategy applies. These samples will be highlighted in the FR by the addition of a comment against the 'Exhibit Notes & FSS Advice' section such as "***Quant & Hold***" or similar. The following steps for processing and result release will occur:

1. Evidence Recovery staff will add an 'Analytical Notation' with a comment alerting Analytical staff that the sample is to be held after the Quantification process is complete – "Quant and Hold"
    a. It is advised that the case manager follow up on the samples to ensure the Analytical Notation has been added to all samples listed in the initial request

2. Collate quantitation information from all samples into Microsoft Excel with the following information – quantification information is located on the PDA page of the individual sample in the 'Profile Analysis' table under the column 'ng/ µL'
    a. Barcode
    b. Description of sample
    c. Total quantitation result (TSAQty)
    d. Male quantitation result (TYQty)
    e. Degradation Index (TSADegIndex)
    f. IPCCT
    g. Volume Remaining (extract volume which will default as ~80 µL)

3. It is recommended the excel spreadsheet titled "Quant and Hold_09032021_Larkin" located G:\ForBiol\AAA Forensic Reporting & Intel\AAA Cold Cases_Missing Persons be used to collate the information requested

4. The information is to be directed to QPS Homicide Cold Case Investigation Unit Forensic Co-ordinator via a 'Request/Task'
    a. It is important to create a new 'Request/Task' and not respond via the initial 'Request/Task' as once the task is completed the information will disappear from the FR – information will exist for the officer initiating the 'Request/Task'
    b. Information to be reviewed prior to adding to the 'Request/Task'

5. Reporting officer to add the result line "QPS Advise No Further Work Required – Results Available" (NWQPSR) at the same time as the 'Request/Task'
    a. If the autogenerated result line "No DNA Detected" (NDNAD) or "DNA Insufficient for Further Processing" (DIFP) is added, NWQPSR is no longer required

6. Reviewer to review result line at the same time the 'Request/Task' is sent

Information regarding the quantification process employed in the laboratory can be sourced via the procedure QIS: 34045 'Quantification of Extracted DNA using the Quantifiler® Trio DNA Quantification Kit'.

Covert Samples Authorised as Reference Samples

Certain cases, such as Cold Cases, may have a covert sample registered by QPS for use as a reference sample. This sample will be identified as 'covert' by information added to the "Exhibit Notes & FSS Advice" field by QPS or in the absence of this information, a 'Notation' added by FSS staff advising of the specific category.

Results of any comparison are to be transferred to QPS via Intelligence Reports only – no exhibit results are to be sent. See QIS: 33773 for full details.

Release of results via email

Where information is released via email, such as an Intel Report, minimum requirements are to be incorporated:

- Results must be as a PDF document
- The phrase "*The pdf document in this email is the report issued by Forensic and Scientific Services. Any other attachments or information provided is not considered to be the issued report.*" must be added to the email.

5 Statement of Witness

An overview of the following process, from statement request through to report publication, has been created and saved as **Appendix 1**.

A process for reporting and reviewing statements under 'Working From Home' conditions has also been created and saved as Appendix 9.

5.1 Casefile Creation and Tracking

A casefile should be available at the time of statement drafting. If not, a request can be forwarded to the Administrative team using the generic Admin email account [redacted] The file is compiled by the Administrative Team as per instruction detailed in Section 9 of document QIS: 34248 'Administrative Team – Case File related duties using the Forensic Register'. This section also lists the contents of the casefile created by Administrative staff.

If however, the reporting scientist needs to create and register the casefile themselves, instructions are available in Section 9 of document QIS: 34248.

Further images and other information can be printed from the FR following the processes referred to in section 9.6 and 9.7 of document QIS: 34248.

5.2 Statement Request (REQUEST)

A statement request is created to identify that a statement is required for the case. A request can be completed with or without a 'Case Officer' in mind. This may be initiated by entering a FR number, the Occurrence number or exhibit barcode located on a worklist, eg, 'Unallocated All' list or by searching on an exhibit barcode and then navigating to the Case Management tab.

This action will be used primarily by QPS to communicate that a statement is required but will also be used by a HP5, SSLU or case manager whenever the need arises – Addendum statement following receipt of additional reference sample(s) or crime scene sample(s); Evidentiary Certificate request; etc.

Where multiple FRs exist under the one Occurrence number, SMU will replicate the statement request on each of the relevant FRs. It is suggested that the reporting scientist check the 'Related Case Files' field within the 'Forensic Case File Record' tab for the existence of multiple FRs and where required create a 'Statement Request' for each FR.

The following will focus on a request made to the reporting scientist. Information concerning managing the statement request will be described in section 7 'Statement Worklists and Milestones'.

5.2.1 Creating a Statement Request and Allocation to a Reporting Officer

This process will usually be initiated by the Queensland Police Service (QPS) or a HP5 or above, however, it can be completed by a reporting officer (HP4).

- From within a Forensic Case File Record (QPS page) select the *Case Management* tab
- Select *Add Record* and the following will display (see **Figure 43**)

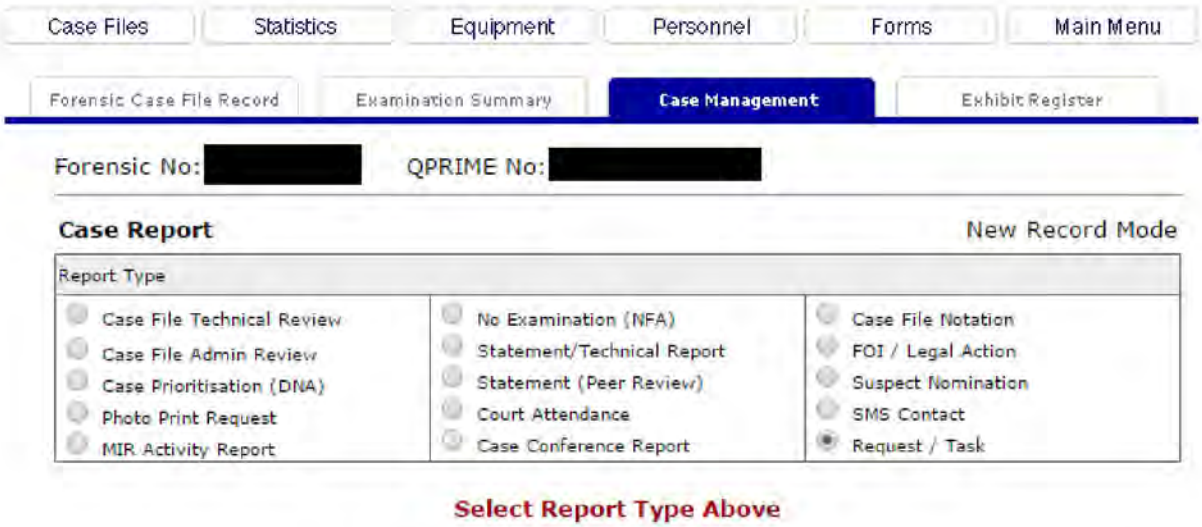


Figure 43 - Statement Request

- Select *Request/Task* which extends page content to display the following fields and complete the following fields
- Complete the following fields (see **Figure 44**):
  - *Case Officer* – allocated case analyst if known (1)
  - *Date Required* – due date for statement (2)
  - *Request Type* – select *Statement* (3)
  - *Priority* – select priority as appropriate (4)
  - *Job/Request Type* – select *Forensic DNA* (5) and relevant case type (6)
    - *Note case type options will not appear until 'Forensic DNA' is selected*

Note – fields (2) and (4) are not required to complete the request.

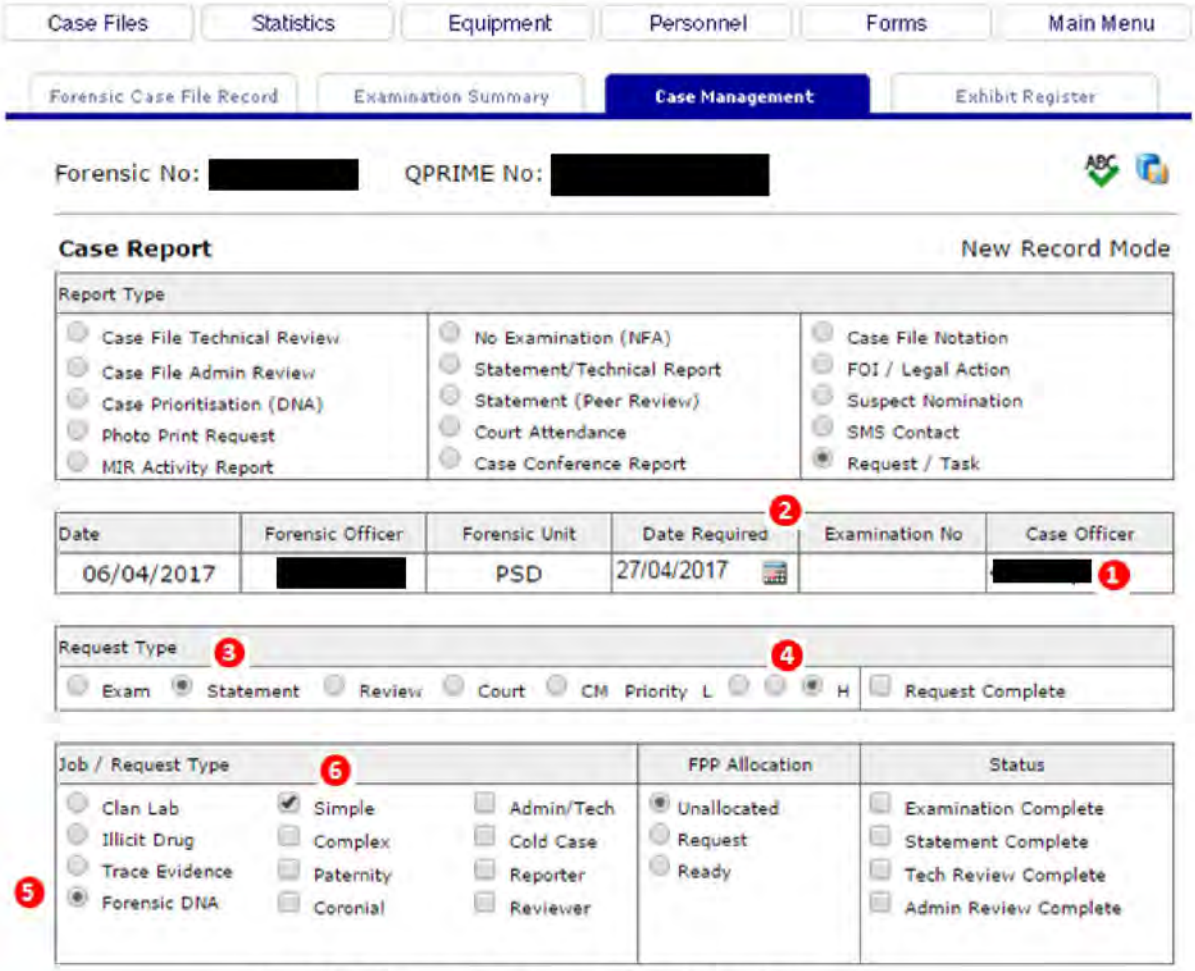


Figure 44 - Statement Request Fields to Complete

- Save the record
- This record can be later updated by selecting *Edit* and saving any changes

When a record is saved a 'request number' (displayed below in red box of **Figure 45**) will be visible in the top right hand corner of the screen. This number can be entered into a search field which will navigate to that specific request.

Note – A 'request number' will be generated when saving any request.

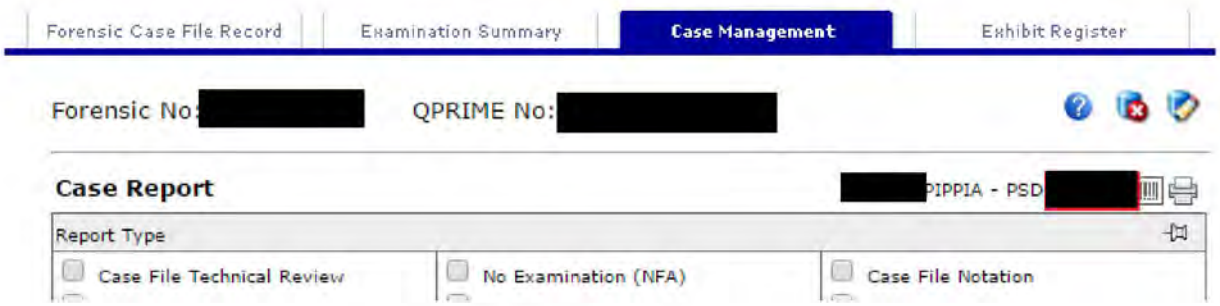


Figure 45 - Record number

If a reporter is nominated, this request will populate the nominated reporters *Personal Work List* (PWL). If a reporter is not nominated, the request will populate the 'Unallocated statements' list. New requests, regardless of the type (case management, peer review) will be highlighted in the staff member's PWL as per **Figure 46**. The number within the red circle indicates the number of new requests.



Figure 46 - PWL Highlight

Upon entering your PWL you may find numerous requests. **Figure 47** shows three such requests sorted on request date and displaying further details such as Occurrence number and FR number. Two of these requests are for statement compilation and release.

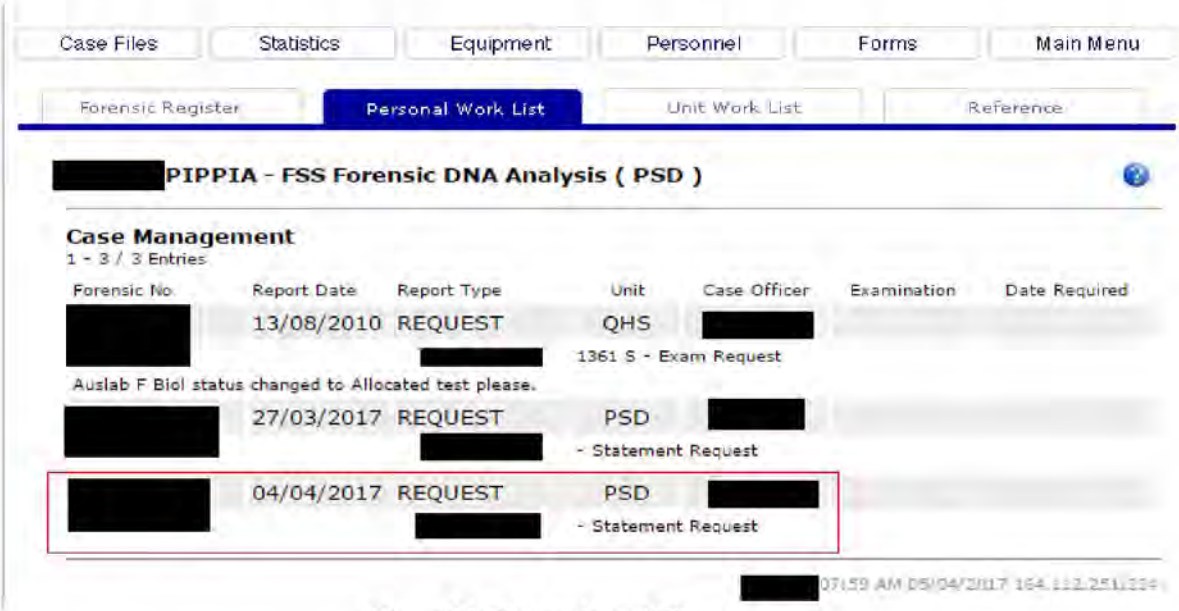


Figure 47 - Requests on PWL

Note - Where multiple requests and records exist, the list can be filtered to sort specific tasks by clicking on the '*Personal Work List* tab and selecting the applicable result. Clicking on the *'Personal Work List'* tab and selecting '*Default List'* will bring back all Case Management entries.

5.3 Statement Record (REPORT)

The statement *REPORT* is the record of the task of writing a report being completed. This record also stores the statement document and updates milestones involved in the creation of the statement. This record should be created by the person preparing/issuing the statement.

Note, the statement record creation applies to all types of reports; Statement of Witness, Addendum statement, Evidentiary Certificate and Intelligence Report. Furthermore, the amount of statements able to be created against a case is limitless.

5.3.1 Creating a report record

- From within a Forensic Case File Record select the *Case Management* tab
- Select *Add Record* and the following will display (see **Figure 48**)

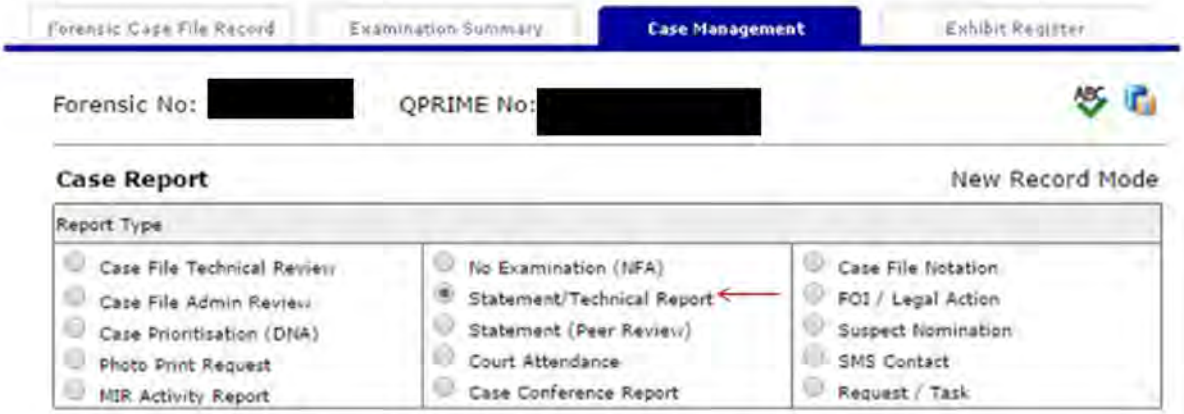


Figure 48 - Creating Statement Record

- Select *Statement/Technical Report* (see **Figure 48**) which extends page content
- Complete the following fields (see **Figure 49**):
  - *Case Officer* – allocated Reporting Scientist (1)
  - *Date Required* – due date for statement (optional) (2)
  - *Priority* – select priority (optional) (3)

Add a description to the *Comments* field to aid in distinguishing linked *RECORDs* where multiple reports are requested eg, 'Statement' – further information is available in Section 5.8 of this document (4)

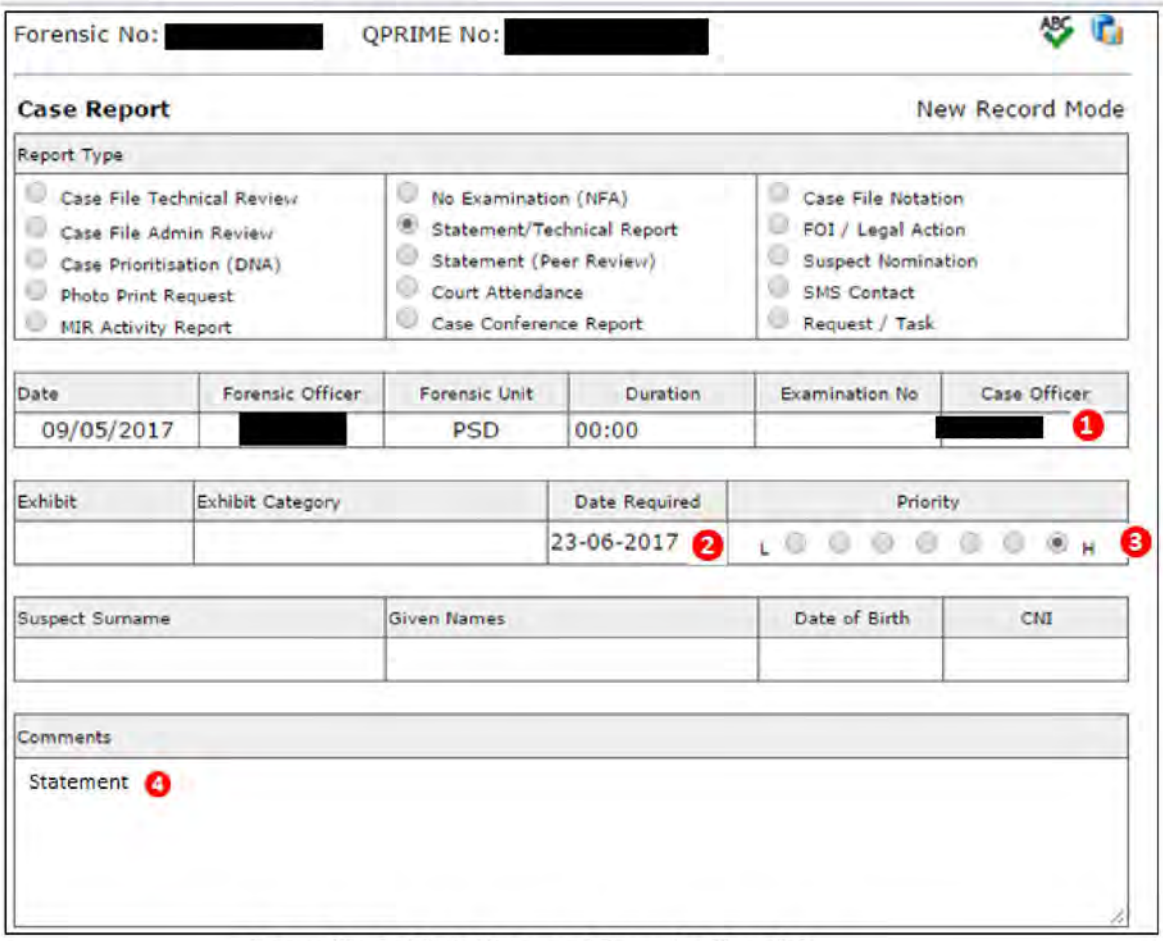


Figure 49 - Fields in Statement Record to Complete

- Save the record

Upon completion, this will create a record under the case management tab for that specific case, as displayed in **Figure 50**:

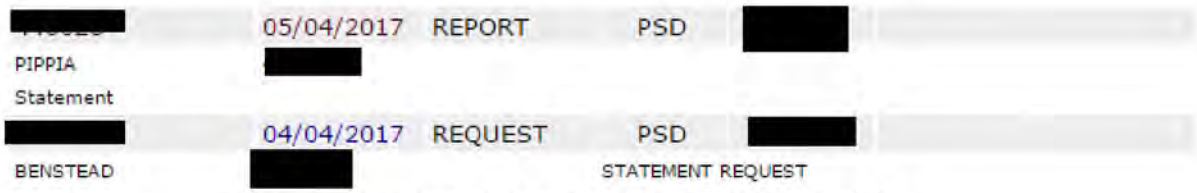


Figure 50 - Statement Record under Case Management tab

5.4 Drafting a Statement

5.4.1 Updating Reporting Scientist Information

When issuing a report it is important that the reporting scientist's personal and professional information is visible on the front page of the statement. This information should include the

full name of the Reporting Scientist, their qualification, membership to an applicable society and other relevant courses.

The following steps outline how to enter and or update this information:

- Navigate to and enter the *Personnel* tab
- On this screen enter your personal record by either entering your *Employee No* or *Surname* into the appropriate fields and press enter.
    - Alternatively, by clicking on the icon this will achieve the same result
- Select *Edit Record*

Employee Name Update

The FR only has fields for *First Name* and *Surname* however issuing a Statement of Witness and other report types requires that the full name of the Reporting Scientist is used

- Add First and Middle name to the *First Name* field (see **Figure 51**)

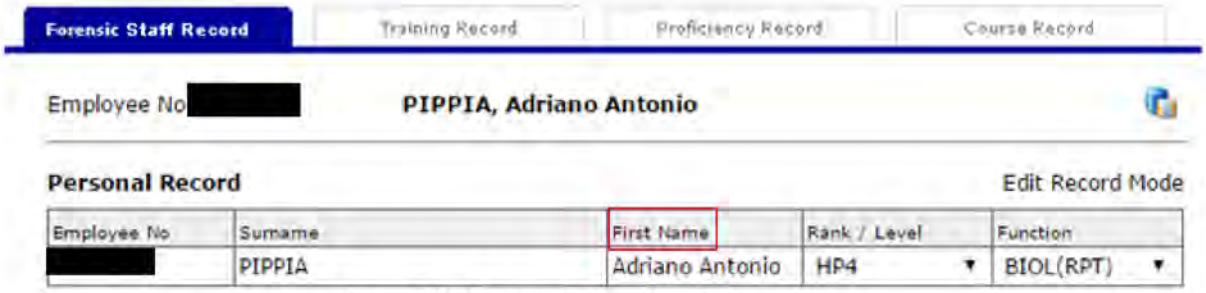


Figure 51 - Employee Name Update

Updating Professional Credentials

- Navigate to the table titled *Statement Preamble*
- Add information as a block of text (see **Figure 52**)

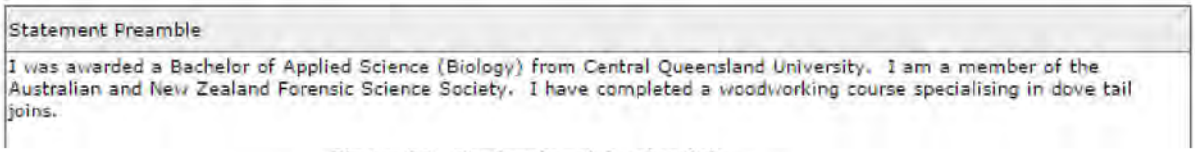
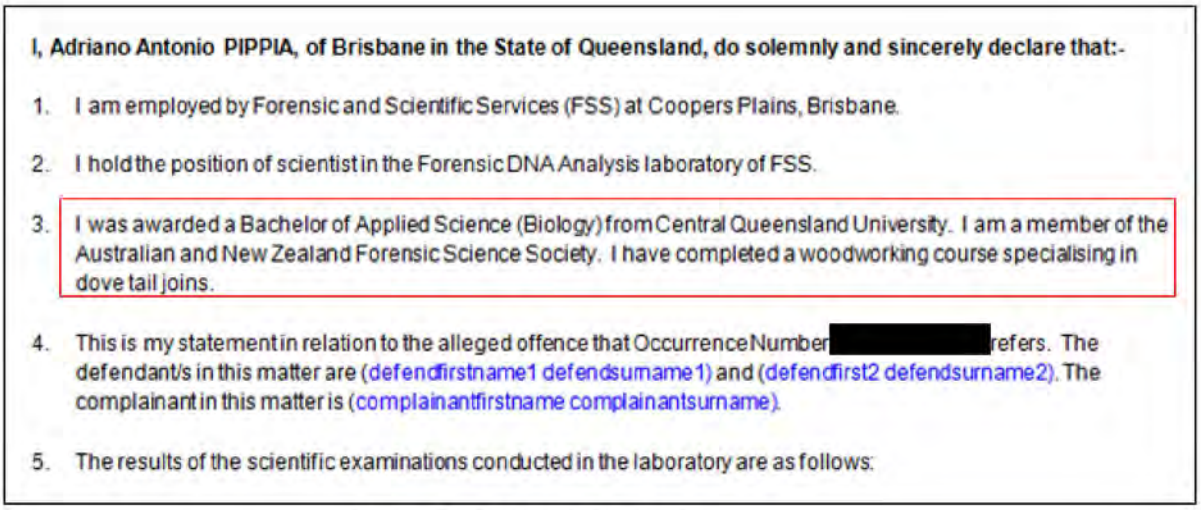


Figure 52 - Professional Credentials

- Save the record

Open the statement, as per instructions in section 5.4.2. The block of text within the '*Statement Preamble*' will be displayed as point 3 (see **Figure 53**).

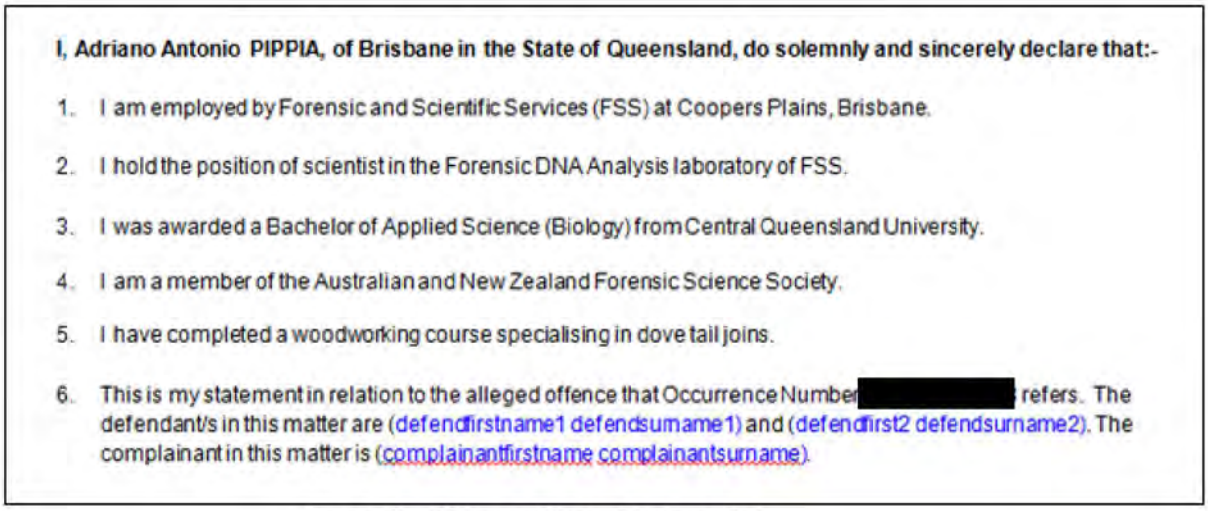


I, Adriano Antonio PIPPIA, of Brisbane in the State of Queensland, do solemnly and sincerely declare that:-

1. I am employed by Forensic and Scientific Services (FSS) at Coopers Plains, Brisbane.
2. I hold the position of scientist in the Forensic DNA Analysis laboratory of FSS.
3. I was awarded a Bachelor of Applied Science (Biology) from Central Queensland University. I am a member of the Australian and New Zealand Forensic Science Society. I have completed a woodworking course specialising in dove tail joins.
4. This is my statement in relation to the alleged offence that Occurrence Number [redacted] refers. The defendant/s in this matter are (defendfirstname1 defendsurname1) and (defendfirst2 defendsurname2). The complainant in this matter is (complainantfirstname complainantsurname).
5. The results of the scientific examinations conducted in the laboratory are as follows:

Figure 53 - Statement Preamble

Separate each portion of information into individual points – entering will create another numbered bullet (see **Figure 54**).



I, Adriano Antonio PIPPIA, of Brisbane in the State of Queensland, do solemnly and sincerely declare that:-

1. I am employed by Forensic and Scientific Services (FSS) at Coopers Plains, Brisbane.
2. I hold the position of scientist in the Forensic DNA Analysis laboratory of FSS.
3. I was awarded a Bachelor of Applied Science (Biology) from Central Queensland University.
4. I am a member of the Australian and New Zealand Forensic Science Society.
5. I have completed a woodworking course specialising in dove tail joins.
6. This is my statement in relation to the alleged offence that Occurrence Number [redacted] refers. The defendant/s in this matter are (defendfirstname1 defendsurname1) and (defendfirst2 defendsurname2). The complainant in this matter is (complainantfirstname complainantsurname).

Figure 54 - Statement Preamble Amended

Now that the Reporting Scientist personal and professional information has been updated, it's time to continue authoring the statement as per section 5.4.2.

5.4.2 Drafting a Statement

*IMPORTANT NOTE: Once you have opened the statement template, save your statement as a **word document** before making any changes, as this will ensure the formatting is maintained.*

- Click on appropriate *REPORT* record in the Case Management tab
- Select the Microsoft Word icon to compile a draft statement

- The Microsoft Word icon will be available as soon as the record is created OR if unable to write the statement at that stage, at a later date navigate to the record under the case management tab and click on the *Forensic Officer* identifier associated to the entry labelled *REPORT*, see **Figure 50**

- Open this document (statement may take a while to open and will be visible at the bottom left corner of the screen)



- The statement is ready to open when the above display changes to the following image



- Save the statement to an appropriate network drive as a '**Word Document**' [default is a *Rich Text Format (*.rtf]* format, using the '*defaultfilename_your initials*'

- This document can be worked on at any stage as required until ready for uploading to the FR

Certain information will be automatically pulled into the statement and include receipt information, the appendix, preamble information, examination information and the DNA profile interpretation. This information should be reviewed to ensure that it is complete and correct. Any additions or subtractions to this should be completed by the reporting scientist.

Any additional details such as opinion evidence will be added by the reporting scientist.

Appendix 8 contains suggested wording for reports created for results obtained using PowerPlex®21 and STRmix.

Receipt Information

Receipt information will be displayed in the draft statement automatically, however in the event this does not occur the following steps can be used to locate this information to add to the statement.

- Navigate to the *Exhibit Register* tab and highlight the *DNA Analysis* drop down menu

- Highlight the *Evidence Cert – Analysis*

This will open a text document containing receipt information along with analytical batch information of all samples that have undergone processing within the laboratory. Receipt information will be displayed at the top of this document. Cut and paste the required information into the statement.

Note, the barcodes associated to a receipt will also contain sample description which historically, was not displayed within the receipt information of the statement. The reporting

officer has the option to remove this information and only have it display in the body of the report.

Individuals Nominated for Report

The FR has only one field for complainant nominations. It is suggested that information within the Case Management tab be reviewed to see if there are extra individuals to be listed in the report. QPS have also advised that it is acceptable to use 'Regina' as the primary complainant in the report where multiple individuals are listed.

Appendix Information

The appendix contains information on procedural overview and test methodology and replaces the need for a separate preamble and appendix, as completed in the past. The appendix is automatically generated by the FR, however this information is not current and needs to be removed from the statement. An appropriate appendix can be selected from **Appendix 2** and content not applicable to the case removed.

Appendix 2 has three appendices available for use in a statement specific to the DNA profiling system used and the STRmix version utilised.

Examination Information

Examination information such as screening and confirmatory tests specific to the case can be viewed by following the process detailed in section 4.4 of this document. This information should be manually added to the statement as required.

5.4.3 Uploading a Draft Statement

- From within a Forensic Case File Record select the *Case Management* tab
- Select the statement record identified as *REPORT* in the *Report Type* column by clicking on the *Forensic Officer* identifier (see **Figure 55**)

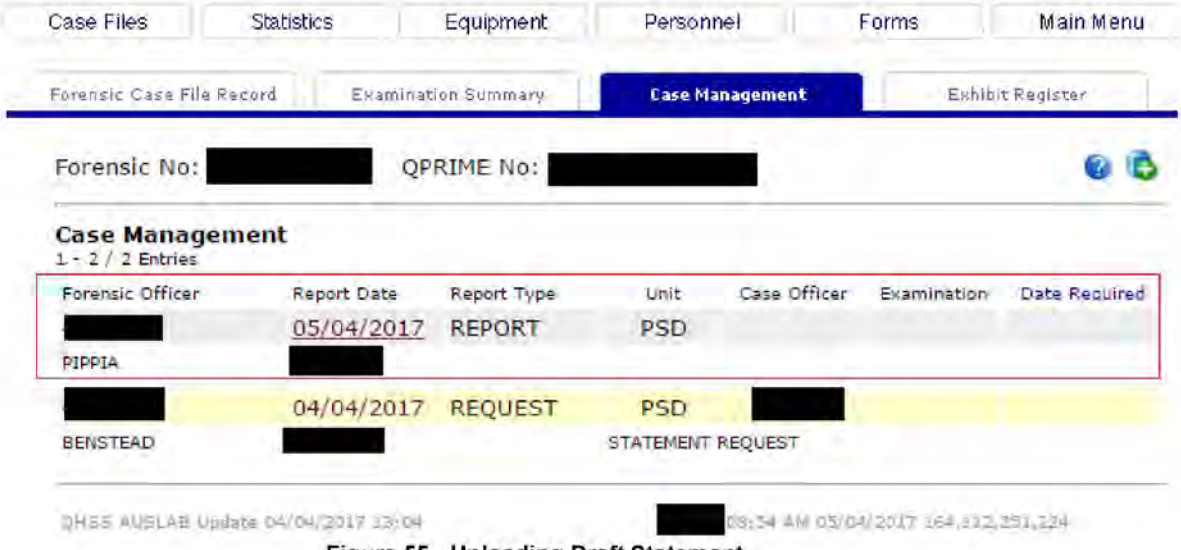


Figure 55 - Uploading Draft Statement

- On the *Statement/Technical Report* record select *Edit Record*
- Upload the statement and select the '*Draft Complete*' checkbox (see **Figure 56**)



Figure 56 - Uploading Draft Statement

- Upload the document by using the *Choose File* option under *Related File* section OR by dragging the document from the stored location to the area to the right of the 'Choose File' box (see **Figure 57**)

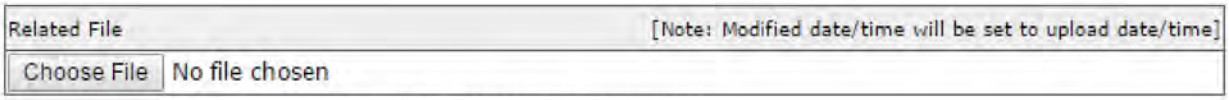


Figure 57 - Uploading Document

- **Figure 58** depicts a draft statement successfully uploaded to the FR



Figure 58 - Uploaded Draft Statement

- Save the record

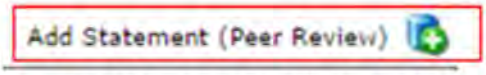
The report record will be updated to show a 'document' icon indicating (**Figure 59**) that a document is available under this record.



Figure 59 - Statement Record with Uploaded Document

If the reporting and reviewing scientist decide that the review process will be completed externally to FR and no draft statement will be uploaded at this point, it is still important that the 'Draft Complete' box is ticked (see **Figure 56**) when the statement is ready to be

reviewed. This is required for the creation of the *REVIEW* record outlined in section 5.5.1 of this document.

If this task is <u>not complete</u> then this 

field will not appear in the *REPORT* record and the reviewing scientist will be unable to create the *REVIEW* record.

5.4.4 Requesting a Statement Review

Once a draft statement has been completed the reporter is to create a request for 'Review'.

A *REVIEW* request can be created by completing the same process as detailed in 5.2.1 with a modification – selecting 'Review' in the 'Request Type' field. If the Reviewing Scientist is known, add the staff members details in the 'Case Officer' field (see **Figure 60**) otherwise leave blank. Adding a date to the 'Date Required' field will ensure the case is added to the 'Unallocated Review' worklist in order of priority and will also highlight the date for statement release to a reviewing scientist on their Personal Worklist.

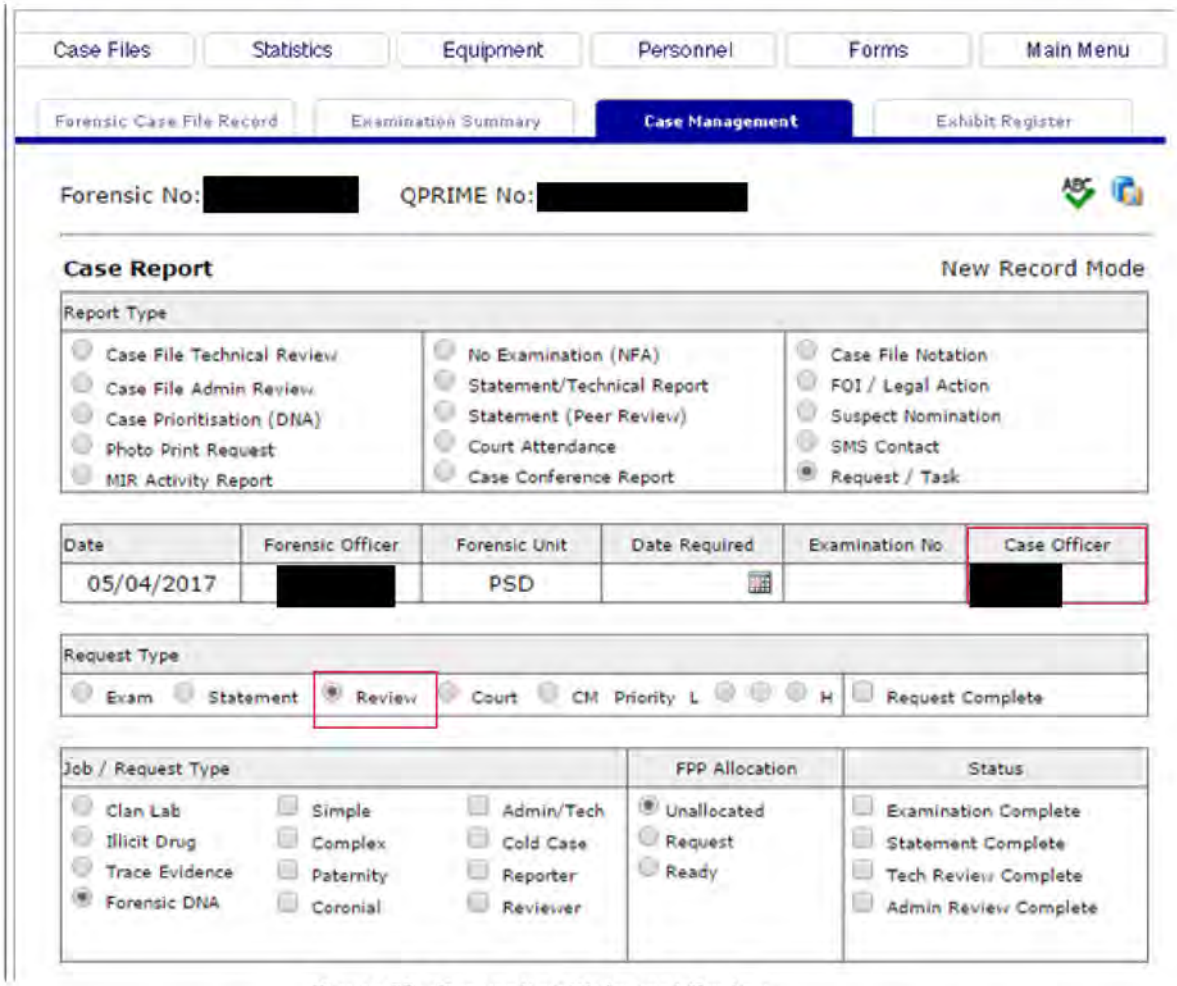


Figure 60 - Requesting Statement Review

Upon completion, this will create a record under the case management tab for that specific case (see **Figure 61)**:



Figure 61 - Statement Review Record

Where a reviewer is allocated, the request will populate the reviewers PWL and be displayed for their attention as follows (see **Figure 62)**:

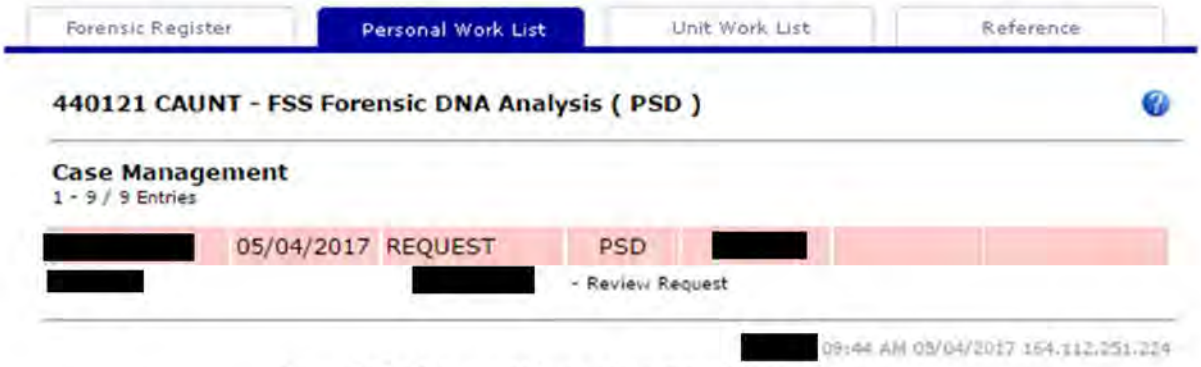


Figure 62 - Statement Review Populates PWL

Where a reviewer has <u>not</u> been nominated, upon saving, this request will populate the 'Unallocated Reviews' worklist. Case reviews can be self-allocated or allocated by a HP5 or above and is completed by simply adding the reviewing scientist's FR ID to the 'Case Officer' field (see **Figure 60**).

5.5 Statement/Report Peer Review

The statement peer review record will document the technical and administrative review completed on all aspects of examination, DNA analysis lab processing, DNA profile interpretation and the drafted statement. All casefiles/statements require a peer reviewer before the information is able to be released.

5.5.1 Creating a Statement Peer Review Record

This action is to be completed by the staff member assigned to perform the peer review and is detailed as follows:

- Navigate to the *REPORT* record located under the *Case Management* tab, **Figure 63** and enter the *REPORT* record which will display as per **Figure 64**



Figure 63 - Find *REPORT* record

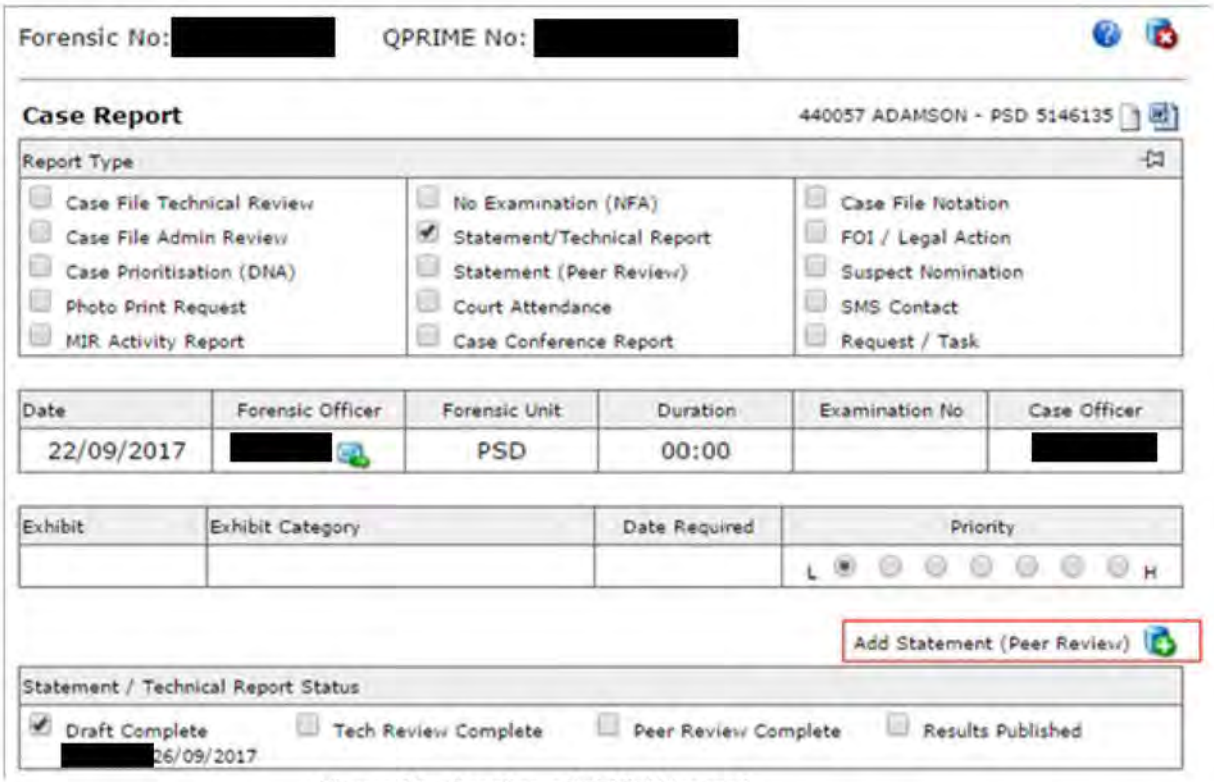


Figure 64 – Creation of REVIEW record

- Click on add icon associated to the 'Add Statement (Peer Review)' field, highlighted in the red box of **Figure 64,** to create a *REVIEW* record as displayed in **Figure 65**

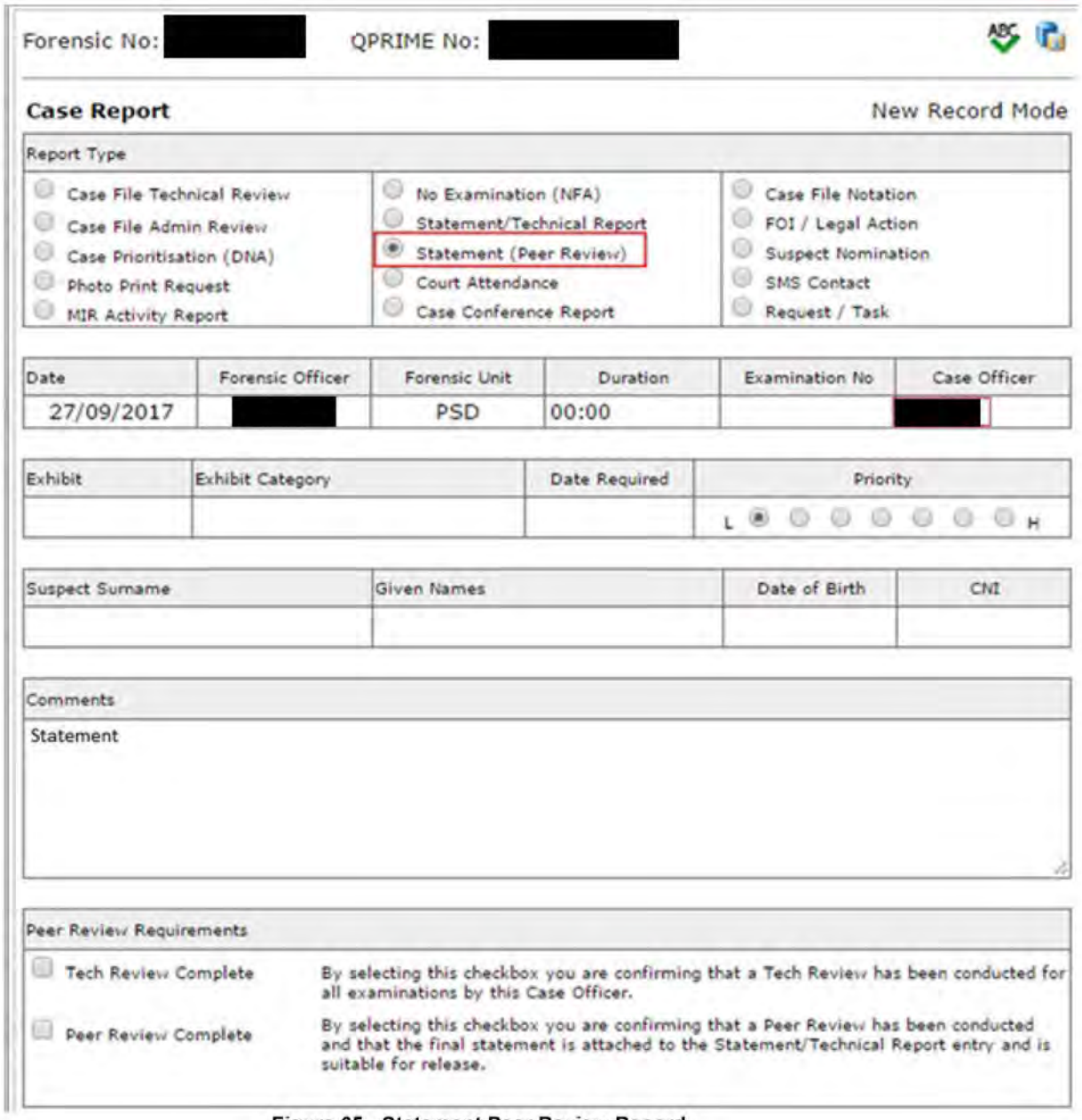


Figure 65 - Statement Peer Review Record

The 'Statement (Peer Review)' report type will be automatically checked.

- Add your FR ID to the 'Case Officer' field
- Add a note to the 'Comments' section – eg, *Statement*
    - this is optional but can aid to distinguish between REVIEW records where multiple reports exist for case
- Save the record

The *REVIEW* record will now be associated to the REPORT record and be visible against the case under the 'Case Management' tab as per **Figure 66**.



Case Management

1 - 11 / 11 Entries

Forensic Officer	Report Date	Report Type	Unit	Case Officer	Examination	Date Required
[redacted]	28/09/2017	REVIEW	PSD	[redacted]		
WILSON	[redacted]					
[redacted]	26/09/2017	REQUEST	PSD	[redacted]		03/10/2017
ADAMSON	[redacted]		REVIEW REQUEST			

Figure 66 - *REVIEW* record

5.5.2 Accessing a Draft Statement

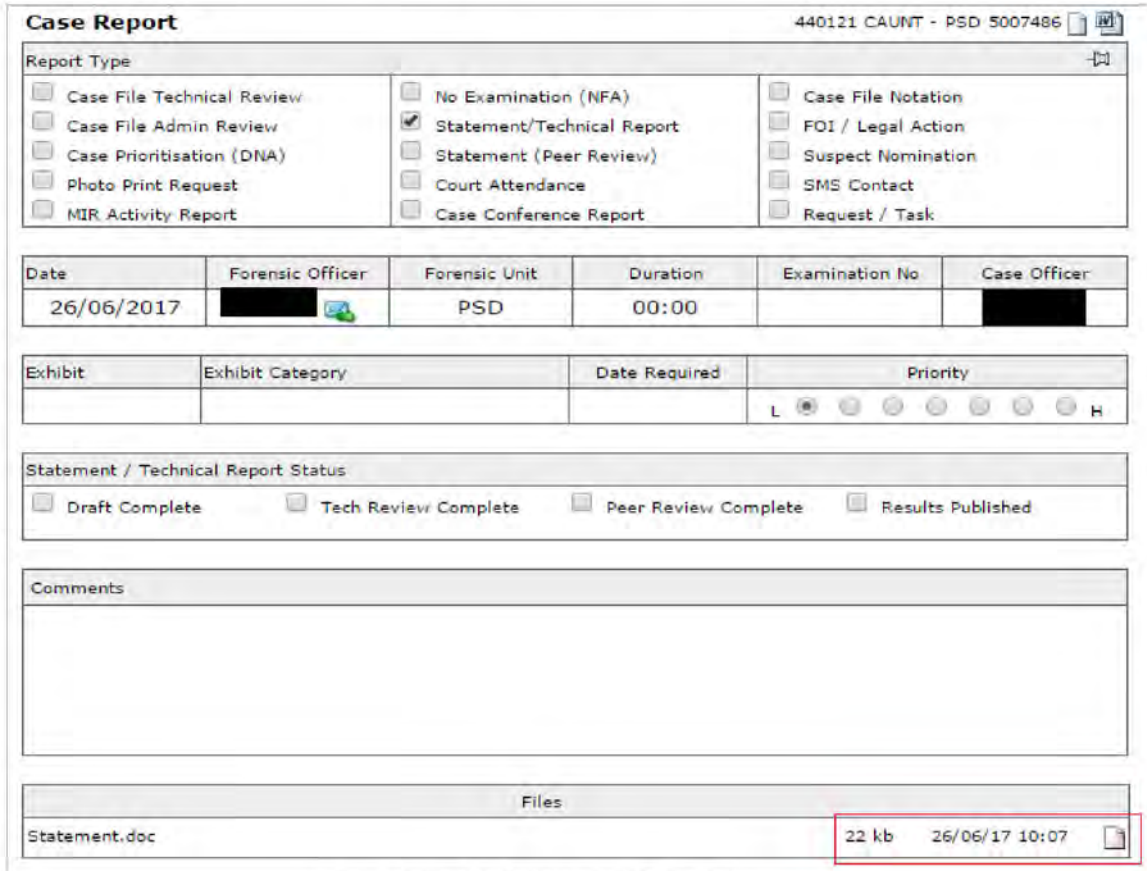
- From within a Forensic Case File Record select the *Case Management* tab
- Select the statement record identified as *REPORT* (**Figure 67)** in the *Report Type* column
  - Be sure to select the right one where multiple *REPORT* records exist

- Enter the record and select the drafted statement, displayed as a document icon (**Figure 68)**, to download the draft statement



[redacted]	26/06/2017	REPORT ☐	PSD	[redacted]
CAUNT	[redacted]			

Figure 67 - *REPORT* record



Case Report 440121 CAUNT - PSD 5007486

Report Type

☐ Case File Technical Review	☐ No Examination (NFA)	☐ Case File Notation
☐ Case File Admin Review	☑ Statement/Technical Report	☐ FOI / Legal Action
☐ Case Prioritisation (DNA)	☐ Statement (Peer Review)	☐ Suspect Nomination
☐ Photo Print Request	☐ Court Attendance	☐ SMS Contact
☐ MIR Activity Report	☐ Case Conference Report	☐ Request / Task

Date	Forensic Officer	Forensic Unit	Duration	Examination No	Case Officer
26/06/2017	[redacted]	PSD	00:00		[redacted]

Exhibit	Exhibit Category	Date Required	Priority
			L ◉ ○ ○ ○ ○ ○ ○ H

Statement / Technical Report Status

☐ Draft Complete ☐ Tech Review Complete ☐ Peer Review Complete ☐ Results Published

Comments

Files

Statement.doc	22 kb	26/06/17 10:07

Figure 68 - Draft statement for review

5.5.3 Perform the Review

Perform a technical and administrative review as per the laboratory protocol as per document QIS: 34322 'Technical and Administrative Review of Records Created in the Forensic Register'.

Note: This section is not intended to describe the requirements of a review, just where to find information to perform the review and where to record notes from said review.

5.5.4 Recording Notes of Review

Following the review of the statement and associated samples, the review and provision of feedback, where applicable, can be completed via the track changes function associated to Microsoft Word against the drafted statement. Corrections regarding typographical errors through to technical observations and suggestions can be recorded against the draft statement as per the below steps.

Note: If the draft statement review process has been completed using a hardcopy then this step is not applicable – this is the current preferred method of feedback within the laboratory.

- Open the word document and add comments/suggestions using track changes (**Figure 65**)
  - Navigate to and click on the 'Review' tab in the tool bar of the word document
  - Navigate to the 'Tracking' group
  - Click on 'Track Changes'

- Save the amended document using the format *defaultfilename_your initials_Review*

- Upload the reviewed document against the '*REVIEW*' record as per the following:
  - From within a Forensic Case File Record select the *Case Management* tab
  - Select the *REVIEW* record, select *Edit Record*
  - Upload the document by using the *Choose File* option and browsing to the location where the reviewed document is temporarily stored OR by dragging the document from the stored location to this area on the page
  - Save the record

Communication to inform the Reporting Officer that the draft is now available for assessment post review can be completed in person or email or you can transfer the review *REQUEST* through the FR which will populate the reporters personal work list. The latter can be done by the following steps:

- Navigate and enter the Review *REQUEST*
- Amend the 'Case Officer' field to reflect the reporters FR ID
- Add an appropriate comment to the 'Comments' section
- Save the record

Bouncing the Review *REQUEST* between the reporter and reviewer can be completed indefinitely until the request has been marked as complete.

5.5.5 Reassessment of the Reviewed Draft Statement

This process refers to the acceptance or rejection of comments/suggestions and corrections added by the reviewing scientist. The following steps outline how to access an electronically reviewed draft statement.

- From within a Forensic Case File Record select the *Case Management* tab
- Select the statement record identified as *REVIEW* in the *Report Type* column
- Select the Microsoft Word icon to download the draft statement (**Figure 69**)
    - Where multiple documents exist, select the latest version



Figure 69 - Reviewed Document

- Open document and assess suggestions/corrections
- Save document and upload against the *REPORT* within the *Case Management* tab as per section 5.4.3

Note: This step can be repeated as many times as required until a final draft has been agreed upon by the reporter and reviewer.

5.5.6 Completing a Peer Review Record

This step is completed once the review process has been completed; eg, information within the statement has been accepted by both parties as being true and correct and the review of all exhibits completed. Completing a *REVIEW* record drives the milestones displayed against the case within the *Statement Review* work list as detailed in section 7 'Statement Worklists and Milestones'.

- From within a Forensic Case File Record select the *Case Management* tab
- Select the peer review record identified as *REVIEW* in the *Report Type* column (**Figure 70**)



Figure 70 - REVIEW record

- Select *Edit Record*

- Change the *Case Officer* ID to reflect the reporting officer (**Figure 71**)
  - Will allow the completion information to be transferred to the *REPORT* record

- Select the *Tech Review Complete and Peer Review Complete* checkboxes (see **Figure 71**)

Case Report Edit Record Mode

Report Type

Case File Technical Review	No Examination (NFA)	Case File Notation
Case File Admin Review	Statement/Technical Report	FOI / Legal Action
Case Prioritisation (DNA)	Statement (Peer Review)	Suspect Nomination
Photo Print Request	Court Attendance	Request / Task
MIR Activity Report	Case Conference Report	

Date	Forensic Officer	Unit Code	Duration	Examination No	Case Officer
04/10/2017	[redacted]	PSD	00:00		[redacted]

Exhibit	Exhibit Category	Date Required	Priority
			L H

Suspect Surname	Given Names	Date of Birth	CNI

Related File - ReportNo[redacted] [Note: Modified date/time will be set to upload date/time]

Choose File No file chosen

Comments

Peer Review Requirements

Tech Review Complete	By selecting this checkbox you are confirming that a Tech Review has been conducted for all examinations by this Case Officer.
Peer Review Complete	By selecting this checkbox you are confirming that a Peer Review has been conducted and that the final statement is attached to the Statement/Technical Report entry and is suitable for release.

Figure 71 - REVIEW Record

- Save the record (**Figure 72**)

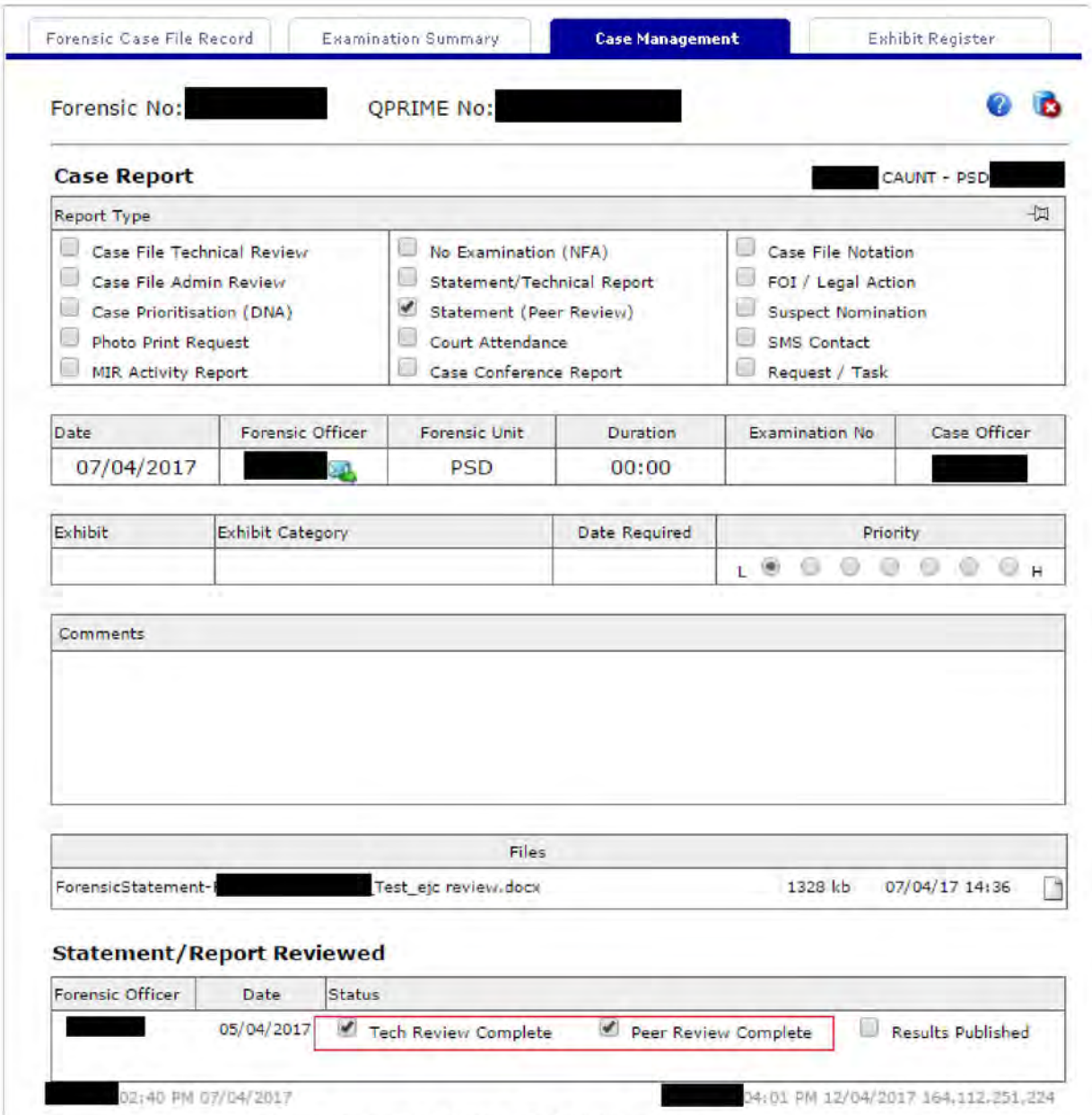


Figure 72 - Saved Details in REVIEW Record

Information from the completion of the *REVIEW* record will transfer to the associated *REPORT* record. As shown in **Figure 73**, the ID of the reviewer and the date the record was completed will be displayed in the *REPORT* record.

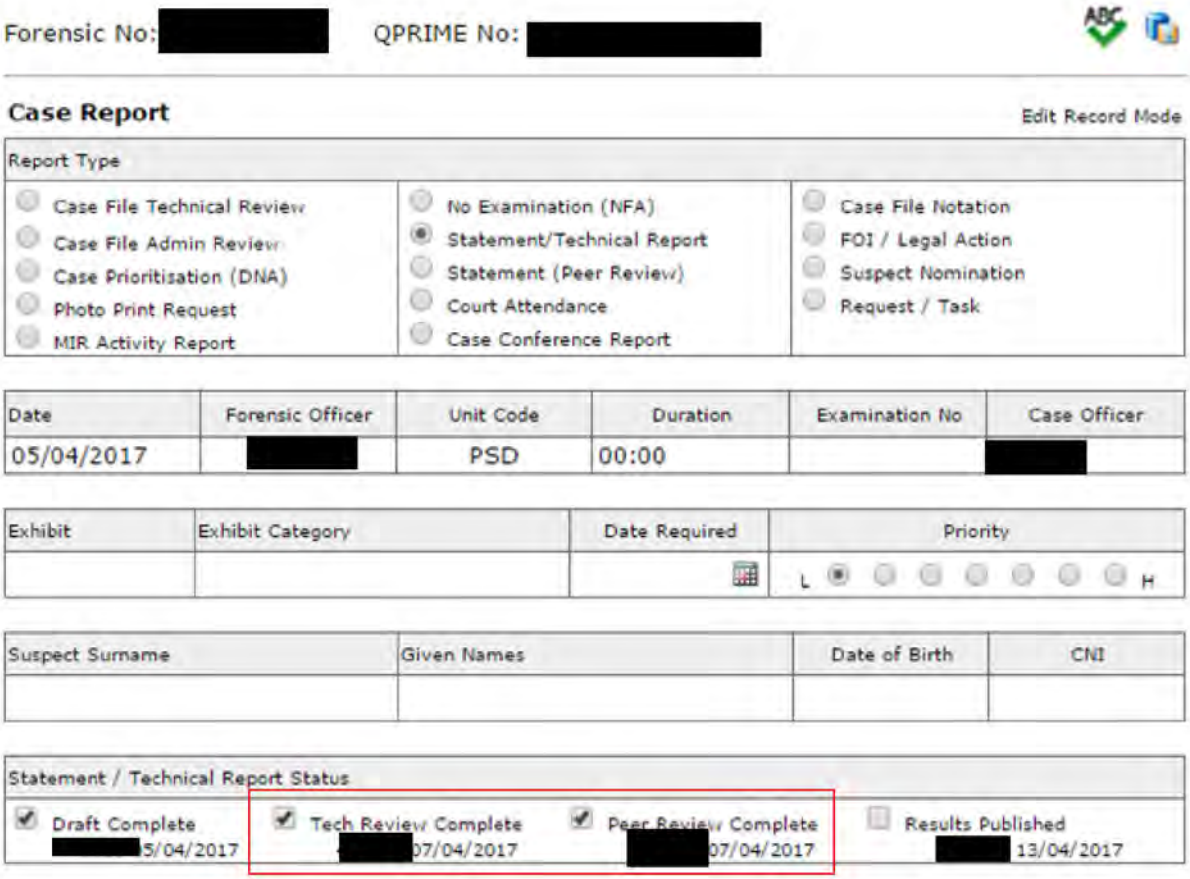


Figure 73 - Review Information Transferred to Report Record

- Update the *REVIEW REQUEST* as per 5.5.7.

5.5.7 Completing the Review Request

Once a task has been completed, the request within the FR must be completed. This action drives the milestones for the case within the *Active Case Files* work list as detailed in Section 7.1.3. This is completed by the following steps:

- Navigate to the *Case Management* tab and select *REQUEST (Review Request)*
- Select *Edit Record*
- Check the following boxes (**Figure 74**):
  - 1 *Request Complete*
  - 2 *Tech Review Complete*
  - 3 *Admin Review Complete*

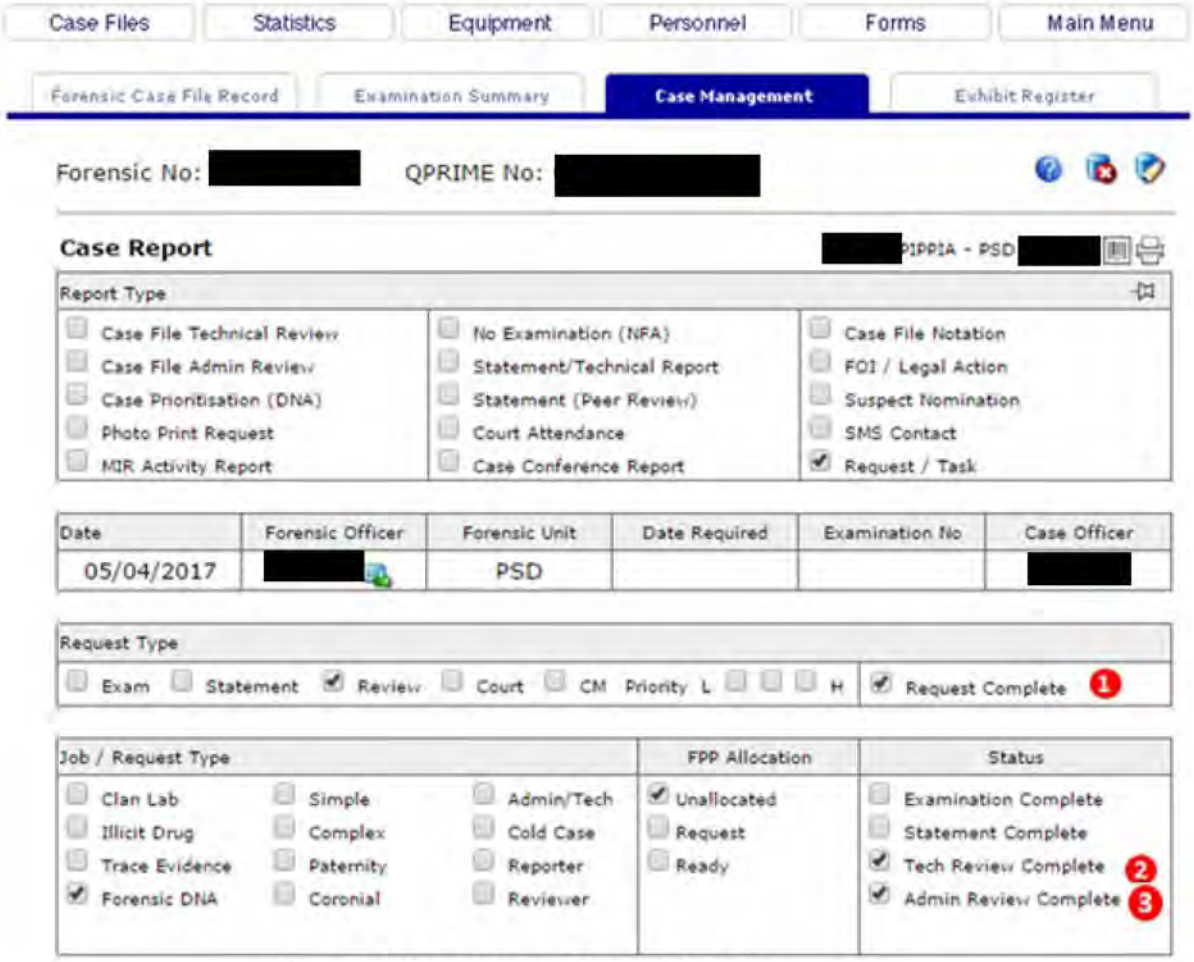


Figure 74 - Completion of Review REQUEST

- Save the record

5.6 Statement Finalisation

When the reporting and reviewing scientists have agreed that a statement is ready for release, the document is to be published in the Forensic Register before the original is sent to the client. This process is completed by the Reporting Scientist in conjunction with the Administrative Team.

Information regarding publishing a statement and finalising a REPORT record can be found in document, QIS: 34249 'Forwarding Statements and Evidentiary Certificates for Cases within the Forensic Register'.

5.6.1 Printing the Final Statement

The Reporting Scientist is to print the final statement. The Reporting and Reviewing Scientist are to sign the relevant sections on the statement; 'Case Analyst' and 'Peer Analyst' fields respectively and the bottom of each page including the 'Justices Act 1886' section. The signed, final statement will be added to the casefile and transferred to the Administrative team to complete the publishing of the statement.

The casefile is to be tracked to the 'Admin In-tray – Statements' as per the tracking process detailed in Section 19.1 and Appendix 7 of the document *QIS:* 33773.

5.6.2 Publishing a Statement and Completing the REPORT Record

Once the final version of the report is completed and is ready for release to the QPS, the following process will be completed by an Administrative Officer:

- Scan a copy of the signed document (PDF) for publishing – section 6.6, QIS: 34249
- Upload the PDF copy of the statement to the FR – section 6.8, QIS: 34249
- Transfer of the hardcopy, original, signed statement to the applicable external officers, DPP, QPS – section 7, QIS: 34249

Publishing the statement completes the *REPORT* record and also drives the milestones for the case within the *Statement Review* work list as detailed in section 7.1.4.

If however, publishing of the statement is to be completed by the reporting scientist, the following process shows how to complete this task.

- Navigate to the *Case Management* tab and select the *REPORT* record – displays as per **Figure 75**
- Select *Edit* and select the *Results Published* checkbox
- Upload the signed PDF as per section 5.4.3
    - To PDF the report, scan the document on a photocopier with scanning capabilities. Send the PDF of the signed report to your email and upload the file to the FR

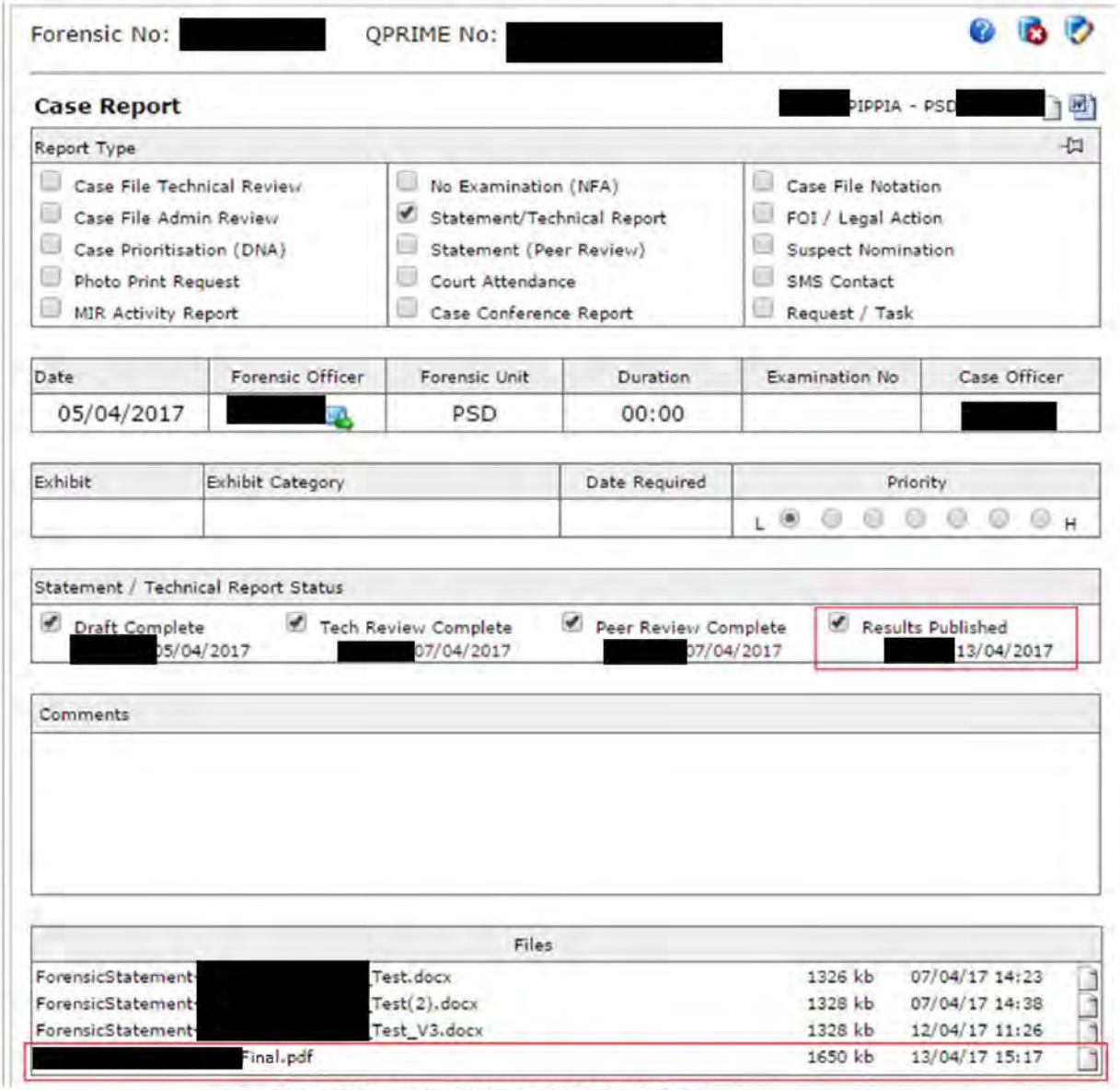


Figure 75 - Completion of REPORT Record

Save the record

5.6.3 Completing the Statement Request

Once the statement has been signed and has been sent to the Administrative team to publish, the *Statement REQUEST* must be completed by the Reporting Scientist. This action drives the milestones displayed against the case within the *Active Case Files* work list as detailed in Section 7.1.3. This is achieved by the following steps:

- Navigate to the *Case Management* tab and select the 'Review Request' REQUEST – displays as **Figure 76**
- Select *Edit*
- Check the following boxes:
  - 1 *Request Complete*

- 2 *Statement Complete*

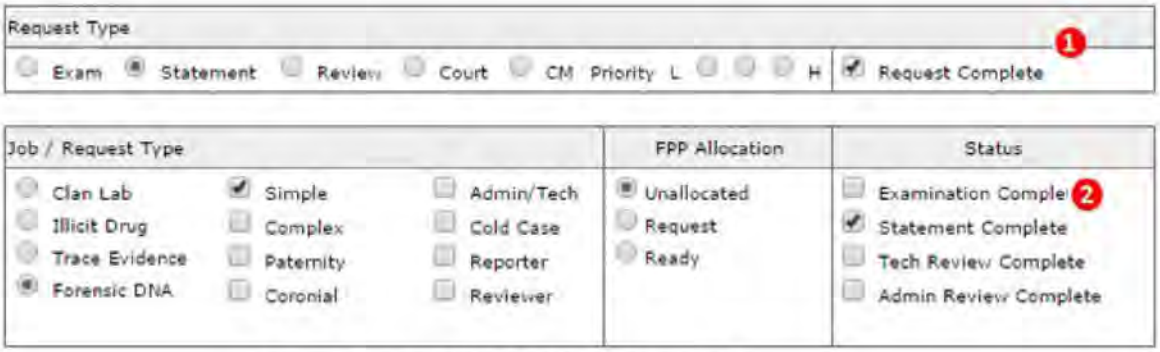


Figure 76 - Completion of Review REQUEST

5.7 Request for Multiple Reports

In the event multiple reports (eg, Statement of Witness and Evidentiary Certificate) are requested at the same time, these can be listed under the one request. However, each report requires an individual *REPORT* and *REVIEW* record. This will allow greater flexibility in the event:

- Multiple reviewers or reporters are required due to differing competencies
- One of the reports is requested to be released prior to the other reports

5.8 Distinguishing between Multiple REQUESTs and RECORDs

In the event multiple records and requests exist within a case eg, statement along with an Evidentiary Certificate, it is suggested the following approach be applied to aid in distinguishing linked requests and records.

When creating a request or record, the officer should add a 'title' in the *Comments* section appropriate to the report being completed. The addition of a title against each *REQUEST/RECORD* is recommended to aid in distiguishing between reports within the *Case Management* tab, described in section 5.3.1, **Figure 49**. This is achieved by adding a specific title in the *Comments* section when selecting the *Report Type* (see below).

A RECORD or REQUESTcan be edited at any stage to add a comment and will display as per **Figure 77**.



Figure 77 - Distinguishing between Reports

5.9 Reallocation of Reporting Scientist and or Reviewing Scientist

Where the reporting scientist and/or reviewing scientist are no longer able to complete the task, new scientists will be allocated.

Reallocation can be completed on the associated *REQUEST* by changing the 'Case Officer' field to the new reporter/reviewer – see section 5.2.1. A *RECORD* on the other hand is unable to be amended and will require that the existing *RECORD* be closed off. Technically, this is unable to be achieved therefore the next best thing is for the original reporter/reviewer to add a comment to the *RECORD* to state the report/review is being completed by another scientist.

The scientist/reviewer can add a comment to the effect "Statement reallocated for reporting/reviewing" as per point 4 of section 5.3.1, **Figure 49**.

6 Filtering of Report Types within a Case

Every request, record, note, etc created for a case can be viewed by clicking on the *Case Management* tab within a case. This list of *Report Types* can get congested and trying to find a specific record, request or communication can be difficult. This is overcome by filtering on the *Report Type* by completing the following:

- Click on to the *Case Management* tab
- Navigate down the list to report type
- Select one of the *Report Types* (see **Figure 78**)

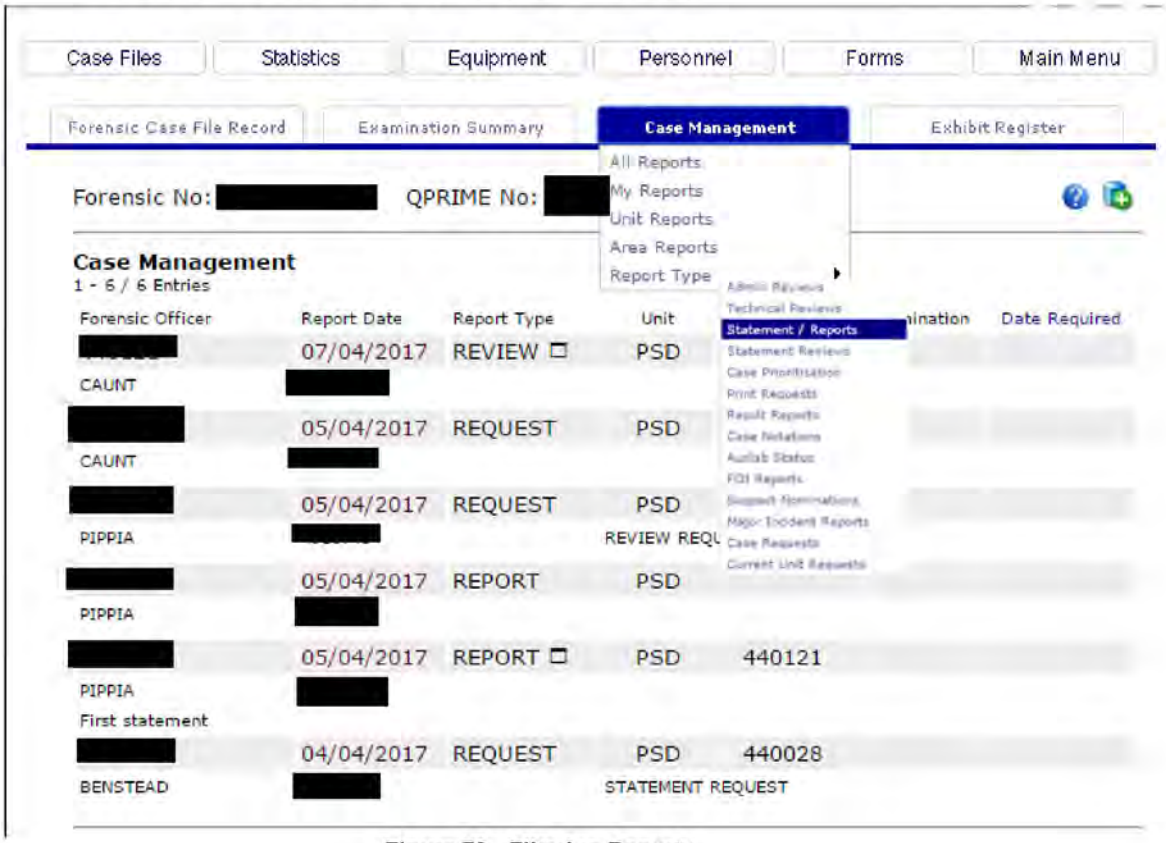


Figure 78 - Filtering Reports

- The filtered list will look like the following (**Figure 79**) based on a filter on 'Statement/Reports



Figure 79 – Filtered Display

To revert back to viewing all the *Report Types*, simply click on the *Case Management* tab and select 'All Reports'.

7 Statement Worklists and Milestones

Worklists are used to manage requests to produce a statement, along with active cases. The following information will describe how worklists can be used by the laboratory, in particular, the managing scientists (HP5 or HP6) to gather information on how a request and or a full case is progressing based on the achievement of milestones.

The *Unit Work List* tab is located on the main menu page and contains all the worklists used from a case management perspective.

7.1 Unallocated Statements

This list identifies cases with a statement request which have not been allocated to a case analyst (**Figure 80**).

This worklist can be accessed as follows:

- *Main Menu*
- *Unit Work List*
- *Unallocated Statements*



Figure 80 - Unallocated Statements list

The HP5 or above, will allocate to a reporting scientist as per section 5.2.1. This will populate the Personal Work List of selected scientist.

7.2 Unallocated Reviews

This list identifies cases which have statements drafted and are awaiting a scientist to perform a review.

This worklist can be accessed as follows:

- *Main Menu*
- *Unit Work List*
- *Unallocated Reviews*

Cases are predominatly self allocated but can be allocated by a HP5 or above as per section 5.4.4. This will populate the Personal Work List of selected scientist.

7.3 Active Case Files Worklist (Case Files PSD)

This list identifies cases with a request allocated to a particular scientist based on the *Case Officer* field of the *REQUEST* record (**Figure 81**).

The worklist also contains information on the job type (rape, paternity, etc), report date, due date and the milestones for the case:

- FPP = receipt of items
- Exam = Examinations completed as requested
- Stmnt = report/statement
- Tech = peer review
- Admin = peer review

A traffic light system reflects when a milestone has been achieved – green box indicates a part of the process has been completed and a red box means a task is yet to be achieved.

This worklist can be accessed as follows:

- *Main Menu*
- *Unit Work List*
- *Active Case Files*

PIPPIA.A

ReportNo	Job Type	Report Date	Due Date	Type	FPP	Exam	Stmnt	Tech	Admin
[redacted]	Murder (Inc. attempts)	10/12/2018		CM (Reporter)	■	■	■	■	■
	Rape	09/08/2019		Review	■	■	■	■	■
	Murder (Inc. attempts)	26/08/2019	01/10/2019	Statement	■	■	■	■	■
	EFRAC	04/09/2019	07/10/2019	Statement	■	■	■	■	■
	EFRAC	06/09/2019	08/10/2019	Statement	■	■	■	■	■
	Rape	06/09/2019	04/10/2019	Review	■	■	■	■	■
	EFRAC	09/09/2019	09/10/2019	Statement	■	■	■	■	■
	Robbery Offences	16/09/2019	16/10/2019	Statement	■	■	■	■	■
	Rape	17/09/2019	14/10/2019	Court	■	■	■	■	■
	SWAB	18/09/2019	11/11/2019	Court	■	■	■	■	■
	Robbery Offences	23/09/2019	14/10/2019	Review	■	■	■	■	■

Figure 81 - Active Case Files list

7.4 Statement Review Audit Worklist (Statement Review PSD)

This list identifies cases with an allocated *Case Officer* and records the progress of the case via the milestones achieved within *RECORDS – REPORT and REVIEW* (**Figure 82**). A traffic light system reflects when a milestone has been achieved – green box indicates a part of the process has been completed and a red box means a task is yet to be achieved.

This list will update according to the following fields on the *REPORT* record and *REVIEW record*:

- *Case Officer* field – records the case (listed by the FR number) to a scientist
- *Draft Complete* checkbox (*section 5.4.3)* – records the '*Draft'* milestone
  - Unallocated: *Case Officer* field is blank and the case appears yellow on the list
  - Allocated: *Case Officer* has reviewer entered (recorded in *Allocated* column)
- *'Tech Review Complete'* and '*Peer Review Complete'* boxes checked and Case Officer filed updated to reporter's ID (section 5.5.6) = records the 'Tech' and 'Peer' milestones
- *'Results Published* (section 5.6.2) = records the '*Pub'* milestone

This worklist can be accessed as follows:

- *Main Menu*
- *Unit Work List*
- *Compliance Audits*
- *Statement Review Audit*



Figure 82 - Statement Review Audit

8 Evidentiary Certificate Statement

8.1 Certificate Details

Refer to Section 95A Evidence Act 1977.

This is a certificate (in an approved form – see **Appendix 4**) that must be signed by an authorised DNA Analyst.

A list of current staff who hold appointments (in accordance with Section 133A of the Evidence Act 1977) as DNA Analysts is held with the Managing Scientist. Refer to QIS: 25608 'Appointment and Cancellation of State Analysts' for details on the process to gain approval for a Reporting Scientist to become a DNA Analyst and the process for publishing in the Government Gazette.

It states that any of the following is evidence of the matter:

- Receipt and testing of the item/s
- Stated DNA Profile (specific barcodes should be requested by QPS)
- That the DNA Analyst examined the records relating to the receipt, storage and testing of the item/s in relation to the matter including any test process that was carried out by someone other than the analyst
- Confirms that the records indicate that all quality assurance procedures for receipt, storage and testing for the item/s that were in place in the laboratory at the time of the test were complied with.

8.2 Sample Batch Information

This is to be completed as per the following:

- Navigate to the *Exhibit Register* tab and highlight the *DNA Analysis* drop down menu
- Highlight the *Evidence Cert – Analysis*

This will open a Html document containing receipt information along with analytical batch information of all samples that have undergone processing within the laboratory. Processing notes that have been added to batches will also be displayed.

This information is to be checked as part of DNA profile interpretation. There is no requirement to print this information as signing of the DNA Evidentiary Certificate by the DNA Analyst confirms that they have read the relevant batch information.

8.3 Storage

Storage of the individual samples and the corresponding sub-samples, spin baskets, slides, etc, can be viewed and reviewed from the 'Exhibit Movement' table located on the Exhibit Testing page on the sample management tab of the FR. Navigating to the individual samples/sub-samples is detailed in Section 4 of this document.

8.4 DNA Profile Table

A table of the DNA profiles generated for sample(s) requested as part of the Evidentiary Certificate are to be added to the bottom of the Evidentiary Certificate report. This is to be completed as per the following:

- Navigate to the *Exhibit Register* tab and highlight the *DNA Analysis* drop down menu
- Highlight the *Evidence Cert – Profiles*

This will open a *html* file with all the DNA profiles generated for each individual sample for the case. This information is to be exported into an Excel spreadsheet and formatted. Add a header and footer with the appropriate details:

- Header = QP number
- Footer = Reporters name; page number eg, '1 of 6' and the date

8.5 Report Drafting

Drafting of the DNA Evidentiary Certificate requires the use of an external template which is provided as **Appendix 4**. Open a new word document and add the template, fill in the required fields and upload the draft evidentiary certificate to the REPORT record as per Section 5.4.3 of this document.

Ensure the applicable appendix, listed in **Appendix 2**, is added to the certificate ensuring the title "Appendix 1" is displayed.

Receipt information can be found on the same document produced for batch reviewing. Refer to section 8.2 of this document for instruction on navigating to this information.

Once the document has been opened the receipt information can be located at the top of the page. Copy and paste this information into the appropriate sections of the Evidentiary Certificate.

8.6 Workflow for Report Creation and Release

Requests and records used during report drafting, report review and publishing are outlined in Sections 5.2, 5.3, 5.4.4, 5.5.1, 5.5.6 and 5.6.3 of this document.

The report review process is detailed in section 5.5 of this document.

Finalisation and publishing of the report is outlined in Section 5.6 of this document.

9 Paternity Reporting

9.1 Report Drafting

Drafting a Paternity Report is completed as per the process described in section 5.4 and applying the appropriate appendix to the statement found in **Appendix 2,** ensuring to remove unnecessary content. Example wording for a paternity report can be found in **Appendix 3.**

Receipt information can be found on the same document produced for batch reviewing. Refer to section 8.2 of this document for instruction on navigating to this information.

Once the document has been opened the receipt information can be located at the top of the page. Copy and paste this information into the appropriate sections of the paternity report.

9.2 Workflow for Report Creation and Release

Requests and records used during report drafting, report review and publishing are outlined in Sections 5.2, 5.3, 5.4.4, 5.5.1, 5.5.6 and 5.6.3 of this document.

The report review process is detailed in section 5.5 of this document.

Finalisation and publishing of the report is outlined in Section 5.6 of this document.

10 Intelligence Reports

If there is information that may not be included in a statement for evidentiary reasons, an Intelligence Report may be produced. This report type should be approved by a Senior Scientist (or higher), and the Senior Scientist of the Intelligence Team should be notified if work is to involve NCIDD. These reports must go through the same peer review process as required for all results released from the laboratory.

Intelligence Reports regarding general casework should be directed to the Senior Sergeant DRMU.

Intelligence Reports written regarding Quality issues should be directed to the Inspector QPS DNA Results Unit (QPS). These are generally written by the Senior Scientist of Quality and Projects and reviewed by a Team Leader.

Matches on NCIDD that are below our standard match reporting stringency can be reported to DRMU via Intelligence Reports.

For further detail refer to document QIS: 34308 'Procedure for Intelligence Reports and Interstate/Interpol Requests in the Forensic Register'.

11 Civil Report

Refer to QIS: 10629 'FSS – Quotation and acceptance of work' for general procedure.

On rare occasions, the laboratory may receive requests for civil work to be conducted. This may be in the situation of a case where a criminal component has been finalised and a civil component is ongoing, or if a profile generated in the laboratory is requested to be compared to DNA profiles generated from other laboratories in, for example, cases of disputed parentage.

Acting upon these requests is at the discretion of the Managing Scientist.

Upon receipt of the request, either the Managing Scientist or Team Leader will confirm arrangements for the work with the requesting party. In confirming this, a written request from the requesting party should be received and timeframes should be negotiated. A cost will be involved and the requesting party should be informed of this.

11.1 Negotiation of Timeframe

The timeframes should be consistent with the timeframes for criminal work. If the matter had a criminal element that meant the processing was complete at the time of the request, then this should be factored into the negotiated timeframe.

11.2 Approval Process

The Managing Scientist or Team Leader are to complete the form QIS: 20401 'Quotation'. This may involve clarification from the requesting party for ABN and other official terms and contact points.

Depending on what testing is required, the fee for service will vary. For further advice on costing, HSQ Finance may be consulted.

This Quote is approved by Executive Director FSS or higher.

When an approved Quote is received, this should be emailed to the requesting party before any work commences. Acceptance of the Quote should be saved on the network and added as a 'Casefile Notation'.

11.3 Report Format

Civil Court reports do not have the same format as Statements of Witness issued for criminal work. Civil work uses the Uniform Civil Procedure Rules 1999 and the format should meet the requirements of these rules.

Some differences to criminal reports include:

- Forensic DNA Analysis is not currently NATA accredited for civil paternity work; therefore, the NATA logo should be removed.
- The Justices Act 1886 should be removed
- Details of procedural overview and test methodology can be detailed in the report by choosing an appropriate appendix used in Criminal matters, refer to **Appendix 2** for an example – NATA references should be removed if the matter is a civil paternity.

- The addition of information on 'Analytical Processes' and 'Quality', detailed in **Appendix 5**, can be added to the Appendix selected in the previous point – has been requested by legal officers in past occasions.

Include the Uniform Civil Procedure Rules 1999 – Sect 428. See **Appendix 6**.

The Magistrates Court of Queensland may request an Affidavit (Form DV25) to be prepared in cases of alleged Domestic Violence in accordance with the Domestic and Family Violence Protection Rules 2014, Rule 35. The Affidavit will require a witness signature of Justice of the Peace, Commissioner for Declarations or Solicitor. In these cases (Civil), the Statement of Witness is not the format for the information to be presented regarding DNA findings. The same information can be transcribed into the template of Form DV25. The current version of the template should be sought in consultation with QPS or the requesting party. An example of the template is G:\ForBiol\AAA Forensic Reporting & Intel\Specific Casework\Civil Casework.

11.4 Issue and Invoice

When the work is complete, the report should be issued as per Section 11.5 below. At this time, the requesting party should be emailed to inform them that the work is complete and that an invoice will be issued.

The Managing Scientist or Team Leader should email [redacted] to ask them to organise issuing the invoice to the requesting party. It is advisable to include the approved quote in this email. This email can be saved within the FR by uploading it under a 'Casefile Notation'.

11.5 Workflow for Report Creation and Release

Requests and records used during report drafting, report review and publishing are outlined in Sections 5.2, 5.3, 5.4.4, 5.5.1, 5.5.6 and 5.6.3 of this document.

The report review process is detailed in section 5.5 of this document.

Finalisation and publishing of the report is outlined in Section 5.6 of this document.

12 Crime and Corruption Commission (CCC) or Ethical Standards unit of the QPS

Due to the confidential nature of these cases, clarification from the QPS requesting officer needs to be sought for the appropriate reporting method – result lines vs Intelligence report Vs email.

This report type shall be approved by the Managing Scientist or Team Leader prior to drafting the report, but will generally be Intelligence Reports sent directly to the Inspector of the QPS DNA Management Unit. In rare situations, the requesting party may bypass the Inspector QPS DNA Management Unit.

Information on authority to upload to NCIDD, and whether Reference Samples will be received should also be sought - QPS will most often make an assessment on this if DNA results are obtained.

This report shall be addressed directly to the Inspector QPS DNA Management Unit, or nominated person and begin with (or equivalent):

" RE : SSFXXXXX (Complainant Jane Smith)

I am writing to summarise the results of examination conducted in the Forensic DNA Analysis laboratory at Forensic and Scientific Services in relation to the above alleged XXXXXXX incident/s."

This report may include the following statement elements to assist in the understanding of the results:

- Receipt details of reference samples and exhibits
- Preamble (Role of a Forensic Scientist, DNA Profiling and appropriate blood or semen preambles)
- List of Reference Samples (and results)
- Results of testing for exhibits submitted
- Items not examined

The report should end with "This information has been peer-reviewed in accordance with standard laboratory Quality Assurance protocols".

This report must go through the same peer review process as required for all results released from the laboratory. The report should be saved within the FR under a 'Notation' or 'Casefile Notation' depending on whether the information is for a single sample or multiple samples.

13 External Testing (Example Low Copy No. or Mitochondrial DNA) in Statements

If the results of tests not performed in the laboratory are included in reports, the source of these results shall be clearly and unambiguously identified in the report/statement. This would be a rare event.

If external testing is discussed with the QPS Investigating Officers, these discussions need to be disclosed to the Inspector (or delegate) of QPS DNA Results Management Unit, or the S/Sgt of the QPS Quality Management Unit. Authorisation for external testing must be given and arranged by QPS.

14 Statements with Coronial Samples

Within the FR, coronial samples will be associated to an Occurrence Number and as such receipting and sample information will be pulled into the statement.

14.1 Coronial and Disaster Victim Identification (DVI) Statement

The report will be the same as a standard statement detailed in Section 5 of this document.

The originals of these types of reports are hand-delivered to the Coronial Support Unit (QPS). A copy of the report is retained in the casefile (as per Statement of Witness above).

The format/template for DVI Preliminary Reports is in QIS: 23955 'Disaster Victim Identification DNA Reports'.

14.2 Workflow for Report Creation and Release

Requests and records used during report drafting, report review and publishing are outlined in Sections 5.2, 5.3, 5.4.4, 5.5.1, 5.5.6 and 5.6.3 of this document.

The report review process is detailed in section 5.5 of this document.

Finalisation and publishing, *this aspect of statement release is subject to further input from the reporting scientist competent in performing this task in conjunction with QPS officers within the Coronial Support Unit (CSU) and the State Coroner.*

15 Tracking of Casefiles

15.1 Casefile

Where a physical casefile is available this needs to be tracked throughout the reporting and review process as per 'Appendix 9 – Creating and tracking a casefile', QIS 33773.

16 Court

16.1 Request to Provide Testimony

Where a reporting scientist is required to provide expert testimony, communication can be completed in the form of a request which will populate the scientist's *Personal Work List*.

The request can be created by a member of the Scientific Services Liaison Unit (SSLU), a HP5, an officer of the Queensland Police Service or by the FSS reporting officer. The request will be completed by the following steps (**Figures 83 and 84**):

- From within a Forensic Case File Record select the *Case Management* tab
- Select *Add Record* and the following will display



Figure 83 - Court Testimony Request

- Select *Request/Task* which extends page content to display the following fields
- Complete the following fields:

- *Case Officer* – allocated case analyst if known 1
- *Date Required* – due date for statement (optional) 2
- *Request Type* – select *Court* 3
- *Priority* – select priority as appropriate (optional) 4
- *Job/Request Type* – select *Forensic DNA* 5

Note – fields 2 and 4 are not required to complete the request.

Date	Forensic Officer	Forensic Unit	Date Required	Examination No	Case Officer
02/05/2017	[redacted]	FSS	31/05/2017 2		[redacted] 1

Request Type 3											Priority 4	L				H	Request Complete
☐ Exam	☐ Statement	☐ Review	☑ Court	☐ CM													

Job / Request Type			FPP Allocation	Status
☐ Clan Lab	☐ Simple	☐ Admin/Tech	☑ Unallocated	☐ Examination Complete
☐ Illicit Drug	☐ Complex	☐ Cold Case	☐ Request	☐ Statement Complete
☐ Trace Evidence	☐ Paternity	☐ Reporter	☐ Ready	☐ Tech Review Complete
☑ Forensic DNA 5	☐ Coronial	☐ Reviewer		☐ Admin Review Complete

Figure 84 - Court Request Specifics

Save the record

16.2 Recording Details of Court Appearance

Following the provision of testimony, details regarding the evidence can be captured within the FR via a *Case Report* record (**Figure 85 and 86**). Fields within this page are searchable and can be used for datamining, collating time spent away from normal duties and how many times staff had to provide evidence. Although the *Date* will contain the date at which the report has been generated this field is able to be amended to reflect the date court was attended.

The 'Comments' section, in particular, can be used to capture specific information in the form of suggested key words to allow this function to work optimally. As such, key words will be used to detail questions posed during evidence in chief and cross examination.

A word document may also be uploaded to this page after the record is saved.

The following steps will be used to create the *Case Report* page:

- From within a Forensic Case File Record select the *Case Management* tab
- Select *Add Record*
- Select *Court Attendance* which extends page content to display the following fields

Case Report [redacted] PIPPIA - PSD [redacted]

Report Type		
☐ Case File Technical Review	☐ No Examination (NFA)	☐ Case File Notation
☐ Case File Admin Review	☐ Statement/Technical Report	☐ FOI / Legal Action
☐ Case Prioritisation (DNA)	☐ Statement (Peer Review)	☐ Suspect Nomination
☐ Photo Print Request	☑ Court Attendance	☐ SMS Contact
☐ MIR Activity Report	☐ Case Conference Report	☐ Request / Task

Date	Forensic Officer	Forensic Unit	Duration 1	Date Concluded 2	Case Officer
03/04/2018	[redacted]	PSD	02:45	03/05/2017	

CourtType 3	Proceedings 4	Appearance 5	Location 6
District Court	Hearing	Person	Brisbane

Comments
Duration in box - 00:50 7 DPP = John Smith Defense = Dapheny Wright Evidence in Chief: Profile Interpretation = why profile changed from Complex Unsuitable to 3 person mixture STRmix = explained process and was asked about weightings of allelic combinations Database = Explained why Aust Caucasian DB was quoted and the other DBs utilised Transfer = digital penetration and whether DNA transfer from anus to vagina expected Cross Examination: STRmix = was system validated by external parties Transfer = posed multiple scenarios; could DNA on digit persist for extended period of time and if so, could foreign DNA be a result of shaking hands 2 hours prior

Figure 85 - Court Report Details

- Complete the following fields:
  - *Duration* – total time of court appearance (time presenting evidence + time waiting to give evidence – time in box will be captured in the *Comments* section) 1
  - *Date Concluded* 2
  - *Court Type* 3
  - *Proceedings* 4
  - *Appearance* - enter whether required in person, on the phone or via video link 5
  - *Location* – free text field for town/city 6
  - *Comments* – as discussed above, this section will be used to summarise the question encountered during evidence and will be used for datamining (use of key words is required) 7
- Save the record

Note – when adding information to the *Comments* section only add information that is significant, eg, no need to record questions relating to name, length of employment and other such standard information.

Furthermore, a *Word* document is able to be uploaded to the court report in the same way the statement is added to a *Report* record (see section 5.4.3, **Figures 57 and 58**)

Upon saving, the record will be viewable from the *Case Management* tab under the 'Report Type' *COURT*.

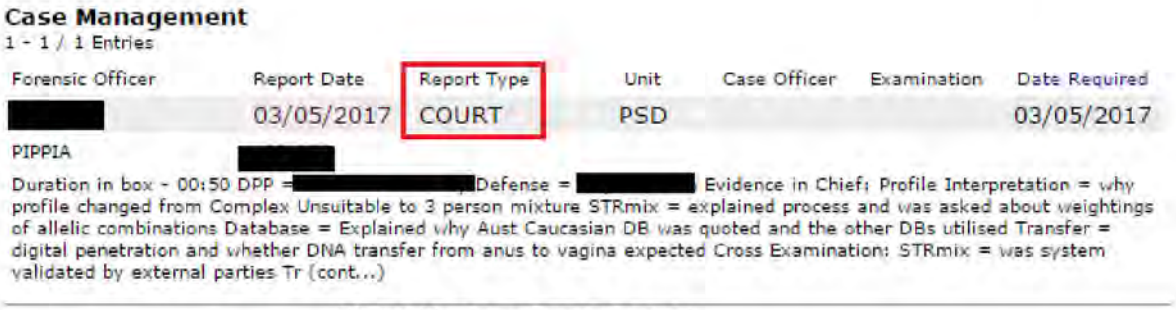


Figure 86 - Court Report Record

16.3 Court Monitoring/Evaluation

Every Reporting Scientist should have their testimony evaluated every 12 months where possible. The evaluation can be performed by another Reporting Scientist, a court official (DPP or Defence) or QPS Officer.

The first page of the QIS: 17047 'Court Testimony Monitoring Evaluation Form' should be filled out by the assessor. This paperwork should be given to the Reporting Scientist's Line Manager or Team Leader to identify any potential training gaps. The second page should then be filled out by the Line Manager and Reporting Scientist and any plans for further training to be documented. The details of the case number, date, type of court, assessor should be added to QIS in the PD module under the 'Other' tab. This should be sent to the Line Manager for verification. The original paperwork should be kept in the Reporting Scientist's training folder.

If court testimony is infrequent such that an evaluation has not been conducted in a 12 month period, the next court appearance should be assessed. Alternatively, a moot court could be held with the Reporting Scientist and two competent senior staff, ideally the Line Manager and Team Leader.

If there was an unusual court experience, or different questions to ones normally expected, a report of that court appearance should be provided orally at a Forensic Reporting and Intelligence Team meeting. This will allow debriefing from what are sometimes stressful events, the sharing of 'real' court questions and current court trends, the refinement of answers through discussions, and the identification of possible areas of improvement for the work unit. It will also help with public speaking, an essential component of court testimony.

16.4 Case Conference Record

Records of case conferences can be added to the FR. To create a record follow the below steps further displayed in **Figure 87 and 88**):

- From within a Forensic Case File Record (QPS page) select the *Case Management* tab
- Select *Add Record*
- Select *Case Conference Report* and the following page will display

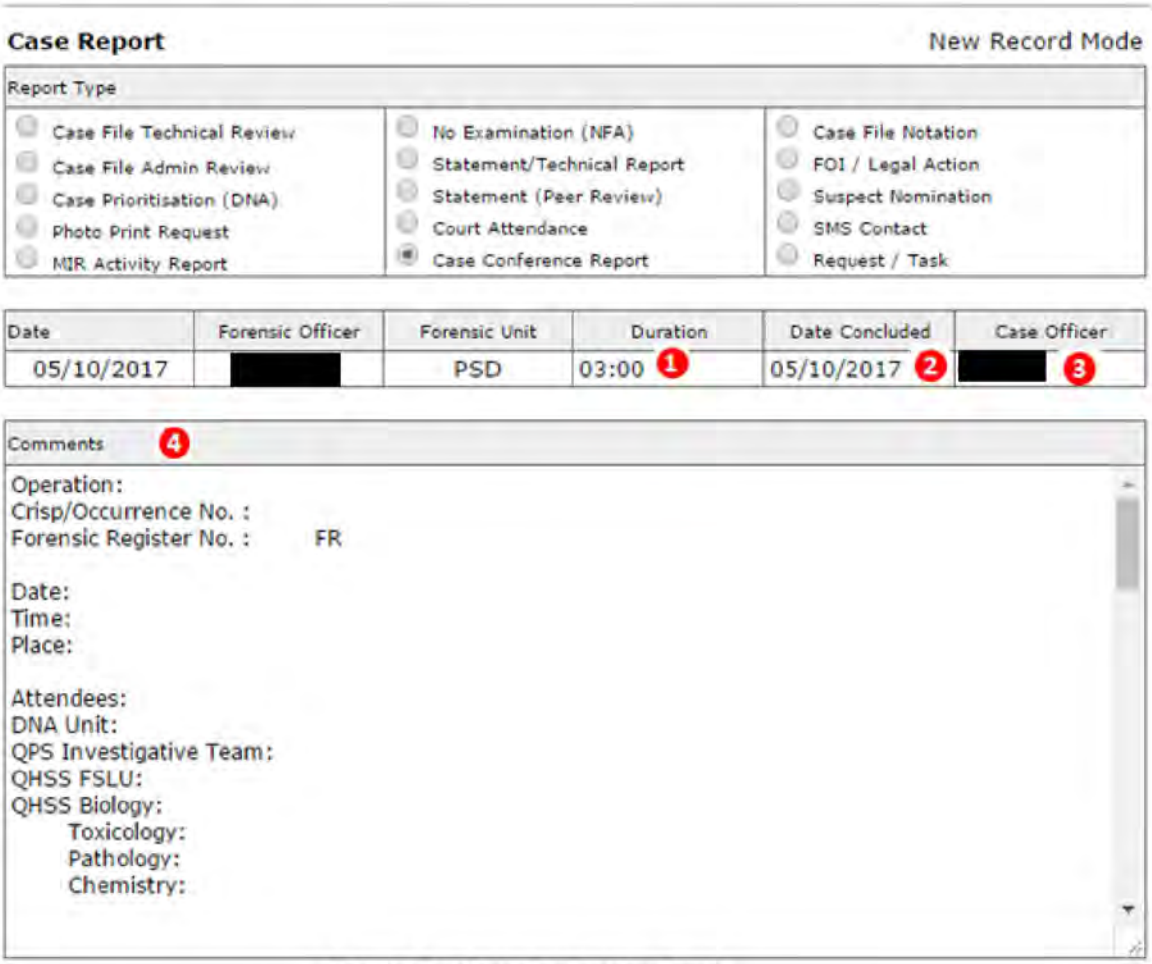


Figure 87 - Case Conference Detail

- Complete the following fields:
  - *Duration* – total time of conference 1
  - *Date Concluded* 2
  - *Case Officer* 3
  - *Comments* – Information discussed during meeting 4

Note – the comments section contains pre-set sections that can be used as a guide. Extend the field to see these options

- Save the record

Furthermore, a *Word* document is able to be uploaded to the court report in the same way the statement is added to a *Report* record (see section 5.4.3, **Figures 57 and 58**).

Upon saving, the record will be viewable from the *Case Management* tab under the 'Report Type' *CASECON* (see **Figure 88**).

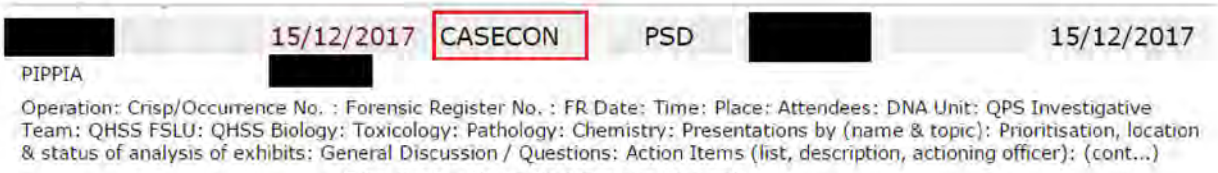


Figure 88 - Case Conference Record

17 Further Documentation Requests

This section refers to the release of information such as audit trails, specific information regarding sample processing or opinion evidence.

A written request should be obtained from DPP or QPS detailing what is specifically requested, ideally with item barcodes listed. When information is received by QHFSS via QPS, or the Office of the DPP (ie. another government department), information can be provided directly to the requesting party. When written requests come directly to QHFSS from Defence Legal representatives, it must be referred on to a Senior Scientist or Team Leader and also forwarded on to QHealth legal (Legal Unit) who will ask the Defence Legal team to subpoena the information. It is preferable to avoid this by asking the Defence Legal team to direct their requests through DPP or QPS.

When providing subpoenaed information, the request should come through FSS Correspondence email address: [redacted] who will track its progress to ensure the information is provided by the timeframe stipulated.

If an audit trail is requested and it is subsequently considered part of the casefile, the pages should be numbered and have the case identifier added. If it is not considered part of the casefile, there is no need for page numbering or identifying numbers to be added, refer QIS: 17117. It is however recommended that this occurs as it is helpful if/when it is referred to in court proceedings.

Documenting the specific information release and the review of this information can be completed in the FR by creating a "Request/Task". The authoring scientist will state the request and the information released within the Request/Task and the scientist performing the review of the information released can add a line in the Request/Task specifically stating who performed the review and when. Alternatively, a Report Record and Review Record can be created in the same way a statement is drafted and released.

If Standard Operating Procedures and internal reports are provided, it is recommended that these are marked to be used in the matter it was requested for only. A watermark is a suggested way to make this point clear.

The requested information can be saved on disc and password-protected. This can be performed on a computer with Adobe Professional. The Investigating Officer will need to be informed of the password to open the files.

It is recommended that the Reporting Scientist negotiate with the requesting party a suitable timeframe for the release of the information. This timeframe should be verified by a Senior Scientist or Team Leader.

18 Associated Documentation

QIS: 17117 – Procedure for Case Management

QIS: 23752 – FSS Court Training Program

QIS: 23955 – Disaster Victim Identification DNA Reports

QIS: 25608 – Appointment and Cancellation of State Analysts

QIS: 29009 – Statement of Witness template – blank – no NATA endorsement

QIS: 29010 – Statement of Witness template – stamp

QIS: 29011 – Generic report template

QIS: 29024 – Use of offline Forensic Reporting templates

QIS: 33744 – Forensic Register Training Manual

QIS: 33773 – Procedure for profile data analysis using the Forensic Register

QIS: 34045 – Quantification of Extracted DNA using the Quantifiler® Trio DNA Quantification Kit

QIS: 34064 – Miscellaneous Analytical Procedures and Tasks

QIS: 34229 – Explanations of Exhibit Results for FR

QIS: 34245 – Reference Sample Result Management

QIS: 34248 – Administrative Team – Case file related duties using the Forensic Register

QIS: 34249 – Forwarding Statements and Evidentiary Certificates for Cases within the Forensic Register

QIS: 34281 – Procedure for the Use and Maintenance of the Forensic DNA Analysis

QIS: 34298 – Validation of Examinations (Forensic Register)

QIS: 34308 – Procedure for Intelligence Reports and Interstate/Interpol Requests in the Forensic Register

QIS: 34322 – Technical and Administrative Review of Records Created in the Forensic Register

19 Amendment history

Version	Date	Author/s	Amendments
1	22/12/2017	Adrian Pippia	First Issue
2	October 2019	Adrian Pippia	- Remove reference to P+ from Section 4.1 and 4.2 - Latest barcode searching tools added to section 4.4.1 - SOP added to Section 4.4.4 for info on exhibit examination validation (red dot '2') – addition of SOP 34298 - Further information on validation options added to 4.4.10 - Addition of section 4.4.11 – Urgent Request workflow - Section 4.4.13 – SOP 17047 replaced with 34229 - New section 4.4.16 added to describe No DNA Detected and Insufficient DNA process - New section 4.4.17 added to describe Quant and Hold release of results and covert samples - Update to Section 9.1 – Paternity draft report using all-inclusive appendix instead of preamble - Addition of due date to 'Review Request' to Section 5.4.4 - Section 11.3 Civil Report has been updated - Appendix 5 has been stripped of all but two paragraphs that can be added to appropriate Appendix - Section 17 – SOP 18034 replaced with 23752 - Associated Documents section updated with above SOP additions and removals - Appendices 3 and 4 removed, preamble no longer separate to appendix in report - Appendix numbering updated and cross referenced within body of SOP
3	25/03/2021	Adrian Pippia	Sections 4.1, 4.1.1 and 4.2 – "Profile Data Analysis Review Worklist" amended to "Profile Review Worklist" as per FR title Section 4.4.6 – Removed wording "Described in section 7" Removed info re QFLAG checks as documented in SOP 34281 Section 4.4.7 – Use of Sample Undergoing Further Testing result lines Section 4.4.9 – Batch acknowledgement by reviewing scientist Section 4.4.13 – update to how PDFs can be uploaded to FR

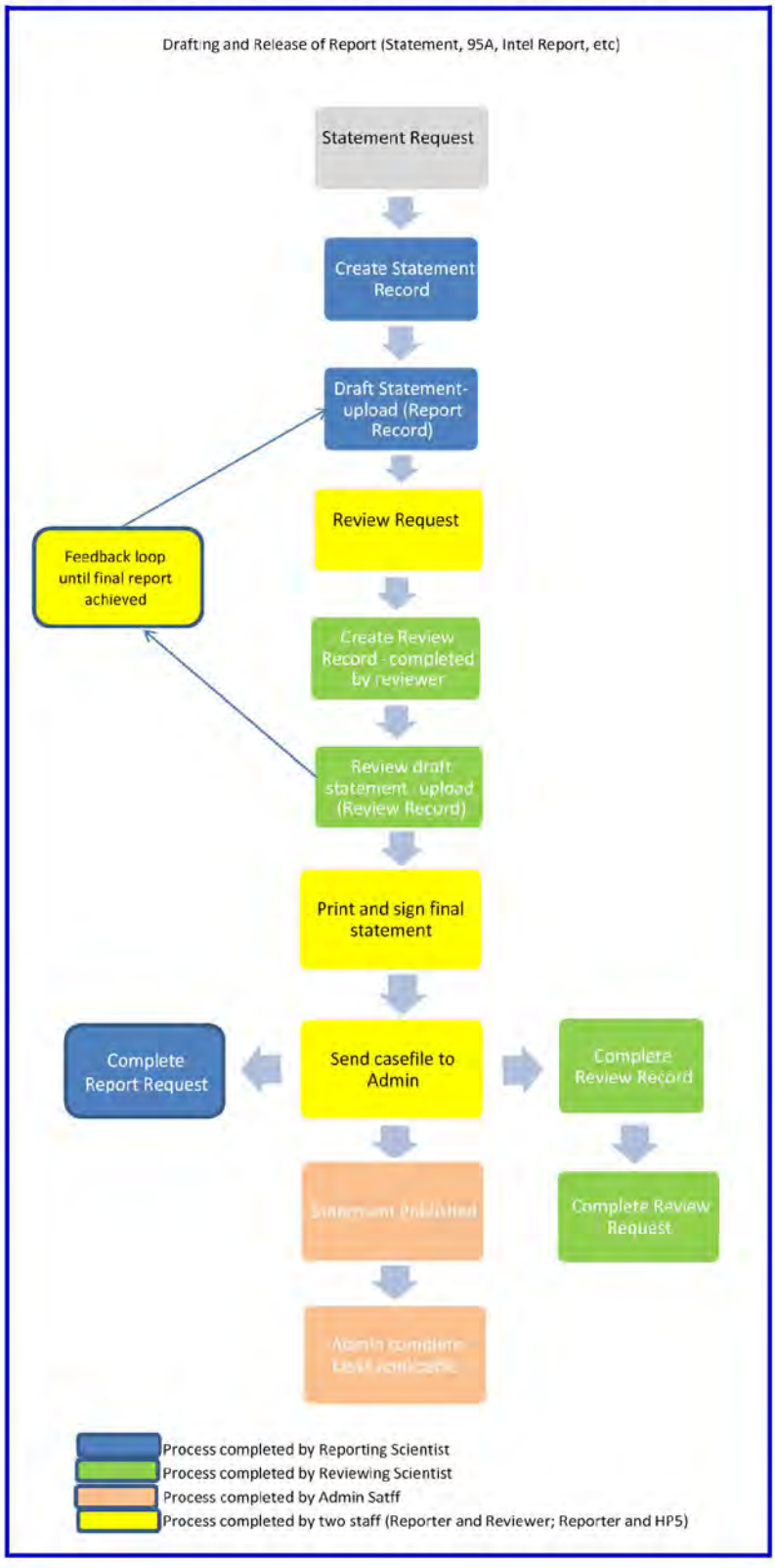
			Section 4.4.17 – Communication for Cold Case to be directed to Cold Case Coordinator Section 5.2 – Existence of multiple FRs Section 5.4.2 – Listing multiple complainants in report Section 5.4.2 – Addition of suggested wording for statement (Appendix 8 created) Section 8.5 – Addition of appropriate appendix titled "Appendix 1" Section 15.1 – reference to Appendix 7 amended to Appendix 9 Section 17 – Addition of new section regarding further documentation request Associated Documents – updates completed Appendix 2 – removed VarNOC appendix; update to Paternity paragraph (propositions) Appendix 7 – Instruction added for NTR of a PM sample Appendix 9 added – work from home information Appendix 10 added – offline statement Section 16.3 – reference to SOP 23752 removed Added header to page 1
4	05/07/2022	Adrian Pippia	<u>Appendix 2</u> – additional phrasing added to statement appendix para "Forensic Biologist"; "The signed Statement is the report issued by Forensic and Scientific Services. Any other attachments or information provided is not considered to be the issued report". - "Semen stains" updated. Appendix 2 – Health Support Queensland removed from laboratory structural. Lab referred to as "Forensic DNA Analysis, Forensic & Scientific Services" <u>Section 11</u> – Magistrates Court of Queensland may request an affidavit (Form DV25) to be prepared in cases of alleged Domestic Violence in accordance with the Domestic and Family Violence Protection Rules 2014, Rule 35 <u>Section 4.4.15</u> – update to process of seeking information on ownership. <u>Section 4.4.16</u> - update to current DNA profiling procedure. <u>Section 4.4.17</u>

			– addition of "Release of result via email" information added

20 Appendices

1. Drafting, Review and Release of Reports (Statement, Evidentiary Certificate, etc)
2. Procedural Overview and Test Methodology (Statement Appendices)
3. Draft Paternity statement
4. DNA Evidentiary Certificate
5. Example of combined preamble and Appendix for Civil casework report
6. Uniform Civil Procedure Rules 1999 – Sect 428
7. Actioning an Exhibit that is No Longer Required for Testing
8. Suggested PowerPlex®21 (and STRmix™) statement wording
9. Working from Home – Statement drafting, reporting and reviewing tasks
10. Offline Statements

20.1 Drafting, Review and Release of Reports (Statement, Evidentiary Certificate, etc)



20.2 Appendix 2 - Procedural Overview and Test Methodology (Statement Appendices)

APPENDIX (Statements Issued using Profiler Plus®)

Procedural and technical overview of DNA profiling at Forensic DNA Analysis, Forensic & Scientific Services

Accreditation

The DNA Analysis Unit first achieved accreditation by the National Association of Testing Authorities (NATA) to conduct forensic DNA analyses in 1998, and has continuously maintained NATA accreditation since this date. NATA ensures continued compliance with the accreditation requirements through routine reassessments (every 3 years) and surveillance visits (18 months).

NATA Accredited facilities are assessed against best international practices based on the ISO/IEC 17025 standard. Laboratories that demonstrate compliance with the standard have shown that they can competently perform activities and testing within the scope of their accreditation.
The parameters assessed during accreditation include:

- Organisation and management
- Quality management system
- Personnel
- Evidence management
- Methods and procedures
- Quality control and Proficiency Testing
- Equipment
- Reporting of results
- Procurement of services and supplies
- Accommodation and safety
- Security and access

For details of the current ISO/IEC 17025 Standard, refer to Standards Australia.

http://www.nata.com.au

Chain of Custody

All DNA Analysis Unit case files and exhibits are electronically tracked, monitored and securely stored to ensure that the appropriate chain of custody and continuity measures are maintained. The Queensland Police Service (QPS) case number and sample submission information is provided by the QPS via an electronic interface to QHFSS, and this information is cross-checked against labelling on exhibit packaging. The packaging and labelling of any exhibit is checked and recorded before the sample is sent for DNA analysis.

Entry into the DNA Analysis Unit is restricted to authorised persons only, via electronically encoded swipe access cards. The DNA Analysis Unit forms part of a Queensland Health campus site which has access controlled and monitored by a security team. Records of Visitors to the DNA Analysis Unit are retained.

Technical information relating to DNA profiling at the Forensic DNA Analysis, Forensic & Scientific Services

DNA (STR) Profiling

STR (Short Tandem Repeat) profiling is the standard technique currently in use for forensic DNA analysis. Deoxyribonucleic acid (DNA) is a complex chemical found in almost all cells of the body. It carries genetic

information which governs a person's physical and biochemical characteristics. Half of a persons DNA is inherited from their mother, and half from their father. A person's DNA is the same in almost all cell types in their body, so that DNA recovered from someone's blood will normally be the same as DNA from their hair roots, saliva or skin cells.

Except for identical twins, each person's total DNA is unique to themselves, although current DNA (STR) profiling techniques do not allow the analysis of the whole of someone's DNA. Instead, specific regions (loci) of the DNA are tested which contain short sequences of DNA (STRs) repeated a number of times end to end. The number of times a particular STR is repeated at each locus (region of DNA) will tend to vary between people, and it is these differences which allow DNA from different people to be compared.

A method known as the Polymerase Chain Reaction (PCR) is used to amplify specific STR regions of the DNA to produce many copies of the original DNA template. In this way, minute amounts of DNA isolated from small or degraded samples can be greatly increased to potentially yield a sufficient quantity of DNA to obtain a DNA profile.

The DNA Analysis Unit currently uses a DNA profiling system called Profiler® Plus which tests nine regions (loci) of DNA containing STRs, and a tenth region which provides an indication of the gender of the DNA source. Another DNA profiling system called COfiler®, although not routinely used at QHFSS, is available if required. The COfiler® system includes two of the regions included in Profiler® Plus, with four additional STR loci. For a list of the loci included in these DNA profiling systems, please refer to Tables 1 and 2 below.

Interpreting DNA Profiles

The individual components of a DNA profile can be represented in a graphical form as a series of peaks, which are measured and given a numerical designation by comparing them against standard sizing DNA components, processed alongside each sample.

If less than the ten regions of DNA tested are present in a DNA profile, this is referred to as a partial or incomplete DNA profile. When more than one person has contributed to a DNA profile, this is referred to as a mixed DNA profile.

A DNA profile obtained from biological material such as blood, semen, saliva or hair can be visually compared with a DNA profile obtained from a reference sample from a person. If each of the individual components within the two DNA profiles have the same corresponding numerical designations, the DNA profiles are said to match each other. If the DNA profiles match then that person, together with anyone else who has the same DNA profile, can be considered as a potential source of the biological material.

If any of the components of the two DNA profiles are different when compared, then the two DNA profiles do not match and the person can normally be excluded as a possible source of the biological material.

The term match does not impart increased significance to the result it describes. Although it may be considered highly unlikely that two unrelated people happen to have matching full DNA profiles, without testing every person in the population we cannot know exactly how many people may share matching DNA profiles.

The Use of Queensland Caucasian Data

The evidential significance of obtaining a match can be evaluated by estimating how common or rare the DNA profile is within a specific population. This can be calculated by estimating the frequency of occurrence of each component in the DNA profile and using a mathematical formula to multiply these frequencies together.

No assumptions are made as to the ethnic origin of any DNA obtained from alleged crime scenes. The DNA Analysis Unit routinely uses Queensland Caucasian data, taken from the largest sub-population in Queensland, for statistical calculations. Calculations using Queensland Aboriginal and Asian data can be provided upon request.

It is laboratory policy to use the Queensland Caucasian data unless the alleged incident occurred off the Queensland mainland, in which case figures from the Queensland Caucasian and Queensland Aboriginal data would both be quoted.

The statistical figure applied to DNA profiles will depend on how closely related people are. The closer the biological relationship (eg. siblings), the greater the chance that the people in question may have DNA profiles which share matching DNA components. However, due to the random nature by which DNA from each parent is combined in their offspring, the probability that two siblings would share the same components at all regions tested is very small. As the relationship becomes more distant, the probability of two relatives having matching DNA profile becomes smaller still. If it is proposed that a relative should be considered as an alternative source of DNA, the best course of action would be to obtain a reference DNA sample from the relative in question, for DNA profiling and comparison.

Validity of the Caucasian Data

The population frequency data used for statistical interpretations in the laboratory have been validated for use by external Forensic Statisticians Dr Simon J WALSH and Dr John S BUCKLETON. The report of their findings is held in the laboratory and is available upon request.

DNA (STR) profiling systems available at the Forensic DNA Analysis, Forensic & Scientific Services

Table 1: Profiler® Plus multiplex system, list of loci:

Abbreviated Name	Scientific Name	Chromosomal Name
D3	D3S1358	3
vWA	HUMVWFA31/A	12
FGA	HUMFIBRA	4
Amel	AMELOGENIN	Sex X and Y
D8	D8S1179	8
D21	D21S11	21
D18	D18S51	18
D5	D5S818	5
D13	D13S317	13
D7	D7S820	7

Table 2: COfiler® multiplex system, list of loci:

Abbreviated Name	Scientific Name	Chromosomal Name
D3	D3S1358	3
D16	D16S539	16
TH01	TH01	11
TPOX	TPOX	2
CSF	CSF	5
D7	D7S820	7
Amel	AMELOGENIN	Sex X and Y

APPENDIX (Statements Issued using PowerPlex® 21 and STRmix v2.0.6)

Procedural and technical overview of DNA profiling at Forensic DNA Analysis, Forensic & Scientific Services

Forensic Biologist

It is a forensic biologist's role to:

1. Report on the examination of items submitted in relation to a case for the presence of possible biological material. If identified, a sample of the biological material is analysed in an attempt to obtain a DNA profile.

2. Report on the DNA profiles obtained from samples submitted by the Queensland Police Service (QPS) in relation to a case.

Any DNA profiles that are obtained from these samples are compared with the DNA profile obtained from an individual's reference sample to assess whether or not the individual may be a contributor of DNA. Where multiple reference DNA profiles are analysed for a case, they are all genetically different to each other unless otherwise specified. That is, they all possess differing allelic designations – see the DNA Profiling section below.

The signed Statement is the report issued by Forensic and Scientific Services. Any other attachments or information provided is not considered to be the issued report.

Examinations

Unless otherwise stated, the examinations of items for biological material were conducted by staff within the QPS. Sub-samples from these items were forwarded to Forensic and Scientific Services (FSS), Health Support Queensland, for the purposes of conducting DNA analysis.

The descriptions of items and/or samples submitted to Forensic DNA Analysis by the QPS, and listed within this Statement, are derived from the descriptions entered by the QPS into the Forensic Register.

Receipt details are listed for items reported in this statement, including reference samples where relevant. The period of testing on these items is from the date of the first submission, to the date of this Statement. Details of specific dates of testing are retained within the Laboratory Information Management System (LIMS). Where relevant, any items that are still in progress at the time of issuing this Statement are identified and final results will be reported in an addendum Statement.

Forensic DNA Analysis operates under the agreement that the QPS are responsible for item prioritisation, sample selection, selection of screening/sampling methods, anti-contamination procedures and the application of Standard Operating Procedures (SOPs) on work undertaken on the items/samples prior to submission to the Forensic DNA Analysis laboratory. As such, forensic biologists may not be able to provide information or opinion on possible biological origin of DNA profiles that may be obtained from these samples.

At the discretion of the QPS, some items may be submitted to this laboratory for the purposes of both examination and DNA profiling. These examinations are performed in accordance with the SOPs of this laboratory. For these items, contemporaneous notes are made during the examination by the examining scientist and these notes form part of the casefile.

Forensic DNA Analysis casefiles and any samples remaining are available for independent examination and/or testing upon request.

As a representative of the laboratory, I am only able to comment on the processes performed within Forensic DNA Analysis.

Chain of Custody

All Forensic DNA Analysis case files and exhibits are electronically tracked, monitored, and securely stored to ensure that appropriate chain of custody and continuity measures are maintained. The QPS case number and sample submission information is provided from the QPS via an electronic interface to FSS, and this information is cross-checked against labelling on the exhibit packaging prior to processing.

Entry into Forensic DNA Analysis is restricted to authorised persons only, via electronic proximity access cards. Forensic DNA Analysis forms part of a Health Support Queensland campus site wherein access is controlled and monitored by a security team. Records of visitors to Forensic DNA Analysis are retained.

Accreditation

Forensic DNA Analysis first achieved accreditation by the National Association of Testing Authorities (NATA) to conduct forensic DNA analyses in 1998 and has continuously maintained NATA accreditation since this date. NATA ensures continued compliance with the accreditation requirements through routine reassessment (every 3 years) and an intermediate surveillance visit (at approximately 18 months between reassessment surveys).

NATA accredited facilities are assessed against best international practices based on the ISO/IEC 17025 standard. Laboratories are deemed able to competently perform testing and analysis activities if the laboratory demonstrates that it meets compliance with the standard within the scope of their accreditation.

The parameters assessed during accreditation include:

- Organisation and management
- Quality management system
- Personnel
- Evidence management
- Methods and procedures
- Quality control and Proficiency Testing
- Equipment
- Reporting of results
- Procurement of services and supplies
- Accommodation and safety
- Security and access

For details of the current ISO/IEC 17025 Standard, refer to Standards Australia.

http://www.nata.com.au

DNA Profiling

Deoxyribonucleic Acid (DNA) is a complex chemical found in almost all cells of the human body. It carries genetic information that determines the physical and chemical characteristics of a person. Forensic DNA Analysis uses two main systems for the generation of DNA profiling results. In this case, the PowerPlex® 21 System was used, which examines 21 regions (loci) of DNA, 20 of which contain highly variable short tandem repeats (STRs). The 21st region gives an indication as to the genotypic sex of the donor (for details see Table 1). The generation of a DNA profile involves a method known as the polymerase chain reaction (PCR), which is used to produce numerous copies of these specific regions of the DNA. In this way, minimal amounts of DNA isolated from small or degraded samples can be increased to a level where the DNA can be detected, profiled, and compared with DNA profiles from other samples.

The individual components (alleles) of a DNA profile are represented by a series of peaks on a graph that are measured and given a designation, using standard sizing ladders. A person will have two alleles (represented graphically as peaks) for each locus, one inherited from the biological mother and one inherited from the biological father. However, if the same allele is inherited from both parents, only one peak will be graphically represented at that locus.

A DNA profile obtained from biological material such as blood, semen, saliva, hair or cellular material (eg. touch DNA) can be compared with the DNA profile obtained from the reference sample from any person.

Table 1: PowerPlex® 21 system, list of loci

Abbreviated Name	Scientific Name	Chromosomal Name
Amel	AMELOGENIN	Sex (X and Y)
D3	D3S1358	3
D1	D1S1656	1
D6	D6S1043	6
D13	D13S317	13
Penta E	Penta E	15
D16	D16S539	16
D18	D18S51	18
D2	D2S1338	2
CSF	CSF1PO	5
Penta D	Penta D	21
TH01	TH01	11
vWA	HUMVWAFA31/A	12
D21	D21S11	21
D7	D7S820	7
D5	D5S818	5
TPOX	TPOX	2
D8	D8S1179	8
D12	D12S391	12
D19	D19S433	19

FGA	HUMFIBRA	4

Statistical Analysis of DNA Profiles

STRmix™ is an expert statistical DNA profile analysis system developed and validated in Australia and New Zealand. Forensic DNA Analysis uses the STRmix™ software to assist in the interpretation of DNA profiles and the calculation of likelihood ratios for DNA profiles generated using the PowerPlex® 21 system.

In order to statistically evaluate DNA profiles, it is necessary to make a reasonable assessment of the number of people who may have contributed DNA to that DNA profile, based on the information observed.

If there is no indication of a contribution by more than one person, then a DNA profile is described as being from a "single contributor". If less than 40 alleles present in a DNA profile, this is referred to as a "partial" or "incomplete" DNA profile. If there are indications of two or more contributors, then a DNA profile is described as being a "mixed" DNA profile.

DNA Profiles Assumed To Originate From One Person (Single Source)

A person can be excluded as a possible source of the biological material if the alleles of the crime-scene DNA profile are different from corresponding alleles of the person's reference DNA profile. If the corresponding alleles of the crime-scene DNA profile contain the same information, then that person, along with any other person who has the same reference DNA profile, can be considered as a potential contributor of the DNA.

The evidential significance of such a match is assessed by considering two competing propositions:

Proposition 1: The crime-scene DNA originated from the person of interest.

Proposition 2: The crime-scene DNA originated from someone other than, and unrelated to, the person of interest.

The resultant figure (termed the 'Likelihood Ratio') compares the two opposing propositions. The likelihood ratio describes how likely the DNA profile obtained from the biological material is to have occurred if Proposition 1 were true (the DNA originated from the person of interest) rather than if Proposition 2 were true (the DNA originated from someone other than, and unrelated to, the person of interest).

The likelihood ratio is calculated by taking into account the characteristics of the DNA profile and the frequency of occurrence of the individual alleles that make up the DNA profile.

If less than the 20 STR regions of DNA are observed in a DNA profile, the likelihood ratio will be smaller than the likelihood ratio calculated for a full DNA profile obtained from the same individual. In other words, the more incomplete a DNA profile is, the greater the likelihood that the obtained DNA profile could have come from someone other than, and unrelated to the person of interest.

DNA Profiles Assumed To Originate From More Than One Person (Mixed DNA Profiles)

In order to assess whether a person may or may not have contributed to a mixed DNA profile, a set of competing propositions (similar to the single source DNA profile example) are considered. For example, for a two-person mixture:

Proposition 1: The crime-scene DNA originated from the person of interest and an unknown person, unrelated to the person of interest.

Proposition 2: The crime-scene DNA originated from two unknown people, both unrelated to the person of interest.

The likelihood ratio provides a statistical assessment of the possibility that the DNA profile obtained was the result of a DNA contribution by the person of interest.

The likelihood ratio will not always favour Proposition 1 (the DNA originated from the person of interest and an unknown person unrelated to the person of interest). The likelihood ratio could favour Proposition 2 (the DNA originated from two unknown people unrelated to the person of interest).

In certain circumstances, if the ownership of an item is established or if the sample was collected from an identified person's body, then it is possible to make the reasonable assumption that the identified person has contributed DNA to the resultant mixed DNA profile. In these cases, a mixed DNA profile can be 'conditioned' on the DNA profile of the assumed contributor, such that the presence of the alleles corresponding with the assumed contributor's reference DNA profile can be factored into the statistical interpretation. This may facilitate a more meaningful statistical analysis of potential second and/or third contributors to the DNA profile. In this situation, the likelihood ratio is based on the following propositions:

Proposition 1: the DNA has originated from the assumed contributor and the person of interest;

Proposition 2: the DNA has originated from the assumed contributor and an unknown individual unrelated to the person of interest.

When a DNA profile is deemed unsuitable for interpretation it may be described as 'complex'. This can occur under the following circumstances:

- When a DNA profile could have a large number of contributors and therefore it is difficult to exclude individuals and/or determine whether a person could be a potential contributor to the DNA profile
- When there is very limited information available and/or the quality of the profile is poor.

If further information is received, such that render the assumptions used in an analysis invalid, the DNA profile will require additional statistical interpretation.

Datasets Used in Statistical Analyses

Three validated datasets consisting of DNA profiles obtained from individuals of the Australian Caucasian, Aboriginal, and South-East Asian populations are used to calculate the likelihood ratio. A population correction factor, θ (theta), is applied to all likelihood ratio calculations in order to correct for the common genetic ancestry of people within a particular population (sharing of DNA components inherited from a common ancestor). The nationally agreed figures for theta are θ=0.02 for the Australian Caucasian dataset, θ=0.03 for the Australian South-East Asian dataset, and θ=0.05 for the Australian Aboriginal dataset. In Forensic DNA Analysis, likelihood ratios are calculated using all three datasets and the most conservative value is reported.

In addition to theta, the calculation of the likelihood ratio also includes an allowance for the sampling variability of the population dataset. In other words, if a new population dataset were generated, this allowance factors in any difference the new dataset might make to the likelihood ratio.

The above-listed values for theta cannot account for close blood relatives. Closely related people, such as siblings, will have a greater chance of sharing similar components within their DNA profiles. However, due to the nature of parental DNA recombination during conception, the probability that two siblings would share the same 40 alleles would be very small. As this relationship becomes more distant, the probability of two relatives having the same DNA profile becomes smaller still. If it were thought that a close blood relative might have been a contributor of DNA, the most meaningful approach to interpretation would be to submit the reference sample from the relative in question for DNA analysis and subsequent direct comparison to the crime-scene DNA profile.

Often the calculated likelihood ratio produces numbers of thousands (1000s) or even millions (1000,000s) of billions. To avoid the use of potentially confusing mathematical terminology, a "ceiling figure" for the likelihood ratio of 100 billion is used (this is called "truncation"). For example, a calculated likelihood ratio of "150 000 billion times more likely", would be reported as "greater than 100 billion times more likely". The actual calculated figure can be provided upon request.

Parentage Testing and Statistical Calculations

In a disputed paternity matter, DNA profiles are obtained from the foetus/child, the biological mother, and the putative father(s). Based on the assumption that the nominated mother is indeed the biological mother of the foetus/child, it is possible to determine which alleles within the DNA profile of the child could have originated from her. Therefore, the remaining alleles within the foetus/child's DNA profile must have originated from the biological father. These are called obligate paternal alleles.

If the DNA profile of a putative father **does not** contain the obligate paternal alleles at three or more of the DNA loci tested, then he is **excluded** as a potential biological father of the foetus/child.

If the DNA profile of a putative father **does contain** the obligate paternal alleles at each of the DNA regions tested, then he is **not excluded** as a potential biological father of the foetus/child. This means that this putative father could be the biological father.

A statistical analysis is performed to calculate a Paternity Index. The Paternity Index (PI) is a ratio of two probabilities conditional upon different competing propositions.

Proposition 1. The alleged father is the true father (and the mother is the true mother).

Proposition 2. A random person who is not related to the alleged father is the ture father (and the mother is the true mother).

The PI reflects how many times more likely it is to see the evidence (i.e. the child's DNA profile) under the first hypothesis compared to the second proposition.

For an inclusion of paternity/maternity the PI must not be less than 1000, according to ISO/IEC 17025 Application Document, Legal (including Forensic Science) – Annex, Parentage Testing for the Australian Family Law Act. See www.nata.com.au

Touch DNA / Transfer of DNA

When a person touches a surface, it is possible for their DNA to be transferred onto that surface. This transferred DNA can often be recovered (sampled) by a swab, tape lift, or excision depending upon the nature of the surface in question, and the sample can then be subjected to DNA profiling.

This transferred DNA can originate from cells or cellular material within sweat and/or oils on the skin. The generation of a DNA profile will depend on many factors. These include the amount of DNA transferred, the nature of the surface being touched, and the amount of genetic material available for transfer. The persistence of any transferred genetic material to a surface will depend largely upon the nature of the surface and the conditions the surface has been subjected to in the time between deposition and recovery of the DNA. For example, DNA could be lost from the surface by washing or mechanical action such as abrasion.

It therefore follows that the inability to obtain a DNA profile from a touched surface does not necessarily mean that a person has not had contact with the surface. It is possible for a person to contact a surface without a detectable amount of their DNA being transferred or subsequently recovered for analysis.

Blood Stains

Potential bloodstains are located in the laboratory by means of their visual appearance and the use of a presumptive chemical test (Tetramethylbenzidine – TMB). A positive result with this test is a good indication that blood may be present, however it does not provide proof as other substances are known to give the same result.

Semen Stains

Semen is the collective name for the mixture of spermatozoa (sperm) and seminal fluid. The presence of semen on an item can be indicated by using a presumptive chemical test that detects a major constituent of seminal fluid, namely Prostate Specific Antigen (PSA / p30). This constituent may exist in other body fluids, such as urine, faecal material, sweat, breast milk and blood, albeit usually at much lower concentrations.

The location or presence of possible semen on items may also be indicated by using a presumptive chemical test that detects another major constituent of seminal fluid (Acid

Phosphatase – AP). This constituent exists in other body fluids, such as vaginal secretions, albeit usually at much lower concentrations.

The presence of semen can be confirmed via the microscopic identification of spermatozoa.

Samples where semen may be present undergo a differential lysis extraction process that aims to separate spermatozoa and epithelial cells into separate fractions. This separation is not always completely effective, and a mixing of fractions can occur. This is often referred to as cellular carryover.

The current practice within Forensic DNA Analysis is for epithelial fractions from internal female sexual assault investigation kit (SAIK) samples to be stored following a differential lysis extraction process. This is because when these fractions are profiled, they are generally found to be a single contributor match to the person from whom the sample was taken. Given the nature of these samples, this finding is not unexpected. These epithelial fractions are stored indefinitely, and can be sent for DNA profiling at a future date if required.

Semen Staining on Items

The presence of semen on an item is normally the result of either direct ejaculation or contact with an item wet with semen (transfer). Any semen that may have been transferred / deposited can subsequently be lost by actions such as washing.

Persistence of Semen in the Vagina

The presence of semen in the vagina is normally the result of vaginal intercourse with internal ejaculation. The chance of detecting semen on a vaginal swab depends upon a number of factors such as:

- the effectiveness of the sampling process;
- the delay between deposition of the semen and sampling during the medical examination;
- the biochemical conditions within the vagina.
- any physiological factors that may affect semen production in the donor

The greater the delay between deposition and sampling, the less chance there is of finding semen. Although highly variable, semen is likely to be found on vaginal swabs if they were taken 1-2 days after the act of vaginal intercourse. Semen is sometimes found on swabs taken between 2-7 days afterwards, but it is unlikely to be detected after 7 days. This is due to a number of factors that can include the following:

- drainage of semen from the vagina;
- loss of semen by bathing or washing (especially on external sites);
- degradation of the spermatozoa and seminal fluid constituents.

Saliva

A presumptive chemical test (Phadebas) may be used to detect the possible presence of saliva. This test exploits the enzyme activity of a constituent of saliva called amylase. Amylase is usually present at a relatively high concentration in saliva, though this can vary considerably between individuals. Amylase may also be detected in other body

fluids such as sweat, vaginal fluid and anal secretions, although usually at much lower concentration than that found in saliva.

The presence of saliva on a surface may be the result of spitting or direct oral contact. Saliva may subsequently be transferred onto other items such as clothing or other areas of the body. Possible saliva stains may then be detected on skin swabs or items of clothing by the Phadebas test, as long as the clothing or skin has not been washed. Cellular material within the saliva, if present in sufficient quantities, can be used to obtain a DNA profile.

JUSTICES ACT 1886

I acknowledge by virtue of Section 110A (6C) (c) of the Justices Act 1886 that:

(i) This written statement by me dated 15 September 2022 and contained in the pages numbered 1 to 100 is true to the best of my knowledge and belief; and

(ii) I make it knowing that, I would be liable to prosecution for stating anything that I know is false.

.....

Reporter

Signed at BRISBANE on 15 September 2022

APPENDIX (Statements Issued using PowerPlex® 21 and STRmix v2.6.0 and beyond)

Procedural and technical overview of DNA profiling at Forensic DNA Analysis, Forensic & Scientific Services

Forensic Biologist

It is a forensic biologist's role to:

1. Report on the examination of items submitted in relation to a case for the presence of possible biological material. If identified, a sample of the biological material is analysed in an attempt to obtain a DNA profile.

2. Report on the DNA profiles obtained from samples submitted by the Queensland Police Service (QPS) in relation to a case.

Any DNA profiles that are obtained from these samples are compared with the DNA profile obtained from an individual's reference sample to assess whether or not the individual may be a contributor of DNA. Where multiple reference DNA profiles are analysed for a case, they are all genetically different to each other unless otherwise specified. That is, they all possess differing allelic designations – see the DNA Profiling section below.

The signed Statement is the report issued by Forensic and Scientific Services. Any other attachments or information provided is not considered to be the issued report.

Examinations

Unless otherwise stated, the examinations of items for biological material were conducted by staff within the QPS. Sub-samples from these items were forwarded to Forensic and Scientific Services (FSS), Health Support Queensland, for the purposes of conducting DNA analysis.

The descriptions of items and/or samples submitted to Forensic DNA Analysis by the QPS, and listed within this Statement, are derived from the descriptions entered by the QPS into the Forensic Register.

Receipt details are listed for items reported in this statement, including reference samples where relevant. The period of testing on these items is from the date of the first submission, to the date of this Statement. Details of specific dates of testing are retained within the Laboratory Information Management System (LIMS). Where relevant, any items that are still in progress at the time of issuing this Statement are identified and final results will be reported in an addendum Statement.

Forensic DNA Analysis operates under the agreement that the QPS are responsible for item prioritisation, sample selection, selection of screening/sampling methods, anti-contamination procedures and the application of Standard Operating Procedures (SOPs) on work undertaken on the items/samples prior to submission to the Forensic DNA Analysis laboratory. As such, forensic biologists may not be able to provide information or opinion on possible biological origin of DNA profiles that may be obtained from these samples.

At the discretion of the QPS, some items may be submitted to this laboratory for the purposes of both examination and DNA profiling. These examinations are performed in accordance with the SOPs of this laboratory. For these items, contemporaneous notes are made during the examination by the examining scientist and these notes form part of the casefile.
Forensic DNA Analysis casefiles and any samples remaining are available for independent examination and / or testing upon request.

As a representative of the laboratory, I am only able to comment on the processes performed within Forensic DNA Analysis.

Chain of Custody

All Forensic DNA Analysis case files and exhibits are electronically tracked, monitored, and securely stored to ensure that appropriate chain of custody and continuity measures are maintained. The QPS case number and sample submission information is provided from the QPS via an electronic interface to FSS, and this information is cross-checked against labelling on the exhibit packaging prior to processing.

Entry into Forensic DNA Analysis is restricted to authorised persons only, via electronic proximity access cards. Forensic DNA Analysis forms part of a Health Support Queensland campus site wherein access is controlled and monitored by a security team. Records of visitors to Forensic DNA Analysis are retained.

Accreditation

Forensic DNA Analysis first achieved accreditation by the National Association of Testing Authorities (NATA) to conduct forensic DNA analyses in 1998, and has continuously maintained NATA accreditation since this date. NATA ensures continued compliance with the accreditation requirements through routine reassessment (every 3 years) and an intermediate surveillance visit (at approximately 18 months between reassessment surveys).

NATA accredited facilities are assessed against best international practices based on the ISO/IEC 17025 standard. Laboratories are deemed able to competently perform testing and analysis activities if the laboratory demonstrates that it meets compliance with the standard within the scope of their accreditation.

The parameters assessed during accreditation include:

- Organisation and management
- Quality management system
- Personnel
- Evidence management
- Methods and procedures
- Quality control and Proficiency Testing
- Equipment
- Reporting of results
- Procurement of services and supplies
- Accommodation and safety
- Security and access

For details of the current ISO/IEC 17025 Standard, refer to Standards Australia.

http://www.nata.com.au

DNA Profiling

Deoxyribonucleic acid (DNA) is a complex chemical found in almost all cells of the human body. It carries genetic information that determines the physical and chemical characteristics of a person. Forensic DNA Analysis uses two main systems for the generation of DNA profiling results. In this case, the PowerPlex® 21 System was used, which examines 21 regions (loci) of DNA, 20 of which contain highly variable short tandem repeats (STRs). The 21st region gives an indication as to the genotypic sex of the donor (for details see Table 1). The generation of a DNA profile involves a method known as the polymerase chain reaction (PCR), which is used to produce numerous copies of these specific regions of the DNA. In this way, minimal amounts of DNA isolated from small or degraded samples can be increased to a level where the DNA can be detected, profiled, and compared with DNA profiles from other samples.

The individual components (alleles) of a DNA profile are represented by a series of peaks on a graph that are measured and given a designation, using standard sizing ladders. A person will have two alleles (represented graphically as peaks) for each locus, one inherited from the biological mother and one inherited from the biological father. However, if the same allele is inherited from both parents, only one peak will be graphically represented at that locus.

A DNA profile obtained from biological material such as blood, semen, saliva, hair or cellular material (eg. touch DNA) can be compared with the DNA profile obtained from the reference sample from any person.

Table 1: PowerPlex® 21 system, list of loci

Abbreviated Name	Scientific Name	Chromosomal Name
Amel	AMELOGENIN	Sex (X and Y)
D3	D3S1358	3
D1	D1S1656	1
D6	D6S1043	6
D13	D13S317	13
Penta E	Penta E	15
D16	D16S539	16
D18	D18S51	18
D2	D2S1338	2
CSF	CSF1PO	5
Penta D	Penta D	21
TH01	TH01	11
vWA	HUMVWAFA31/A	12
D21	D21S11	21
D7	D7S820	7
D5	D5S818	5
TPOX	TPOX	2
D8	D8S1179	8
D12	D12S391	12
D19	D19S433	19
FGA	HUMFIBRA	4

Statistical Analysis of DNA Profiles

STRmix™ is an expert statistical DNA profile analysis system developed and validated in Australia and New Zealand. Forensic DNA Analysis uses the STRmix™ software to assist in the interpretation of DNA profiles and the calculation of likelihood ratios for DNA profiles generated using the PowerPlex® 21 system.

In order to statistically evaluate DNA profiles, it is necessary to make a reasonable assessment of the number of people who may have contributed DNA to that DNA profile, based on the information observed.

If there is no indication of a contribution by more than one person, then a DNA profile is described as being from a "single contributor". If less than 40 alleles present in a DNA profile, this is referred to as a "partial" or "incomplete" DNA profile. If there are indications of two or more contributors, then a DNA profile is described as being a "mixed" DNA profile.

DNA Profiles Assumed To Originate From One Person (Single Source)

A person can be excluded as a possible source of the biological material if the alleles of the crime-scene DNA profile are different from the corresponding alleles of the person's reference DNA profile. If the corresponding alleles of the crime-scene DNA profile contain the same information, then that person, along with any other person who has the same corresponding alleles as the crime-scene DNA profile, can be considered as a potential contributor of the DNA.

The evidential significance of such a finding is assessed by considering two competing propositions:

Proposition 1: The crime-scene DNA originated from the person of interest.

Proposition 2: The crime-scene DNA originated from someone other than, and unrelated to, the person of interest.

The resultant figure (termed the 'Likelihood Ratio') compares the two opposing propositions. The likelihood ratio describes how likely the DNA profile obtained from the biological material is to have occurred if Proposition 1 were true (the DNA originated from the person of interest) rather than if Proposition 2 were true (the DNA originated from someone other than, and unrelated to, the person of interest).

The likelihood ratio is calculated by taking into account the characteristics of the DNA profile and the frequency of occurrence of the individual alleles that make up the DNA profile.

If less than the 20 STR regions of DNA are observed in a DNA profile, the likelihood ratio will be smaller than the likelihood ratio calculated for a full DNA profile obtained from the same individual. In other words, the more incomplete a DNA profile is, the greater the likelihood that the obtained DNA profile could have come from someone other than, and unrelated to the person of interest.

DNA Profiles Assumed To Originate From More Than One Person (Mixed DNA Profiles)

In order to assess whether a person may or may not have contributed to a mixed DNA profile, a set of competing propositions (similar to the single source DNA profile example) are considered. For example, for a two-person mixture:

Proposition 1: The crime-scene DNA originated from the person of interest and an unknown person, unrelated to the person of interest.

Proposition 2: The crime-scene DNA originated from two unknown people, both unrelated to the person of interest.

The likelihood ratio provides a statistical assessment of the possibility that the DNA profile obtained was the result of a DNA contribution by the person of interest.

The likelihood ratio will not always favour Proposition 1 (the DNA originated from the person of interest and an unknown person unrelated to the person of interest). The likelihood ratio could favour Proposition 2 (the DNA originated from two unknown people unrelated to the person of interest).

In certain circumstances, if the ownership of an item is established or if the sample was collected from an identified person's body, then it is possible to make the reasonable assumption that the identified person has contributed DNA to the resultant mixed DNA profile. In these cases, a mixed DNA profile can be 'conditioned' on the DNA profile of the assumed contributor, such that the presence of the alleles corresponding with the assumed contributor's reference DNA profile can be factored into the statistical interpretation. This may facilitate a more meaningful statistical analysis of potential second and/or third contributors to the DNA profile. In this situation, the likelihood ratio is based on the following propositions:

Proposition 1: the DNA has originated from the assumed contributor and the person of interest.

Proposition 2: the DNA has originated from the assumed contributor and an unknown individual, unrelated to the person of interest.

DNA profiles with an uncertain number of contributors

Forensic DNA Analysis is currently validated for the interpretation of DNA profiles with 1-4 contributors. Once the assessment of the number of contributors has been made, this information is used in the STRmix™ analysis.

When a DNA profile is deemed unsuitable for interpretation it may be described as 'complex'. This can occur under the following circumstances:

- When a DNA profile could have a large number of contributors and therefore it is difficult to exclude individuals and/or determine whether a person could be a potential contributor to the DNA profile
- When there is very limited information available and/or the quality of the profile is poor.

It is important to note that should further information be received that renders the assumptions used in an analysis invalid, the DNA profile will require additional statistical interpretation.

Datasets Used in Statistical Analyses

Three validated datasets consisting of DNA profiles obtained from individuals of the Australian Caucasian, Aboriginal, and South-East Asian populations are used to calculate the likelihood ratio. A population correction factor, θ (theta), is applied to all likelihood ratio calculations in order to correct for the common genetic ancestry of people within a particular population (sharing of DNA components inherited from a common ancestor). In Forensic DNA Analysis, a likelihood ratio that represents a stratified population statistic is reported irrespective of whether the DNA profile of interest is single source or a mixed DNA Profile.

The likelihood ratio is calculated using all three datasets and the relative proportions of each ethnic grouping in the overall Australian population based on data sourced from the Australian Bureau of Statistics. This calculation, which is known as stratification, allows for the possibility that a random unknown person, unrelated to the person of interest, from anywhere in Australia could have contributed to the DNA profile obtained. Therefore, the likelihood ratio is not dependent on the ethnicity of the person of interest, but it is representative of the relative proportion of the person of interest's ethnic population within the larger Australian population.

Theta cannot account for close blood relatives. Closely related people, such as siblings, will have a greater chance of sharing similar components within their DNA profiles. However, due to the nature of parental DNA recombination during conception, the probability that two siblings would share the same 40 alleles would be very small. As this relationship becomes more distant, the probability of two relatives having the same DNA profile becomes smaller still. If it were thought that a close blood relative might have been a contributor of DNA, the most meaningful approach to interpretation would be to submit the reference sample from the relative in question for DNA analysis and subsequent direct comparison to the crime-scene DNA profile.

Often the calculated likelihood ratio produces numbers of thousands (1000s) or even millions (1000,000s) of billions. To avoid the use of potentially confusing mathematical terminology, a "ceiling figure" for the likelihood ratio of 100 billion is used (this is called "truncation"). For example, a calculated likelihood ratio of "150 000 billion times more likely", would be reported as "greater than 100 billion times more likely". The actual calculated figure can be provided upon request.

Parentage Testing and Statistical Calculations

In a disputed paternity matter, DNA profiles are obtained from the foetus/child, the biological mother, and the putative father(s). Based on the assumption that the nominated mother is indeed the biological mother of the foetus/child, it is possible to determine which alleles within the DNA profile of the child could have originated from her. Therefore, the remaining alleles within the foetus/child's DNA profile must have originated from the biological father. These are called *obligate paternal alleles*.

If the DNA profile of a putative father *does not* contain the obligate paternal alleles at three or more of the DNA loci tested, then he is *excluded* as a potential biological father of the foetus/child.

If the DNA profile of a putative father *does* contain the obligate paternal alleles at each of the DNA regions tested, then he is *not excluded* as a potential biological father of the foetus/child. This means that this putative father could be the biological father.

A statistical analysis is performed to calculate a *Paternity Index (PI)*. The PI is a ratio of two probabilities conditional upon different competing propositions.

Proposition 1. The alleged father is the true father (and the mother is the true mother).

Proposition 2. A random person who is not related to the alleged father is the true father (and the mother is the true mother).

The PI reflects how many times more likely it is to see the evidence (i.e. the child's DNA profile) under the first proposition compared to the second proposition.

For an inclusion of paternity/maternity the PI must not be less than 1000, according to ISO/IEC 17025 Application Document, Legal (including Forensic Science) – Annex, Parentage Testing for the Australian Family Law Act. See www.nata.com.au

Touch DNA / Transfer of DNA

When a person touches a surface, it is possible for their DNA to be transferred onto that surface. This transferred DNA can often be recovered (sampled) by a swab, tape lift, or excision depending upon the nature of the surface in question, and the sample can then be subjected to DNA profiling.

This transferred DNA can originate from cells or cellular material within sweat and/or oils on the skin. The generation of a DNA profile will depend on many factors. These include the amount of DNA transferred, the nature of the surface being touched, and the amount of genetic material available for transfer. The persistence of any transferred genetic material to a surface will depend largely upon the nature of the surface and the conditions the surface has been subjected to in the time between deposition and recovery of the DNA. For example, DNA could be lost from the surface by washing or mechanical action such as abrasion.

It therefore follows that the inability to obtain a DNA profile from a touched surface does not necessarily mean that a person has not had contact with the surface. It is possible for a person to contact a surface without a detectable amount of their DNA being transferred or subsequently recovered for analysis.

Blood Stains

Potential bloodstains are located in the laboratory by means of their visual appearance and the use of a presumptive chemical test (Tetramethylbenzidine – TMB). A positive result with this test is a good indication that blood may be present, however it does not provide proof as other substances are known to give the same result.

Semen Stains

Semen is the collective name for the mixture of spermatozoa (sperm) and seminal fluid. The presence of semen on an item can be indicated by using a presumptive chemical test that detects a major constituent of seminal fluid, namely Prostate Specific Antigen (PSA / p30). This constituent may exist in other body fluids, such as urine, faecal material, sweat, breast milk and blood, albeit usually at much lower concentrations.

The location or presence of possible semen on items may also be indicated by using a presumptive chemical test that detects another major constituent of seminal fluid (Acid Phosphatase – AP). This constituent exists in other body fluids, such as vaginal secretions, albeit usually at much lower concentrations.

The presence of semen can be confirmed via the microscopic identification of spermatozoa.

Samples where semen may be present undergo a differential lysis extraction process that aims to separate spermatozoa and epithelial cells into separate fractions. This separation is not always completely effective, and a mixing of fractions can occur. This is often referred to as cellular carryover.

The current practice within Forensic DNA Analysis is for epithelial fractions from internal female sexual assault investigation kit (SAIK) samples to be stored following a differential lysis extraction process. This is because when these fractions are profiled, they are generally found to be a single contributor match to the person from whom the sample was taken. Given the nature of these samples, this finding is not unexpected. These epithelial fractions are stored indefinitely, and can be sent for DNA profiling at a future date if required.

Semen Staining on Items

The presence of semen on an item is normally the result of either direct ejaculation or contact with an item wet with semen (transfer). Any semen that may have been transferred / deposited can subsequently be lost by actions such as washing.

Persistence of Semen in the Vagina

The presence of semen in the vagina is normally the result of vaginal intercourse with internal ejaculation. The chance of detecting semen on a vaginal swab depends upon a number of factors such as:

- the effectiveness of the sampling process;
- the delay between deposition of the semen and sampling during the medical examination;
- the biochemical conditions within the vagina.
- any physiological factors that may affect semen production in the donor

The greater the delay between deposition and sampling, the less chance there is of finding semen. Although highly variable, semen is likely to be found on vaginal swabs if they were taken 1-2 days after the act of vaginal intercourse. Semen is sometimes found on swabs taken between 2-7 days afterwards, but it is unlikely to be detected after 7 days. This is due to a number of factors that can include the following:

- drainage of semen from the vagina;
- loss of semen by bathing or washing (especially on external sites);
- degradation of the spermatozoa and seminal fluid constituents.

Saliva

A presumptive chemical test (Phadebas) may be used to detect the possible presence of saliva. This test exploits the enzyme activity of a constituent of saliva called amylase. Amylase is usually present at a relatively high concentration in saliva, though this can vary considerably between individuals. Amylase may also be detected in other body fluids such as sweat, vaginal fluid and anal secretions, although usually at much lower concentration than that found in saliva.

The presence of saliva on a surface may be the result of spitting or direct oral contact. Saliva may subsequently be transferred onto other items such as clothing or other areas of the body. Possible saliva stains may then be detected on skin swabs or items of clothing by the Phadebas test, as long as the clothing or skin has not been washed. Cellular material within the saliva, if present in sufficient quantities, can be used to obtain a DNA profile.

JUSTICES ACT 1886

I acknowledge by virtue of Section 110A (6C) (c) of the Justices Act 1886 that:

(i) This written statement by me dated 15 September 2022 and contained in the pages numbered 1 to 109 is true to the best of my knowledge and belief; and

(ii) I make it knowing that, I would be liable to prosecution for stating anything that I know is false.

.....

Reporter

Signed at BRISBANE on 15 September 2022

20.3 Appendix 3 – Draft paternity statement

Paternity trio evaluation wording

XX. The results of the scientific examinations conducted in this laboratory are as follows:

Reference Samples

nn: XX - mother
nn: XY - suspect
nn: CC - child

DNA profiles were obtained from these reference samples. These DNA profiles were different to each other.

Information was observed within the DNA profile of CC, supporting the assumption that XX is indeed the biological mother of CC.

The DNA profile obtained from the reference sample from XY was compared to the DNA profiles obtained from the reference samples of XX and CC in order to assist in the determination of the possible paternity of CC.

XY possesses all of the obligate paternal alleles. In my opinion, it is possible that XY is the biological father of CC given that XX is the natural mother. The following statistical weighting has been calculated in support of this opinion:

The DNA profile from CC is n times more likely to have occurred if CC was the offspring of XX and XY rather than if CC was the offspring of XX and a random man unrelated to XY <population data set>

Paired kinship evaluation wording

XX. The results of the scientific examinations conducted in this laboratory are as follows:

Reference Samples

nn: XY - suspect
nn: CC – child

DNA profiles were obtained from these reference samples. These DNA profiles were different to each other.

The DNA profile obtained from the reference sample of XY was compared to the DNA profile obtained from the reference sample of CC in order to assist in the determination of the possibility of paternity of CC.

In my opinion, it is possible that XY is the biological father of CC. The following statistical weighting has been calculated in support of this opinion:

The DNA profile from CC is approximately x times more likely to have occurred if CC was the offspring XY rather than if CC was the offspring of a random man unrelated to XY.

20.4 Appendix 4 - DNA Evidentiary Certificate

Section 95A
Evidence Act 1977
Form 3 Version 2

DNA EVIDENTIARY CERTIFICATE

I, name, state

1. I am a DNA Analyst employed by Queensland Health Scientific Services

2. I am a Scientist in the DNA Analysis Unit.

3. My qualifications are: fill in

4. I hold appointment as a DNA Analyst under the Evidence Act 1977.

5. Appendix 1 to this certificate sets out the procedures and methodology used by Queensland Health Scientific Services in DNA testing. These procedures are carried out in accordance with the requirements of the National Association of Testing Authorities (NATA).

6. On the DD day of MM, YYYY, insert delivery officer delivered a number of items to Queensland Health Scientific Services, which were then received and registered under laboratory number: 123456789.

7. These things were:

8. On the ...

9. On (or between) the date of initial receipt and the statement date, these things, namely insert specified items here

Reference samples:

Items

were tested by me (and other laboratory staff):

11. I have examined the laboratory's records relating to the receipt, storage and testing of the things referred to in paragraph 10 (including where the testing process was done by someone other than me) and confirm that the records indicate that all quality assurance procedures for the receipt, storage and testing of the things that were in place in the laboratory at the time of the testing were complied with.

12. The results of the testing of the things referred to in paragraph 10 are as follows:
Refer to attached table of results.

Signed _____

Name **Your Name**

DNA Analyst _____

Date _____

Notes:

A. A party intending to rely on this DNA Evidentiary Certificate must give a copy to each other party in the proceeding at least 10 business days before the hearing day

B. The DNA Analyst giving the certificate will be called to give evidence at the hearing where the certificate is to be used.

C. Any party may request from the Chief Executive of the Department of Health a copy of the laboratory's records relating to the receipt, storage and testing of any things referred to in this certificate.

D. If any party intends to challenge any matter stated in this certificate that party must give written notice of the matter to be challenged (in form 4) to the Chief Executive of the Department of Health and each other party at least 3 business days before the hearing.

20.5 Appendix 5 – Further paragraphs for civil casework report

Analytical Techniques

In order to perform the DNA profiling process, DNA must first be isolated from the sub-sample obtained during examination. This is achieved by separating the cell containing the DNA from the substrate (eg, swab, tape lift, fabric, etc) by performing a number of washes and agitative steps. The cell is then broken open to release the DNA. During this step the DNA is separated from the cellular debris. This phase is termed 'DNA Extraction'.

The next phase is known as 'Quantitation' and is used to assess the amount of DNA within the sample. This information is then used to optimise the next stage called 'Amplification'. Amplification is a process designed to make many copies of the targeted DNA regions within the extracted DNA of a specific sample. This procedure is based on the laboratory technique called the 'Polymerase Chain Reaction' (PCR) and can be thought of as a DNA photocopier.

The amplified DNA is then separated based on the size of the targeted DNA fragments during a process called 'Capillary Electrophoresis'. This information is then analysed during a data analysis process aimed at labelling the individual fragments according to the relative size.

The result of the above processes is a DNA profile which displays as peaks on a graph which are assessed by a reporting scientist.

Quality

All testing completed by the Forensic DNA Analysis laboratory is conducted under a strict quality framework to ensure the utmost reliability and integrity of all results released. This is achieved by establishing and maintaining the following quality measures, to name a few:

- Use of Standard Operating Procedures (SOPs)
- Intensive training schedule for staff associated to individual processes to ensure that only competent staff are conducting the tasks
- Maintenance of continuity throughout the processes with the use of electronic batch /audit records and tracking of each exhibit/sample
- Review of all work and results prior to release
- Use of control and blank samples with every analytical processes
- Internal validation of all techniques utilised within the Forensic DNA laboratory
- Establishment and maintenance of staff and QPS DNA elimination databases
- Environmental monitoring and cleaning of the individual laboratory spaces
- Use of Personal Protective Equipment (PPE) throughout sample processing
- Restricted access to the laboratory including specific areas within the laboratory

20.6 Appendix 6 – Uniform Civil Procedure Rules 1999 – Sect 428

Uniform Civil Procedure Rules 1999 – Sect 428

In accordance with the Uniform Civil Procedure Rules 1999 – Sect 428, I confirm that:

(a) the factual matters stated in the report are, as far as the expert knows, true; and

(b) the expert has made all enquiries considered appropriate; and

(c) the opinions stated in the report are genuinely held by the expert; and

(d) the report contains reference to all matters the expert considers significant; and

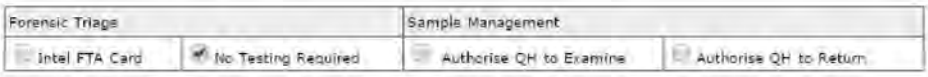
(e) the expert understands the expert's duty to the court and has complied with the duty.

.....

XXXXX
Signed at BRISBANE on DD Month YYYY

20.7 Appendix 7 – Actioning an exhibit that is no longer required for testing

If the QPS decide that no further work is required on an exhibit they will check the 'No Testing Required' box on the within the 'Forensic Triage' field.



This will automatically enter the 'No further work required as per advice from QPS' (NWQPS) exhibit result line against the exhibit which will be highlighted in red. This line requires manual validation.



If the exhibit has child exhibits then these children will also get the NWQPS exhibit result line, for example in the case of a SAIK that is no longer required, the SAIK and each of the swabs from the SAIK will have this line.

If the sample is in the process of being profiled then it will be flagged on the batch worklists for analytical staff to cease processing depending on where the sample is.

If the sample continues through analytical then the sample will populate the PDA worklists. The profile analyst will see the NWQPS line when entering into that sample for interpretation and will action the request for no further work.

If interpretation has already been completed and the sample is on the Profile Review worklists when the NWQPS line is added then the reviewer will see the NWQPS line when entering into that sample and will action the request for no further work.

Actioning No Further Work requests for samples on the PDA worklist

If a scientist enters into a sample on the PDA worklist that has the NWQPS exhibit result line then they will action this request as follows:

1. If there is a 'Calculation' process requiring validation, the scientist should enter a note into the calculation stating that the calculation has not been reviewed as no further work is required. They will then ask another scientist to validate the 'Calculation'.

2. Validate the NWQPS exhibit result line.

3. Order a 'Reallocate' process to remove the sample from the PDA worklist.

Actioning No Further Work requests for samples on the Profile Review worklist

If a scientist enters into a sample on the Profile Review worklist that has the NWQPS exhibit result line then they must action this request as follows:

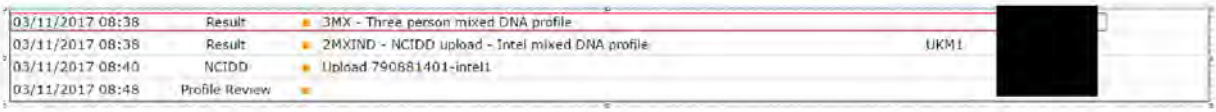
If the DNA profile has been correctly interpreted as a single source profile then the reviewer is to complete the review of the result as per section 4.4.10 of this document. The NWQPS exhibit result line is to be validated as well as this will reflect the sample audit and ensure the sample is not accidentally added to the statement with a result.

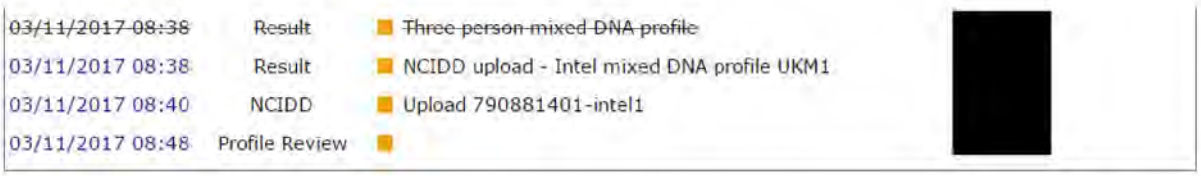
If however the DNA profile is anything other than a single source profile or it appears the initial assessment of a single source DNA profile is not correct then the following

1. If there is a 'Calculation' process requiring validation, the scientist should enter a note into the calculation stating that the calculation has not been reviewed as no further work is required. They will then ask another scientist to validate the 'Calculation'.

2. If there are profiles in the Profile Record table, the scientist should clear the Profile Record table by clicking on the icon whilst in edit mode.

3. Enter into each 'Result' that has an exhibit result line and 'incorrect' the line by clicking the icon.





4. If there is a 'NCIDD' test then this should be 'incorrected' by clicking on the icon.

5. Validate the 'Profile Review'.

6. Validate the 'NWQPS' line.

If advice is received that no further testing is required of a Post Mortem (PM) sample the 'No Testing Required' box within the 'Forensic Triage' field can be completed by a Senior Scientist or above. Staff at the HP4 and below level do not have access within the FR to complete this task

20.8 Appendix 8 – Suggested PowerPlex®21 (and STRmixTM) statement wording

NOTE 1:
When wording your statement it is important to remember that the comparison is being performed by STRmix™ and therefore the conclusions are based on statistical interpretation. Intuitive checking is performed only to ensure that STRmix™ is giving an appropriate interpretation. Therefore, statements such as 'Mr X cannot be excluded as having contributed to this profile and therefore I have considered the following propositions' are not appropriate under this model. Your statement should refer only to your assumptions and the statistical interpretation.

NOTE 2:
A link between the profile obtained and the assumption of number of contributors is recommended.

This could be written for mixtures in the following ways:

- *The mixed DNA profile(s) obtained from this sample indicates the presence of DNA from three contributors. As such, an assumption of three contributors has been made for statistical analysis.*

Or

- *A mixed DNA profile has been obtained from this sample. Based on the information within this DNA profile, an assumption of three contributors has been made for statistical analysis.*

This could be written for single source in the following ways:

- *The DNA profile(s) obtained from this sample indicates the presence of DNA from a single contributor. As such, this DNA profile matches the reference DNA profile of XY.*

Or

- *The DNA profile(s) obtained from this sample matches the DNA profile of XY.*

NOTE 3:

Rounding of LRs should be in the following conservative format:
- *if the LR = 157 232, round to LR = 150 thousand.*
- *If the LR = 129, round to LR = 120*
- *If the LR =72, no rounding performed..*
- *If the LR = 2.3, round to LR = 2*
- *If the LR favours Hd and = 157 232, round to 160 thousand*
- *If the LR favours Hd and = 129, round to 130*
- *If the LR favours Hd and =72, no rounding performed.*
- *If the LR favours Hd and = 2.3, round to LR = 3*

Example wording

Unknowns [redacted] **Swab (A), near rear door**

[redacted] **Swab (D), floor in foyer near charge counter**

The DNA profiles obtained from these samples *[match each other and]* do not match the reference DNA profiles associated with this matter. Each of these DNA profiles indicated male gender.

Single Source [redacted] **Swab (E), floor in charge area**

The DNA profile(s) obtained from this sample indicates the presence of DNA from a single contributor. As such, this DNA profile matches the reference DNA profile of XY.

Based on statistical analysis, it is estimated that the DNA profile obtained is greater than 100 billion times more likely to have occurred if the DNA originated from Mr X, rather than if the DNA originated from someone other than Mr X.

OR

The DNA profile obtained from this sample matches the DNA profile of Mr X.

Based on statistical analysis, it is estimated that the DNA profile obtained is greater than 100 billion times more likely to have occurred if Mr X had contributed DNA rather than if he had not.

Non-conditioned Mixture [redacted] **Swab (B), floor near cells**

The mixed DNA profile(s) obtained from this sample indicates the presence of DNA from three contributors. As such, an assumption of three contributors has been made for statistical analysis.

The reference DNA profiles of John, Sam and Carol have been compared with this mixed DNA profile separately, in order to assess whether or not any of them may have contributed DNA. Based on statistical analyses, the results are as follows:

In favour of contribution:

John - It is estimated that the mixed DNA profile obtained is approximately 4 times more likely to have occurred if he has contributed DNA rather than if he has not.

In favour of non-contribution:

Carol – It is estimated that the mixed DNA profile obtained is approximately 100,000 times more likely to have occurred if she has not contributed DNA rather than if she has contributed DNA.

Inconclusive:

Sam – It is estimated that the mixed DNA profile obtained is equally likely if he has contributed DNA rather than if he has not.

Conditioned Mixture

Conditioned Mixture

The mixed DNA profile(s) obtained from this sample indicates the presence of DNA from X contributors, one of whom could be Carol. Since this sample is said to have been collected from Carol, it would not be unexpected to find DNA which could have come from her. In order to interpret this mixed DNA profile an assumption of DNA from X contributors, one of whom is Carol, has been made.

The reference DNA profile of John has been compared to this mixed DNA profile, to assess whether or not he may have contributed DNA along with Carol.

Based on statistical analysis it is estimated that:

In favour of contribution:

John - It is estimated that the mixed DNA profile obtained is approximately 4 times more likely to have occurred if he has contributed DNA *[along with Carol]* rather than if he has not.

In favour of non-contribution:

John - It is estimated that the mixed DNA profile obtained is approximately 4 times more likely to have occurred if he has not contributed DNA rather than if he has contributed DNA.

Inconclusive:

John - It is estimated that the mixed DNA profile obtained is equally likely to have occurred if he has contributed DNA rather than if he has not.

Excluded:

Based on the assumption of X contributors and the presence of DNA from Carol, the following reference samples are excluded as potential contributors to the mixed DNA profile obtained: John et al

Not unexpected findings

Rectal swab
Anterior lower gum swab

The DNA profiles obtained from these samples *[match each other and also]* match the reference DNA profile of Carol. As these samples are said to have been taken from Carol, the finding of DNA which could have come from her is not unexpected, and therefore no statistical analysis has been performed.

Insufficient DNA

[redacted] **Graph 21; swab; pop bottle**

This sample contained insufficient DNA to be suitable for analysis and was not tested further.

No DNA Detected

[redacted]
Graph 9; swab; cot
Graph 2; swab; flyscreen

DNA was not detected in these samples and therefore they were not tested further.

Complex – no STRmix [redacted] **Graph 11; swab; right thong**
Item 6; tapelift; back of hand

The complex mixed DNA profiles obtained from these samples indicate the presence of DNA from more than three contributors and are therefore unsuitable for statistical analysis.

Complex – unsuitable [redacted] **Graph 5**

Due to the complex nature of this DNA profile, including uncertainty as to the number of contributors, in my opinion this DNA profile is not suitable for meaningful interpretation

20.9 Appendix 9 – Working from Home – Statement drafting, reporting and reviewing tasks

Drafting a statement

- Complete paperless process as described in Section 5 of this document
  - It is important that a casefile is available at the time of statement release as the Admin staff need to locate the hardcopy of the statement to a physical location. The reporting scientist is to request that a file is created by the Admin staff via email (as per Section 5.1) as soon as possible.

- In statement template, DO NOT DELETE the Peer Reviewer line on top left (signing block). The Options below are all written with no changes to the current statement template.

- If there are urgent statements needing to be released, please communicate with your Supervisor on potential adjustments to the options below.

- When the review is finalised, the options are:

1. **Original statement sent to Admin, to process as per normal**

   a. Print and sign statement as per normal
   b. Send statement in pre-paid envelope to FSS DNA Admin in supplied pre-paid envelopes.
   c. Email [redacted] to notify them a statement is in the mail
   d. Admin continue to process statement as per SOP.
      i. Admin will seek Reviewer's initials for the statement if they are at work
      ii. Admin will add initials of Peer Reviewer if they are also absent/working from home eg. 'JAH as per FR record'
      iii. Admin to add Casefile Notation that initials have been added in Reviewer's absence as per FR record.

   Works for staff working 100% at home and includes Admin final check (very worthwhile). Requires staff to have a number of pre-paid envelopes with them.

2. **Organise to attend work and process as per normal**

   a. Organise to attend work at a convenient time and to an area to minimise contact with other personnel if need be.
   b. Sign statement paperwork while at work
   c. Deliver statement to Admin for processing.
      i. Admin to write initials of Peer Reviewer if they are absent as per Option 1 (above).
   d. Reporting Scientist can choose to go through paper record of casefile at that stage, or not (and add a Casefile Notation that paper record has not been used at this stage).
   e. Add Casefile Notation detailing the process that has been followed.

Processed through Admin, SSLU, Records in the same way as current process. Can work for cases with generous timeframes and for staff not working 100% at home.

Reviewing a Statement

- Follow QIS 34006 and the paperless process described
- Complete FR Review records as per SOP
- If reviewer is present (even if the Reporting Scientist is not present but they have signed the statement), sign the relevant section of the statement and the date issued.
- If reviewer is not present and the statement needs to be issued, Reporting Scientist/Admin/delegate can add Reviewer's initials as per Option 1 above.
- Casefile Notation to be added to say peer reviewed remotely.

20.10 Appendix 10 – Offline Statements

If a Statement of Witness needs to be written outside of the FR (eg, system is down), the templates are available in QIS. Templates exist for Statements of Witness and Intelligence Reports - see the following documents:

QIS: 29010 – Statement of Witness template – stamp
QIS: 29009 – Statement of Witness template – blank – no NATA endorsement
QIS: 29024 – Use of offline Forensic Reporting templates
QIS: 29011 – Generic report template

This type of statement may be utilised in cases where someone other than the Reporting Scientist is requested to write a Statement of Witness. This may be, for example, by the examining scientist, or an analytical scientist. These statements should use the template without the stamp, as the stamp refers to the Reporting Scientist.

These statements should be scanned into the FR upon completion or when the system is available and be accompanied by a Report record and Review record as per section 5 of this document

Queensland Health
Forensic and Scientific Services

Validation of Examinations

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1 Purpose

The purpose of this procedure is to describe the validation process for samples within Evidence Recovery, Forensic DNA Analysis.

2 Scope

This procedure applies to all Evidence Recovery staff required to perform validations.

3 Definitions

ERT:	Evidence Recovery Team
CSSE:	Crime Scene Sample Envelope (packaging used by QPS to store items collected at a scene)
QPS:	Queensland Police Service
FR:	Forensic Register

4 General Principles

4.1 Competency

The validation process must be performed by a person who is competent in the process being reviewed.

4.2 Validation

The Forensic Register will not allow the validation process to be completed by the user who performed the examination; therefore, a second user must complete the validation. If the second user finds an error and wishes to correct it themselves, they can no longer validate that examination. In most instances, when an error needs to be corrected it should be given back to the user who completed the examination, refer to section 6.1.

The following processes will auto-validate:

- Notations
- Subsamples
- Analytical notes
- Specific result lines refer to Appendix 1 in QIS 33800 and Appendix 1 and 2 in QIS 33798.

Although these processes do not need to be validated, the user performing the validation must ensure the information within these processes is correct.

4.3 Worklists

The following worklists are used by ERT staff performing validations:

-  icon > Worklist > click Worklist tab > Awaiting Review > **In-tube check**
    - Validator to ensure no in-tube checks are outstanding
-  icon > Worklist > click Worklist tab > Awaiting Review > **Item Exam**

- Validator to validate Item Exams

-  icon > Worklist > click Worklist tab > Awaiting Review > **Microscopic**
  - Validator to validate Microscopic processes
-  icon > Worklist > click Worklist tab > Awaiting Review > **Presumptive**
  - Validator to validate Presumptive processes
-  icon > Worklist > click Worklist tab > Awaiting Review > **Result** (this worklist must be filtered to show only ER and NWQPS results)
  - ER – validator to validate result lines
  - NWQPS – validator to validate result line and follow up items not yet examined or in the process of being examined
-  icon > Worklist > click Worklist tab > **On Hold** – (this worklist must be filtered to show only Awaiting Advice)
  - Validator to check if requests that are >10 days have been actioned, details of exhibits that remain outstanding are to be sent to the Senior Scientist.
-  icon > Worklist > click Worklist tab > Audit > **28 Day Audit Case Work**
  - Validator to check the worklist for items that require an INT result line
-  icon > Worklist > click Worklist tab > **Received**
  - Validator transfers items for HP3 examination from the received worklist to either the Examination worklist or the On-hold worklist.
  - SAIKs cannot be transferred until FR details have been checked and an examination strategy has been formulated, refer to QIS 33798 for the SAIK strategy process.
  - Send request/tasks where necessary to confirm testing requirements (PM samples).
- Click the "bdna" logo > **Unit Work List** tab
  - Validator to complete or delegate case management requests of absent staff.
- Click the "bdna" logo > Unit Work List tab (click twice) > Compliance Audits > **Major Crime Tech Review**
  - Validator to validate Examination Summaries (or get the original case validator to validate them)

General guidelines for using worklists to validate:

- The user performing validations should work from one worklist at a time.
- When performing a validation on an exhibit, all outstanding process are to be validated at the same time for that item, as well as any outstanding validations for subsamples and child exhibits created from that exhibit.
- When a validation is performed, the sample will drop off the awaiting review worklist for that test type. Review all the awaiting review worklists to ensure no validations have been missed.

5 Procedure

5.1 Validation Process

1. Check testing requirements for the item, including the forensic category, description, location/owner, exhibit notes and analysis advice, forensic biology analytical advice, presumptive screening test and whether no testing required has been ticked.

Note: The no testing required box will only display if it has been ticked.

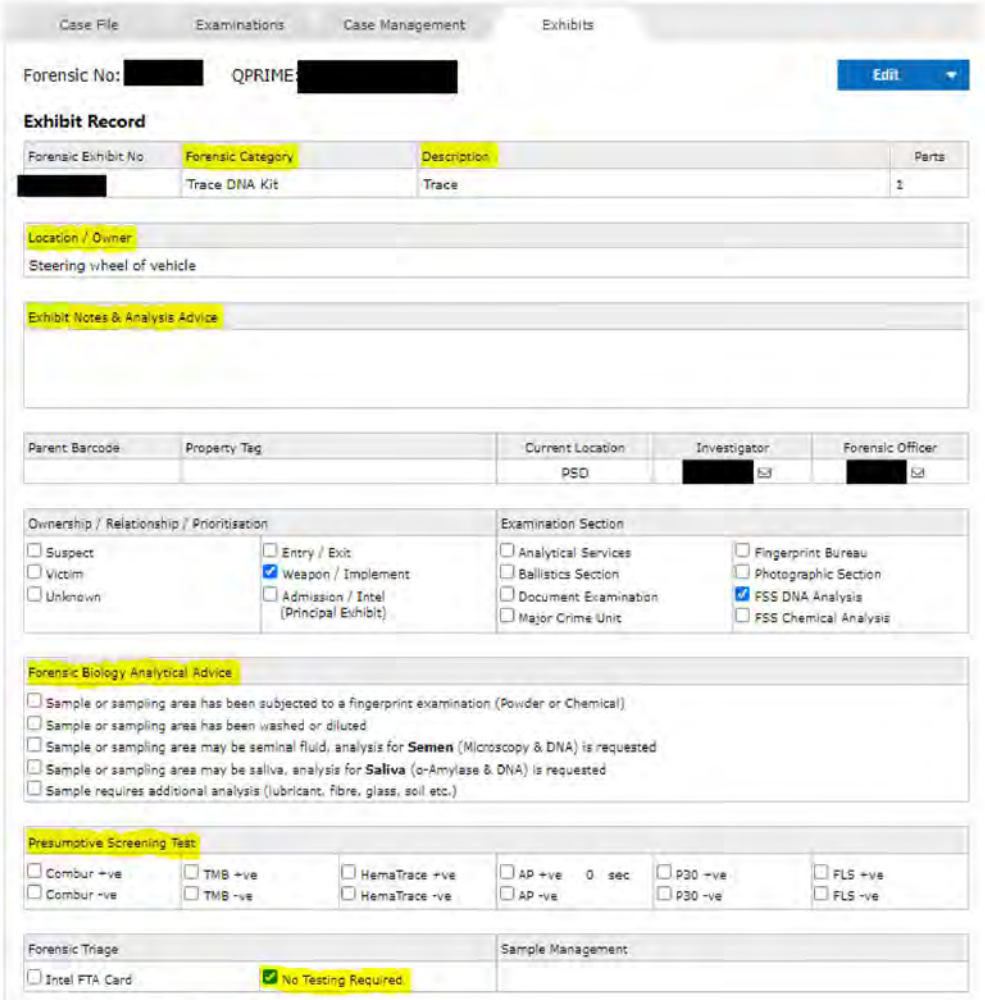

Figure 1 – Testing requirements

2. Review any associated and relevant information in the case management reports table or the case management tab for Forensic DNA Analysis.
3. Ensure the QPS image (if present) matches all information on the exhibit record page, including the barcode, QP and FR numbers, forensic category, description, and location/owner fields. Ensure a request/task has been sent if there are any discrepancies.

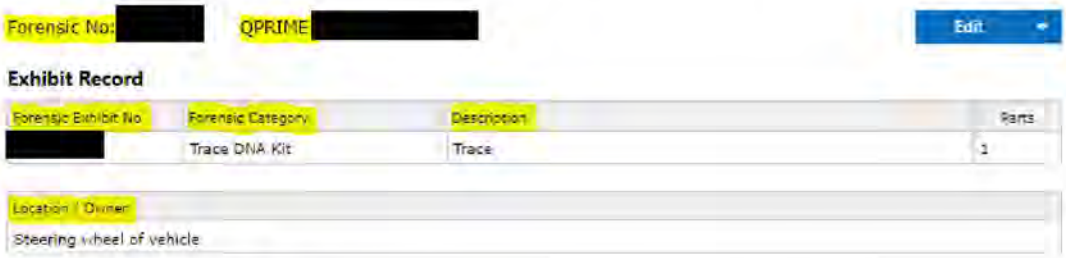

Figure 2 – Image check

4. In the exhibit movement table, ensure the sample has been tracked correctly including the examination bench number and if it is currently stored to an appropriate location.
5. Ensure the link chart is correct.
6. Validate all processes with orange traffic lights under the examinations and exhibit analytical/testing tables excluding microscopic and presumptives, if present. See sections 5.2 – 5.5 for details on specific processes.
7. Add samples to the appropriate extraction worklist, see appendix 10.2. Ensure the appropriate worklist is selected based on case notes and the examination strategy for SAIKs.
8. Validate microscopic and presumptive processes.
9. Check that the information entered in auto-validated processes (notations, subsamples, and analytical notes) are correct.
    - Notations – Ensure the notes are correct
    - Subsamples – Ensure a SubID has been entered and the correct SubType has been selected. Check that the notes correctly describe what the subsample is. Ensure the subsample has been stored correctly and a tube lot number has been entered if required (storage and tube lot numbers are not entered here if the subsample has been converted to a child exhibit).
    - Analytical notes – Check that the notes are correct and are present if required.
10. Ensure a correct result line has been selected and is validated if required; refer to SOP 33800 appendix 1, and SOP 33798 appendices 1 and 2 for information on which actions trigger automatic result lines and which items need manual result lines. Please note that result lines may be under the parent exhibit and/or the child exhibit.

11. To change the priority (i.e. P1) add a notation "Priority changed to P1 as per case notes" and click the P1 Priority radio button in the priority field.

12. Add an INT (Item has been examined / sub-sampled) result line to finalise any item/exhibit that will not have a final DNA profile result (e.g. no DNA detected, Single Source DNA profile etc.) and has been subsampled. The following are examples of exhibits that require an INT result line:

    - SAIK parent barcode
    - Fabric that is being returned to QPS after sampling
    - Post mortem samples parent barcode
    - SAIK swab where the microscopic and p30 tests are negative

5.2 Examination Record

If an examination record is present it will be listed in the Examinations table on the exhibit record page, check that the following fields are complete and correct:

1. Exam date/time
2. Duration
3. Check that the 'general', 'photo general' and 'no case file' boxes have been ticked. These boxes are located in the 'Examination Location - Scene / Subject Type' and 'Recording Method' fields.
4. Examination notes (check that these are consistent with the notes written in the item exam on the exhibit record page).
5. The item barcode is listed in the exhibits examined field.
6. Ensure the components of the item are listed in the exhibits collected field.
7. Check the examination images. Ensure all images of packaging match the information on the exhibit record page. **Note:** If the examination time field is later than the time that the photos were taken, a message will appear underneath the photos. If this occurs, then the examination time must be edited by the examiner.

If the above information is complete and correct, then a tech and admin review must be performed.

1. Click the [Create Tech Review] button, a new window with the "Case File Technical Review" check box selected will be visible, press the save button.
2. Click the [Create Admin Review] button, a new window with the "Case File Admin Review" check box selected will be visible, press the save button.
3. The two traffic lights next to the examination in the examinations table will now be green.

5.3 Item exam

1. In the notes field, check that the following have been mentioned and described appropriately:
    a. Packaging and seals including:
        - Type of seal
        - If intact
        - Whether it is signed and dated
    b. Package labelling
    c. A description of the item including (if relevant):
        - What it is
        - Size
        - Colour
        - Labelling/brand
        - Staining (including any presumptive tests conducted)
        - Physical appearance of damage
    d. A description of staining including (if relevant):
        - Shape
        - Distribution
        - Colour
        - Size (including measurements)
        - Intensity
        - Which side of the item the stain may have originated from
        - Any presumptive tests performed
        - Odour if applicable
    e. Presumptive results (AP and phadebas).
    f. How the sample was processed.

Note: The 'the sample was observed to meet requirements for next process' tick box is an in-tube specific line and should never be recorded for items.

1. Ensure a tube lot number has been entered if required.
2. The tube has been tracked to an ERT-AS box.

3. If all details are correct click the [CLICK TO VALIDATE] bar, which will turn green.

5.4 Microscopic

1. Check that the following fields are complete and correct:
    a. SubID
    b. SLIDE is selected in the SubType field
    c. Equipment number
    d. Result of the microscopy examination
    e. The H+E stains are entered in the reagents field
    f. The notes are completed including any England Finder coordinates
2. Ensure the slide has been stored correctly.
3. If all details are correct click the [CLICK TO VALIDATE] bar, which will turn green.

5.5 Presumptive

1. Consider whether the presumptive process is performed on the correct exhibit (parent exhibit or child exhibit). If the presumptive was performed on the parent exhibit, then it should be recorded against the parent exhibit. If the parent exhibit was subsampled (e.g. swab taken, fabric excised) and then the presumptive performed on this subsample, then the presumptive should be recorded against the child exhibit.
2. Ensure any result/s have been correctly ticked in the result field
3. For a positive AP result, ensure a time has been entered in the comments field
4. For phadebas, ensure a time has been entered in the notes field, with a description of the positive areas including size and location. Ensure the examiner has discussed what areas were positive at 10 minutes and what areas were positive at 40 minutes.
5. If an annotated image has been uploaded in an examination, ensure all marked areas are discussed in the notes field.
6. Check that one or more reagents have been correctly entered into the reagent field.
7. If all details are correct click the [CLICK TO VALIDATE] bar, which will turn green.

5.6 Child Exhibits

1. Clicking on the child exhibit in the link chart will take you to the exhibit record page for the child exhibit.



Figure 3 – Child exhibit in link chart

2. Check that the forensic category, description and location/owner are correct on the exhibit record page.
3. From the exhibit movement table ensure the sample has been tracked correctly and is currently in an appropriate storage location.
4. Complete steps 6 - 10 of section 5.1 for the child exhibit.

5.7 Audits

1. Exhibit room shelves – ensure all items physically located match the relevant worklist in FR (received or examination) and action if necessary.
2. On-hold box – ensure all items physically located within the on-hold box match the On-Hold worklist in FR and action if necessary.
3. Freezer boxes – ensure all items physically located are stored correctly and match the relevant worklist in FR (received, examination or on-hold) and action if necessary.

6 Actions

6.1 Requesting a correction

If the examination being validated is found to be incorrect or incomplete, then the user who completed the examination must be notified following the steps below.

1. If an error is found during validation, then return to the review worklist and click on the barcode hyperlink for the sample that needs correcting.
2. Click on the "View Analysis" button in the top right corner.
3. Click on the edit button under profile analysis.

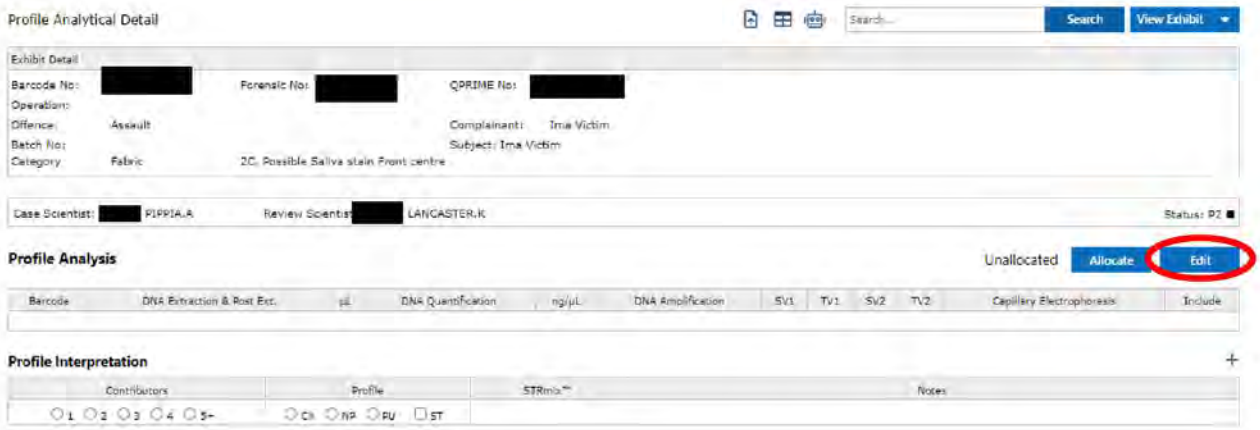

Figure 4 – Profile data analysis page

4. Type your initials into the notes field.



Figure 5 – Notes field on PDA page

5. Press the save button.

6. This will now display in the review worklist in the PDA notes column. **Note:** The PDA note will display in all review worklists where the sample has outstanding processes.

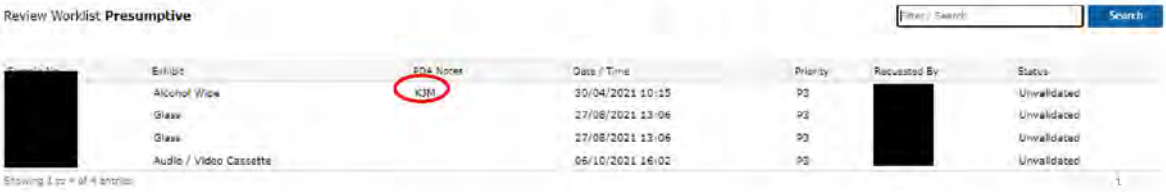

Figure 6 – PDA notes column

7. Email the examiner informing them of the corrections required. If the original examiner is absent, another examiner can perform the correction if necessary.

8. The examiner is to make the corrections required and send a return email stating that the corrections have been made.

9. Check that the corrections have been made and validate the required processes.

10. Follow steps 1 - 5 to edit the PDA notes and remove your initials.

Note: The PDA note will only display against the barcode that it is recorded against, and not child/parent exhibits.

6.2 Incorrect exhibit result lines and incorrect or duplicate examinations

If there is an error in the exhibit analytical/testing table, the line which contains the error must be marked as incorrect by the user who made the error, examples of this include:

- An incorrect exhibit result line has been selected
- An incorrect examination has been performed
- The examination is duplicated

A line within the exhibit analytical/testing table can only be marked as incorrect by the examiner if it has not yet been validated, refer to QIS 33800 for the process to incorrect. If the line has been validated, or it is a line that auto-validates, it can only be incorrected by a Senior Scientist.

Note: The examiner should delete all information within the record before it is incorrected.

7 Associated Documentation

QIS: 17185 – Detection of Azoospermic Semen in Casework Samples
QIS: 17186 – The Acid Phosphatase screening test for seminal stains
QIS: 17189 – Examination For & Of Spermatozoa
QIS: 17190 – Tetramethylbenzidine Screening Test for Blood
QIS: 22857 – Anti-contamination Procedure
QIS: 23849 – Common Forensic DNA Analysis Terms and Acronyms
QIS: 23959 – Storage Guidelines for Forensic DNA Analysis
QIS: 33798 – Examination of Sexual Cases
QIS: 33771 – Examination of in-tube samples
QIS: 33998 – Phadebas test for saliva
QIS: 33800 – Examination of Items

8 References

Nil.

9 Amendment History

QIS² Edition			
Version	**Date**	**Updated By**	**Amendments**
1	15/06/2017	Chelsea Savage	First Issue
2	29/11/2018	Chelsea Savage	Amendments to reflect changes in processes.
3	05/08/2020	Abbie Ryan	Removed "Forensic Register" from document title. 5.1 Amended process – validator to add samples to extraction worklists. Amended appendix 1 to include addition to extraction worklist. Added Appendix 2.
4	26/04/2022	J Seymour-Murray, K Morton	New template, updated screenshots and content to reflect current processes. Removed the process to incorrect exhibit testing processes, to be moved to QIS 33800.

10 Appendices

1 Appendix 1: Checklist for ValidationsAppendix 1:
2 Appendix 2: Extraction Worklist Selection

10.1 Appendix 1: Checklist for Validations

1	Check testing requirements
2	Check any reports in the case management reports table
3	Check images
4	Check tracking and that the sample is stored correctly in sample movement table
5	Check link chart
6	Check the following information in the examination record (if present) – exam date/time, duration, the 'general', 'photo general' and 'no case file' boxes have been ticked, examination notes, item barcode is entered in the exhibits examined, the components of the exhibit are listed in the exhibits collected field and exam images are uploaded.
7	Validate: Item exam – Ensure seals, labelling, description of item and staining and how the sample is processed is included in the notes field, and a tube lot number is entered if required.
8	Add the sample to the relevant extraction worklist.
9	Validate: Microscopic – Ensure the SubID, SubType, equipment number, result of microscopy examination, reagents and notes fields are correct and complete Presumptive – Ensure the results, comments, notes, and reagents fields are correct and complete.
10	Check the information in auto-validated processes
11	Validate manual result lines if required. Ensure any relevant auto-generated result lines are present.
12	Check that an analytical note has been entered if required
13	Check that the details entered into the exhibit record page for child exhibits are correct. Check storage for the child exhibit and complete steps 6 - 12 in section 5.1

10.2 Appendix 2: Extraction Worklist Selection

Sample Type	Extraction Worklist
Cells	QIAsymphony Pre-Lysis
Saliva	Retain Supernatant DNA IQ
Semen	Differential Lysis DNA IQ
Chewing Gum (cells)	Maxwell 16 DNA IQ
Semen/Saliva	Diff Lysis Retain Supernatant
Reference	Maxwell 16 DNA IQ
Bones	Organic Bone
Urgent P1 samples (cells)	Maxwell 16 DNA IQ

Queensland Health
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Technical and Administrative Review of Records Created in the Forensic Register

1 Purpose

The purpose of this document is to describe the procedure for the technical and administrative review of sample and case records created in the Forensic Register.

2 Scope

This procedure applies to all Forensic DNA Analysis staff who are required to perform technical and administrative reviews.

This procedure does not include the guidelines for the scientific interpretation of DNA profiling results. This information can be found in QIS 33773 *Procedure for Profile Data Analysis using the Forensic Register*.

3 Definitions

Case Record	Records of the case in FR, or a hardcopy case file containing FR records
FR	Forensic Register
EPG	Electropherogram
OQI	Opportunity for quality improvement
QPS	Queensland Police Service

4 Administrative and Technical Reviews

An *administrative review* is a review performed to ensure the completeness and correctness of case records and reports issued; a *technical review* is a review of a case record that checks the validity of the results and opinions contained within a report.

The Forensic Register contains the primary Case File record for all cases entirely received after 15 June 2017. All records pertaining to the Administrative and Technical review are stored within the Forensic Register.

An administrative and technical review can be performed at the same time by the same person but must not be performed by a person on their own work.

A person performing a technical review must be competent in the process that they are reviewing e.g. if a case contains mixed DNA profiles, the reviewer must be competent to interpret mixed DNA profiles to the appropriate level.

Results can be reported to the client in two ways:

- Electronically in the FR using Exhibit Reports
- In a paper statement or report

An administrative and technical review is performed on 100% of results released by the laboratory, including electronic Exhibit Reports, links and statements.

When a result is released by the Evidence Recovery team, a technical and administrative review is conducted which includes checking sample records and packaging images. Refer to QIS 34298 for the review process conducted by the Evidence Recovery team.

Once a DNA profile has been obtained for a sample, that sample will automatically populate the PDA worklists. Once interpretation has been performed the sample will populate a review worklist regardless of whether a paper case file exists.

When reviewing a result where a paper case file exists the reviewer must also perform an administrative review of the paper records pertaining to that result. This includes checking transcriptions and annotations on epgs. By validating the result, the scientist is acknowledging that both the technical and administrative aspects relating to this sample record (both paper and electronic) have been reviewed.

5 Review of Statements and Reports

The review of the statement of witness is the final step in the DNA profile interpretation process. At this stage the reviewer should check that all records in the FR have been reviewed and that any statistical calculations and opinions in the statement of witness have been appropriately reported. All profile interpretations in the FR should be consistent with those in the statement.

A statement may be accompanied by a paper file e.g. sexual assault and large cases. If a paper file exists, the reviewer should check:

- that any descriptions or interpretations noted on the EPG are correct (note that annotations of EPGs in the casefile are not compulsory)
- that the case file has all relevant communications and case notes included

If a review is being completed remotely, the paper case file may be unable to be checked. In this instance, a case file notation should be added to the FR to explain the departure from procedure. An administrative review of the case file should be completed prior to taking the file to court.

Administrative staff (or delegate) will:

- stamp the case file, if it exists, with the case identifier and write the total number of pages on the front of the case file or on the Case Files Particulars page (QIS 34307)
- ensure the original report is sent to the client and place a copy in the paper case file
- if report is also faxed, include a copy of fax cover sheet in the case file. These pages are included in the total number of pages in the case file
- in all instances a copy of the statement is uploaded to the FR. No paper records are kept for cases with no case file.

6 Additional information

Discuss any comments or discrepancies with the Reporting Scientist, or relevant scientist. If there are major discrepancies that affect the results, it may be necessary to consult QIS 36061 – *Procedure for Resolving DNA Profile Interpretation Differences of Opinion* or raise an OQI as a record of the investigation and implementation of corrective and preventive actions. Any discrepancies must be resolved to the satisfaction of the relevant parties. If problems cannot be resolved, a Senior Scientist, or Team Leader should be consulted.

The reviewer must use their approved number of initials, either two or three initials, as per NATA guidelines (refer 17088).

The following scenarios are acceptable:

- Sample result gets entered by Person A and validated/reviewed by Person B. Person A writes statement (containing all sample results) and this is reviewed by Person B.
- Sample result gets entered by Person A and validated/reviewed by Person B. Person B writes statement (containing all sample results) and this is reviewed by Person A.
- Sample result gets entered by Person A and validated/reviewed by Person B. Person C writes statement (containing all sample results) and this is reviewed by Person A.
- Sample result gets entered by Person A and validated/reviewed by Person B. Person C writes statement (containing all sample results) and this is reviewed by Person B.

7 Associated Documentation

QIS 17088	Procedure for recording handwriting specimens in Police services
QIS 33773	Procedure for Profile Data Analysis using the Forensic Register
QIS 34006	Procedure for the Release of Results using the Forensic Register
QIS 34298	Validation of Examinations
QIS 17168	Basics of DNA profile interpretation
QIS 34247	Creating and Reviewing Links - FR
QIS 34229	Explanation of Exhibit Results for FR
QIS 35007	Use of STRmix Software
QIS 34307	Forensic DNA Analysis – Case File Particulars
QIS 36061	Procedure for Resolving DNA Profile Interpretation Differences of Opinion

8 References

National Association of Testing Authorities (NATA). Legal-Forensic Science ISO/IEC 17025 Appendix. Refer to NATA website: http://www.nata.com.au

9 Amendment History

Version	Date	Updated By	Amendments
1	June 2017	E Caunt	First issue
2	January 2019	E Caunt	Reference updated, hyperlinks and associated documentation updated
3	Sept 2020	E Caunt	Reference to remote working and inability to check file added.

4	June 2022	E Caunt	Updated template. Referred to when a paper file does not exist. Added what happens in admin when no file. Referred to QIS 36061

CA-98

AS ISO/IEC 17025:2018
ISO/IEC 17025:2017

AS ISO/IEC 17025:2018

Australian STANDARD

General requirements for the competence of testing and calibration laboratories

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STANDARDS Australia

AS ISO/IEC 17025:2018

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General requirements for the competence of testing and calibration laboratories

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Preface

This Standard was prepared by the Australian members of the Joint Standards Australia/Standards New Zealand Committee QR-010, Conformity Assessment, to supersede AS ISO/IEC 17025—2005, *General requirements for the competence of testing and calibration laboratories.*

After consultation with stakeholders in both countries, Standards Australia and Standards New Zealand decided to develop this Standard as an Australian Standard rather than an Australian/New Zealand Standard.

The objective of this Standard is to specify the general requirements for the competence, impartiality and consistent operation of laboratories. This Standard is applicable to all organizations performing laboratory activities, regardless of the number of personnel.

This Standard is identical with, and has been reproduced from ISO/IEC 17025:2017, *General requirements for the competence of testing and calibration laboratories.*

As this document has been reproduced from an International Standard, a full point substitutes for a comma when referring to a decimal marker.

Australian or Australian/New Zealand Standards that are identical adoptions of international normative references may be used interchangeably. Refer to the online catalogue for information on specific Standards.

The terms 'normative' and 'informative' are used in Standards to define the application of the appendices or annexes to which they apply. A 'normative' appendix or annex is an integral part of a Standard, whereas an 'informative' appendix or annex is only for information and guidance.

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Foreword

ISO (the International Organization for Standardization) is a worldwide federation of national standards bodies (ISO member bodies). The work of preparing International Standards is normally carried out through ISO technical committees. Each member body interested in a subject for which a technical committee has been established has the right to be represented on that committee. International organizations, governmental and non-governmental, in liaison with ISO, also take part in the work. In the field of conformity assessment, ISO and the International Electrotechnical Commission (IEC) develop joint ISO/IEC documents under the management of the ISO Committee on Conformity assessment (ISO/CASCO).

The procedures used to develop this document and those intended for its further maintenance are described in the ISO/IEC Directives, Part 1. In particular the different approval criteria needed for the different types of ISO documents should be noted. This document was drafted in accordance with the editorial rules of the ISO/IEC Directives, Part 2 (see www.iso.org/directives).

Attention is drawn to the possibility that some of the elements of this document may be the subject of patent rights. ISO shall not be held responsible for identifying any or all such patent rights. Details of any patent rights identified during the development of the document will be in the Introduction and/or on the ISO list of patent declarations received (see www.iso.org/patents).

Any trade name used in this document is information given for the convenience of users and does not constitute an endorsement.

For an explanation on the voluntary nature of standards, the meaning of ISO specific terms and expressions related to conformity assessment, as well as information about ISO's adherence to the World Trade Organization (WTO) principles in the Technical Barriers to Trade (TBT) see the following URL: www.iso.org/iso/foreword.html.

This document was prepared by the ISO Committee on Conformity Assessment (CASCO) and circulated for voting to the national bodies of both ISO and IEC, and was approved by both organizations.

This third edition cancels and replaces the second edition (ISO/IEC 17025:2005), which has been technically revised.

The main changes compared to the previous edition are as follows:

— the risk-based thinking applied in this edition has enabled some reduction in prescriptive requirements and their replacement by performance-based requirements;

— there is greater flexibility than in the previous edition in the requirements for processes, procedures, documented information and organizational responsibilities;

— a definition of "laboratory" has been added (see 3.6).

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Introduction

This document has been developed with the objective of promoting confidence in the operation of laboratories. This document contains requirements for laboratories to enable them to demonstrate they operate competently, and are able to generate valid results. Laboratories that conform to this document will also operate generally in accordance with the principles of ISO 9001.

This document requires the laboratory to plan and implement actions to address risks and opportunities. Addressing both risks and opportunities establishes a basis for increasing the effectiveness of the management system, achieving improved results and preventing negative effects. The laboratory is responsible for deciding which risks and opportunities need to be addressed.

The use of this document will facilitate cooperation between laboratories and other bodies, and assist in the exchange of information and experience, and in the harmonization of standards and procedures. The acceptance of results between countries is facilitated if laboratories conform to this document.

In this document, the following verbal forms are used:

— "shall" indicates a requirement;

— "should" indicates a recommendation;

— "may" indicates a permission;

— "can" indicates a possibility or a capability.

Further details can be found in the ISO/IEC Directives, Part 2.

For the purposes of research, users are encouraged to share their views on this document and their priorities for changes to future editions. Click on the link below to take part in the online survey:

17025_ed3_usersurvey

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Australian Standard®

General requirements for the competence of testing and calibration laboratories

1 Scope

This document specifies the general requirements for the competence, impartiality and consistent operation of laboratories.

This document is applicable to all organizations performing laboratory activities, regardless of the number of personnel.

Laboratory customers, regulatory authorities, organizations and schemes using peer-assessment, accreditation bodies, and others use this document in confirming or recognizing the competence of laboratories.

2 Normative references

The following documents are referred to in the text in such a way that some or all of their content constitutes requirements of this document. For dated references, only the edition cited applies. For undated references, the latest edition of the referenced document (including any amendments) applies.

ISO/IEC Guide 99, *International vocabulary of metrology — Basic and general concepts and associated terms (VIM)*[1)]

ISO/IEC 17000, *Conformity assessment — Vocabulary and general principles*

3 Terms and definitions

For the purposes of this document, the terms and definitions given in ISO/IEC Guide 99 and ISO/IEC 17000 and the following apply.

ISO and IEC maintain terminological databases for use in standardization at the following addresses:

— ISO Online browsing platform: available at https://www.iso.org/obp

— IEC Electropedia: available at http://www.electropedia.org/

3.1
impartiality
presence of objectivity

Note 1 to entry: Objectivity means that conflicts of interest do not exist, or are resolved so as not to adversely influence subsequent activities of the *laboratory* (3.6).

Note 2 to entry: Other terms that are useful in conveying the element of impartiality include "freedom from conflict of interests", "freedom from bias", "lack of prejudice", "neutrality", "fairness", "open-mindedness", "even-handedness", "detachment", "balance".

[SOURCE: ISO/IEC 17021-1:2015, 3.2, modified — The words "the certification body" have been replaced by "the laboratory" in Note 1 to entry, and the word "independence" has been deleted from the list in Note 2 to entry.]

1) Also known as JCGM 200.

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3.2
complaint
expression of dissatisfaction by any person or organization to a *laboratory* (3.6), relating to the activities or results of that laboratory, where a response is expected

[SOURCE: ISO/IEC 17000:2004, 6.5, modified — The words "other than appeal" have been deleted, and the words "a conformity assessment body or accreditation body, relating to the activities of that body" have been replaced by "a laboratory, relating to the activities or results of that laboratory".]

3.3
interlaboratory comparison
organization, performance and evaluation of measurements or tests on the same or similar items by two or more laboratories in accordance with predetermined conditions

[SOURCE: ISO/IEC 17043:2010, 3.4]

3.4
intralaboratory comparison
organization, performance and evaluation of measurements or tests on the same or similar items within the same *laboratory* (3.6) in accordance with predetermined conditions

3.5
proficiency testing
evaluation of participant performance against pre-established criteria by means of *interlaboratory comparisons* (3.3)

[SOURCE: ISO/IEC 17043:2010, 3.7, modified — Notes to entry have been deleted.]

3.6
laboratory
body that performs one or more of the following activities:

— testing;

— calibration;

— sampling, associated with subsequent testing or calibration

Note 1 to entry: In the context of this document, "laboratory activities" refer to the three above-mentioned activities.

3.7
decision rule
rule that describes how measurement uncertainty is accounted for when stating conformity with a specified requirement

3.8
verification
provision of objective evidence that a given item fulfils specified requirements

EXAMPLE 1 Confirmation that a given reference material as claimed is homogeneous for the quantity value and measurement procedure concerned, down to a measurement portion having a mass of 10 mg.

EXAMPLE 2 Confirmation that performance properties or legal requirements of a measuring system are achieved.

EXAMPLE 3 Confirmation that a target measurement uncertainty can be met.

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Note 1 to entry: When applicable, measurement uncertainty should be taken into consideration.

Note 2 to entry: The item may be, for example, a process, measurement procedure, material, compound, or measuring system.

Note 3 to entry: The specified requirements may be, for example, that a manufacturer's specifications are met.

Note 4 to entry: Verification in legal metrology, as defined in VIML, and in conformity assessment in general, pertains to the examination and marking and/or issuing of a verification certificate for a measuring system.

Note 5 to entry: Verification should not be confused with calibration. Not every verification is a *validation* (3.9).

Note 6 to entry: In chemistry, verification of the identity of the entity involved, or of activity, requires a description of the structure or properties of that entity or activity.

[SOURCE: ISO/IEC Guide 99:2007, 2.44]

3.9
validation
verification (3.8), where the specified requirements are adequate for an intended use

EXAMPLE A measurement procedure, ordinarily used for the measurement of mass concentration of nitrogen in water, may be validated also for measurement of mass concentration of nitrogen in human serum.

[SOURCE: ISO/IEC Guide 99:2007, 2.45]

4 General requirements

4.1 Impartiality

4.1.1 Laboratory activities shall be undertaken impartially and structured and managed so as to safeguard impartiality.

4.1.2 The laboratory management shall be committed to impartiality.

4.1.3 The laboratory shall be responsible for the impartiality of its laboratory activities and shall not allow commercial, financial or other pressures to compromise impartiality.

4.1.4 The laboratory shall identify risks to its impartiality on an on-going basis. This shall include those risks that arise from its activities, or from its relationships, or from the relationships of its personnel. However, such relationships do not necessarily present a laboratory with a risk to impartiality.

NOTE A relationship that threatens the impartiality of the laboratory can be based on ownership, governance, management, personnel, shared resources, finances, contracts, marketing (including branding), and payment of a sales commission or other inducement for the referral of new customers, etc.

4.1.5 If a risk to impartiality is identified, the laboratory shall be able to demonstrate how it eliminates or minimizes such risk.

4.2 Confidentiality

4.2.1 The laboratory shall be responsible, through legally enforceable commitments, for the management of all information obtained or created during the performance of laboratory activities. The laboratory shall inform the customer in advance, of the information it intends to place in the public domain. Except for information that the customer makes publicly available, or when agreed between the

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laboratory and the customer (e.g. for the purpose of responding to complaints), all other information is considered proprietary information and shall be regarded as confidential.

4.2.2 When the laboratory is required by law or authorized by contractual arrangements to release confidential information, the customer or individual concerned shall, unless prohibited by law, be notified of the information provided.

4.2.3 Information about the customer obtained from sources other than the customer (e.g. complainant, regulators) shall be confidential between the customer and the laboratory. The provider (source) of this information shall be confidential to the laboratory and shall not be shared with the customer, unless agreed by the source.

4.2.4 Personnel, including any committee members, contractors, personnel of external bodies, or individuals acting on the laboratory's behalf, shall keep confidential all information obtained or created during the performance of laboratory activities, except as required by law.

5 Structural requirements

5.1 The laboratory shall be a legal entity, or a defined part of a legal entity, that is legally responsible for its laboratory activities.

NOTE For the purposes of this document, a governmental laboratory is deemed to be a legal entity on the basis of its governmental status.

5.2 The laboratory shall identify management that has overall responsibility for the laboratory.

5.3 The laboratory shall define and document the range of laboratory activities for which it conforms with this document. The laboratory shall only claim conformity with this document for this range of laboratory activities, which excludes externally provided laboratory activities on an ongoing basis.

5.4 Laboratory activities shall be carried out in such a way as to meet the requirements of this document, the laboratory's customers, regulatory authorities and organizations providing recognition. This shall include laboratory activities performed in all its permanent facilities, at sites away from its permanent facilities, in associated temporary or mobile facilities or at a customer's facility.

5.5 The laboratory shall:

a) define the organization and management structure of the laboratory, its place in any parent organization, and the relationships between management, technical operations and support services;

b) specify the responsibility, authority and interrelationship of all personnel who manage, perform or verify work affecting the results of laboratory activities;

c) document its procedures to the extent necessary to ensure the consistent application of its laboratory activities and the validity of the results.

5.6 The laboratory shall have personnel who, irrespective of other responsibilities, have the authority and resources needed to carry out their duties, including:

a) implementation, maintenance and improvement of the management system;

b) identification of deviations from the management system or from the procedures for performing laboratory activities;

c) initiation of actions to prevent or minimize such deviations;

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d) reporting to laboratory management on the performance of the management system and any need for improvement;

e) ensuring the effectiveness of laboratory activities.

5.7 Laboratory management shall ensure that:

a) communication takes place regarding the effectiveness of the management system and the importance of meeting customers' and other requirements;

b) the integrity of the management system is maintained when changes to the management system are planned and implemented.

6 Resource requirements

6.1 General

The laboratory shall have available the personnel, facilities, equipment, systems and support services necessary to manage and perform its laboratory activities.

6.2 Personnel

6.2.1 All personnel of the laboratory, either internal or external, that could influence the laboratory activities shall act impartially, be competent and work in accordance with the laboratory's management system.

6.2.2 The laboratory shall document the competence requirements for each function influencing the results of laboratory activities, including requirements for education, qualification, training, technical knowledge, skills and experience.

6.2.3 The laboratory shall ensure that the personnel have the competence to perform laboratory activities for which they are responsible and to evaluate the significance of deviations.

6.2.4 The management of the laboratory shall communicate to personnel their duties, responsibilities and authorities.

6.2.5 The laboratory shall have procedure(s) and retain records for:

a) determining the competence requirements;

b) selection of personnel;

c) training of personnel;

d) supervision of personnel;

e) authorization of personnel;

f) monitoring competence of personnel.

6.2.6 The laboratory shall authorize personnel to perform specific laboratory activities, including but not limited to, the following:

a) development, modification, verification and validation of methods;

b) analysis of results, including statements of conformity or opinions and interpretations;

c) report, review and authorization of results.

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6.3 Facilities and environmental conditions

6.3.1 The facilities and environmental conditions shall be suitable for the laboratory activities and shall not adversely affect the validity of results.

NOTE Influences that can adversely affect the validity of results can include, but are not limited to, microbial contamination, dust, electromagnetic disturbances, radiation, humidity, electrical supply, temperature, sound and vibration.

6.3.2 The requirements for facilities and environmental conditions necessary for the performance of the laboratory activities shall be documented.

6.3.3 The laboratory shall monitor, control and record environmental conditions in accordance with relevant specifications, methods or procedures or where they influence the validity of the results.

6.3.4 Measures to control facilities shall be implemented, monitored and periodically reviewed and shall include, but not be limited to:

a) access to and use of areas affecting laboratory activities;

b) prevention of contamination, interference or adverse influences on laboratory activities;

c) effective separation between areas with incompatible laboratory activities.

6.3.5 When the laboratory performs laboratory activities at sites or facilities outside its permanent control, it shall ensure that the requirements related to facilities and environmental conditions of this document are met.

6.4 Equipment

6.4.1 The laboratory shall have access to equipment (including, but not limited to, measuring instruments, software, measurement standards, reference materials, reference data, reagents, consumables or auxiliary apparatus) that is required for the correct performance of laboratory activities and that can influence the results.

NOTE 1 A multitude of names exist for reference materials and certified reference materials, including reference standards, calibration standards, standard reference materials and quality control materials. ISO 17034 contains additional information on reference material producers (RMPs). RMPs that meet the requirements of ISO 17034 are considered to be competent. Reference materials from RMPs meeting the requirements of ISO 17034 are provided with a product information sheet/certificate that specifies, amongst other characteristics, homogeneity and stability for specified properties and, for certified reference materials, specified properties with certified values, their associated measurement uncertainty and metrological traceability.

NOTE 2 ISO Guide 33 provides guidance on the selection and use of reference materials. ISO Guide 80 provides guidance to produce in-house quality control materials.

6.4.2 When the laboratory uses equipment outside its permanent control, it shall ensure that the requirements for equipment of this document are met.

6.4.3 The laboratory shall have a procedure for handling, transport, storage, use and planned maintenance of equipment in order to ensure proper functioning and to prevent contamination or deterioration.

6.4.4 The laboratory shall verify that equipment conforms to specified requirements before being placed or returned into service.

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6.4.5 The equipment used for measurement shall be capable of achieving the measurement accuracy and/or measurement uncertainty required to provide a valid result.

6.4.6 Measuring equipment shall be calibrated when:

— the measurement accuracy or measurement uncertainty affects the validity of the reported results, and/or

— calibration of the equipment is required to establish the metrological traceability of the reported results.

NOTE Types of equipment having an effect on the validity of the reported results can include:

— those used for the direct measurement of the measurand, e.g. use of a balance to perform a mass measurement;

— those used to make corrections to the measured value, e.g. temperature measurements;

— those used to obtain a measurement result calculated from multiple quantities.

6.4.7 The laboratory shall establish a calibration programme, which shall be reviewed and adjusted as necessary in order to maintain confidence in the status of calibration.

6.4.8 All equipment requiring calibration or which has a defined period of validity shall be labelled, coded or otherwise identified to allow the user of the equipment to readily identify the status of calibration or period of validity.

6.4.9 Equipment that has been subjected to overloading or mishandling, gives questionable results, or has been shown to be defective or outside specified requirements, shall be taken out of service. It shall be isolated to prevent its use or clearly labelled or marked as being out of service until it has been verified to perform correctly. The laboratory shall examine the effect of the defect or deviation from specified requirements and shall initiate the management of nonconforming work procedure (see 7.10).

6.4.10 When intermediate checks are necessary to maintain confidence in the performance of the equipment, these checks shall be carried out according to a procedure.

6.4.11 When calibration and reference material data include reference values or correction factors, the laboratory shall ensure the reference values and correction factors are updated and implemented, as appropriate, to meet specified requirements.

6.4.12 The laboratory shall take practicable measures to prevent unintended adjustments of equipment from invalidating results.

6.4.13 Records shall be retained for equipment which can influence laboratory activities. The records shall include the following, where applicable:

a) the identity of equipment, including software and firmware version;

b) the manufacturer's name, type identification, and serial number or other unique identification;

c) evidence of verification that equipment conforms with specified requirements;

d) the current location;

e) calibration dates, results of calibrations, adjustments, acceptance criteria, and the due date of the next calibration or the calibration interval;

f) documentation of reference materials, results, acceptance criteria, relevant dates and the period of validity;

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g) the maintenance plan and maintenance carried out to date, where relevant to the performance of the equipment;

h) details of any damage, malfunction, modification to, or repair of, the equipment.

6.5 Metrological traceability

6.5.1 The laboratory shall establish and maintain metrological traceability of its measurement results by means of a documented unbroken chain of calibrations, each contributing to the measurement uncertainty, linking them to an appropriate reference.

NOTE 1 In ISO/IEC Guide 99, metrological traceability is defined as the "property of a measurement result whereby the result can be related to a reference through a documented unbroken chain of calibrations, each contributing to the measurement uncertainty".

NOTE 2 See Annex A for additional information on metrological traceability.

6.5.2 The laboratory shall ensure that measurement results are traceable to the International System of Units (SI) through:

a) calibration provided by a competent laboratory; or

NOTE 1 Laboratories fulfilling the requirements of this document are considered to be competent.

b) certified values of certified reference materials provided by a competent producer with stated metrological traceability to the SI; or

NOTE 2 Reference material producers fulfilling the requirements of ISO 17034 are considered to be competent.

c) direct realization of the SI units ensured by comparison, directly or indirectly, with national or international standards.

NOTE 3 Details of practical realization of the definitions of some important units are given in the SI brochure.

6.5.3 When metrological traceability to the SI units is not technically possible, the laboratory shall demonstrate metrological traceability to an appropriate reference, e.g.:

a) certified values of certified reference materials provided by a competent producer;

b) results of reference measurement procedures, specified methods or consensus standards that are clearly described and accepted as providing measurement results fit for their intended use and ensured by suitable comparison.

6.6 Externally provided products and services

6.6.1 The laboratory shall ensure that only suitable externally provided products and services that affect laboratory activities are used, when such products and services:

a) are intended for incorporation into the laboratory's own activities;

b) are provided, in part or in full, directly to the customer by the laboratory, as received from the external provider;

c) are used to support the operation of the laboratory.

NOTE Products can include, for example, measurement standards and equipment, auxiliary equipment, consumable materials and reference materials. Services can include, for example, calibration services, sampling services, testing services, facility and equipment maintenance services, proficiency testing services and assessment and auditing services.

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6.6.2 The laboratory shall have a procedure and retain records for:

a) defining, reviewing and approving the laboratory's requirements for externally provided products and services;

b) defining the criteria for evaluation, selection, monitoring of performance and re-evaluation of the external providers;

c) ensuring that externally provided products and services conform to the laboratory's established requirements, or when applicable, to the relevant requirements of this document, before they are used or directly provided to the customer;

d) taking any actions arising from evaluations, monitoring of performance and re-evaluations of the external providers.

6.6.3 The laboratory shall communicate its requirements to external providers for:

a) the products and services to be provided;

b) the acceptance criteria;

c) competence, including any required qualification of personnel;

d) activities that the laboratory, or its customer, intends to perform at the external provider's premises.

7 Process requirements

7.1 Review of requests, tenders and contracts

7.1.1 The laboratory shall have a procedure for the review of requests, tenders and contracts. The procedure shall ensure that:

a) the requirements are adequately defined, documented and understood;

b) the laboratory has the capability and resources to meet the requirements;

c) where external providers are used, the requirements of 6.6 are applied and the laboratory advises the customer of the specific laboratory activities to be performed by the external provider and gains the customer's approval;

NOTE 1 It is recognized that externally provided laboratory activities can occur when:

— the laboratory has the resources and competence to perform the activities, however, for unforeseen reasons is unable to undertake these in part or full;

— the laboratory does not have the resources or competence to perform the activities.

d) the appropriate methods or procedures are selected and are capable of meeting the customers' requirements.

NOTE 2 For internal or routine customers, reviews of requests, tenders and contracts can be performed in a simplified way.

7.1.2 The laboratory shall inform the customer when the method requested by the customer is considered to be inappropriate or out of date.

7.1.3 When the customer requests a statement of conformity to a specification or standard for the test or calibration (e.g. pass/fail, in-tolerance/out-of-tolerance), the specification or standard and the decision rule shall be clearly defined. Unless inherent in the requested specification or standard, the decision rule selected shall be communicated to, and agreed with, the customer.

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NOTE For further guidance on statements of conformity, see ISO/IEC Guide 98-4.

7.1.4 Any differences between the request or tender and the contract shall be resolved before laboratory activities commence. Each contract shall be acceptable both to the laboratory and the customer. Deviations requested by the customer shall not impact the integrity of the laboratory or the validity of the results.

7.1.5 The customer shall be informed of any deviation from the contract.

7.1.6 If a contract is amended after work has commenced, the contract review shall be repeated and any amendments shall be communicated to all affected personnel.

7.1.7 The laboratory shall cooperate with customers or their representatives in clarifying the customer's request and in monitoring the laboratory's performance in relation to the work performed.

NOTE Such cooperation can include:

a) providing reasonable access to relevant areas of the laboratory to witness customer-specific laboratory activities;

b) preparation, packaging, and dispatch of items needed by the customer for verification purposes.

7.1.8 Records of reviews, including any significant changes, shall be retained. Records shall also be retained of pertinent discussions with a customer relating to the customer's requirements or the results of the laboratory activities.

7.2 Selection, verification and validation of methods

7.2.1 Selection and verification of methods

7.2.1.1 The laboratory shall use appropriate methods and procedures for all laboratory activities and, where appropriate, for evaluation of the measurement uncertainty as well as statistical techniques for analysis of data.

NOTE "Method" as used in this document can be considered synonymous with the term "measurement procedure" as defined in ISO/IEC Guide 99.

7.2.1.2 All methods, procedures and supporting documentation, such as instructions, standards, manuals and reference data relevant to the laboratory activities, shall be kept up to date and shall be made readily available to personnel (see 8.3).

7.2.1.3 The laboratory shall ensure that it uses the latest valid version of a method unless it is not appropriate or possible to do so. When necessary, the application of the method shall be supplemented with additional details to ensure consistent application.

NOTE International, regional or national standards or other recognized specifications that contain sufficient and concise information on how to perform laboratory activities do not need to be supplemented or rewritten as internal procedures if these standards are written in a way that they can be used by the operating personnel in a laboratory. It can be necessary to provide additional documentation for optional steps in the method or additional details.

7.2.1.4 When the customer does not specify the method to be used, the laboratory shall select an appropriate method and inform the customer of the method chosen. Methods published either in international, regional or national standards, or by reputable technical organizations, or in relevant scientific texts or journals, or as specified by the manufacturer of the equipment, are recommended. Laboratory-developed or modified methods can also be used.

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7.2.1.5 The laboratory shall verify that it can properly perform methods before introducing them by ensuring that it can achieve the required performance. Records of the verification shall be retained. If the method is revised by the issuing body, verification shall be repeated to the extent necessary.

7.2.1.6 When method development is required, this shall be a planned activity and shall be assigned to competent personnel equipped with adequate resources. As method development proceeds, periodic review shall be carried out to confirm that the needs of the customer are still being fulfilled. Any modifications to the development plan shall be approved and authorized.

7.2.1.7 Deviations from methods for all laboratory activities shall occur only if the deviation has been documented, technically justified, authorized, and accepted by the customer.

NOTE Customer acceptance of deviations can be agreed in advance in the contract.

7.2.2 Validation of methods

7.2.2.1 The laboratory shall validate non-standard methods, laboratory-developed methods and standard methods used outside their intended scope or otherwise modified. The validation shall be as extensive as is necessary to meet the needs of the given application or field of application.

NOTE 1 Validation can include procedures for sampling, handling and transportation of test or calibration items.

NOTE 2 The techniques used for method validation can be one of, or a combination of, the following:

a) calibration or evaluation of bias and precision using reference standards or reference materials;

b) systematic assessment of the factors influencing the result;

c) testing method robustness through variation of controlled parameters, such as incubator temperature, volume dispensed;

d) comparison of results achieved with other validated methods;

e) interlaboratory comparisons;

f) evaluation of measurement uncertainty of the results based on an understanding of the theoretical principles of the method and practical experience of the performance of the sampling or test method.

7.2.2.2 When changes are made to a validated method, the influence of such changes shall be determined and where they are found to affect the original validation, a new method validation shall be performed.

7.2.2.3 The performance characteristics of validated methods, as assessed for the intended use, shall be relevant to the customers' needs and consistent with specified requirements.

NOTE Performance characteristics can include, but are not limited to, measurement range, accuracy, measurement uncertainty of the results, limit of detection, limit of quantification, selectivity of the method, linearity, repeatability or reproducibility, robustness against external influences or cross-sensitivity against interference from the matrix of the sample or test object, and bias.

7.2.2.4 The laboratory shall retain the following records of validation:

a) the validation procedure used;

b) specification of the requirements;

c) determination of the performance characteristics of the method;

d) results obtained;

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e) a statement on the validity of the method, detailing its fitness for the intended use.

7.3 Sampling

7.3.1 The laboratory shall have a sampling plan and method when it carries out sampling of substances, materials or products for subsequent testing or calibration. The sampling method shall address the factors to be controlled to ensure the validity of subsequent testing or calibration results. The sampling plan and method shall be available at the site where sampling is undertaken. Sampling plans shall, whenever reasonable, be based on appropriate statistical methods.

7.3.2 The sampling method shall describe:

a) the selection of samples or sites;

b) the sampling plan;

c) the preparation and treatment of sample(s) from a substance, material or product to yield the required item for subsequent testing or calibration.

NOTE When received into the laboratory, further handling can be required as specified in 7.4.

7.3.3 The laboratory shall retain records of sampling data that forms part of the testing or calibration that is undertaken. These records shall include, where relevant:

a) reference to the sampling method used;

b) date and time of sampling;

c) data to identify and describe the sample (e.g. number, amount, name);

d) identification of the personnel performing sampling;

e) identification of the equipment used;

f) environmental or transport conditions;

g) diagrams or other equivalent means to identify the sampling location, when appropriate;

h) deviations, additions to or exclusions from the sampling method and sampling plan.

7.4 Handling of test or calibration items

7.4.1 The laboratory shall have a procedure for the transportation, receipt, handling, protection, storage, retention, and disposal or return of test or calibration items, including all provisions necessary to protect the integrity of the test or calibration item, and to protect the interests of the laboratory and the customer. Precautions shall be taken to avoid deterioration, contamination, loss or damage to the item during handling, transporting, storing/waiting, and preparation for testing or calibration. Handling instructions provided with the item shall be followed.

7.4.2 The laboratory shall have a system for the unambiguous identification of test or calibration items. The identification shall be retained while the item is under the responsibility of the laboratory. The system shall ensure that items will not be confused physically or when referred to in records or other documents. The system shall, if appropriate, accommodate a sub-division of an item or groups of items and the transfer of items.

7.4.3 Upon receipt of the test or calibration item, deviations from specified conditions shall be recorded. When there is doubt about the suitability of an item for test or calibration, or when an item does not conform to the description provided, the laboratory shall consult the customer for further instructions

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before proceeding and shall record the results of this consultation. When the customer requires the item to be tested or calibrated acknowledging a deviation from specified conditions, the laboratory shall include a disclaimer in the report indicating which results may be affected by the deviation.

7.4.4 When items need to be stored or conditioned under specified environmental conditions, these conditions shall be maintained, monitored and recorded.

7.5 Technical records

7.5.1 The laboratory shall ensure that technical records for each laboratory activity contain the results, report and sufficient information to facilitate, if possible, identification of factors affecting the measurement result and its associated measurement uncertainty and enable the repetition of the laboratory activity under conditions as close as possible to the original. The technical records shall include the date and the identity of personnel responsible for each laboratory activity and for checking data and results. Original observations, data and calculations shall be recorded at the time they are made and shall be identifiable with the specific task.

7.5.2 The laboratory shall ensure that amendments to technical records can be tracked to previous versions or to original observations. Both the original and amended data and files shall be retained, including the date of alteration, an indication of the altered aspects and the personnel responsible for the alterations.

7.6 Evaluation of measurement uncertainty

7.6.1 Laboratories shall identify the contributions to measurement uncertainty. When evaluating measurement uncertainty, all contributions that are of significance, including those arising from sampling, shall be taken into account using appropriate methods of analysis.

7.6.2 A laboratory performing calibrations, including of its own equipment, shall evaluate the measurement uncertainty for all calibrations.

7.6.3 A laboratory performing testing shall evaluate measurement uncertainty. Where the test method precludes rigorous evaluation of measurement uncertainty, an estimation shall be made based on an understanding of the theoretical principles or practical experience of the performance of the method.

NOTE 1 In those cases where a well-recognized test method specifies limits to the values of the major sources of measurement uncertainty and specifies the form of presentation of the calculated results, the laboratory is considered to have satisfied 7.6.3 by following the test method and reporting instructions.

NOTE 2 For a particular method where the measurement uncertainty of the results has been established and verified, there is no need to evaluate measurement uncertainty for each result if the laboratory can demonstrate that the identified critical influencing factors are under control.

NOTE 3 For further information, see ISO/IEC Guide 98-3, ISO 21748 and the ISO 5725 series.

7.7 Ensuring the validity of results

7.7.1 The laboratory shall have a procedure for monitoring the validity of results. The resulting data shall be recorded in such a way that trends are detectable and, where practicable, statistical techniques shall be applied to review the results. This monitoring shall be planned and reviewed and shall include, where appropriate, but not be limited to:

a) use of reference materials or quality control materials;

b) use of alternative instrumentation that has been calibrated to provide traceable results;

c) functional check(s) of measuring and testing equipment;

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d) use of check or working standards with control charts, where applicable;

e) intermediate checks on measuring equipment;

f) replicate tests or calibrations using the same or different methods;

g) retesting or recalibration of retained items;

h) correlation of results for different characteristics of an item;

i) review of reported results;

j) intralaboratory comparisons;

k) testing of blind sample(s).

7.7.2 The laboratory shall monitor its performance by comparison with results of other laboratories, where available and appropriate. This monitoring shall be planned and reviewed and shall include, but not be limited to, either or both of the following:

a) participation in proficiency testing;

NOTE ISO/IEC 17043 contains additional information on proficiency tests and proficiency testing providers. Proficiency testing providers that meet the requirements of ISO/IEC 17043 are considered to be competent.

b) participation in interlaboratory comparisons other than proficiency testing.

7.7.3 Data from monitoring activities shall be analysed, used to control and, if applicable, improve the laboratory's activities. If the results of the analysis of data from monitoring activities are found to be outside pre-defined criteria, appropriate action shall be taken to prevent incorrect results from being reported.

7.8 Reporting of results

7.8.1 General

7.8.1.1 The results shall be reviewed and authorized prior to release.

7.8.1.2 The results shall be provided accurately, clearly, unambiguously and objectively, usually in a report (e.g. a test report or a calibration certificate or report of sampling), and shall include all the information agreed with the customer and necessary for the interpretation of the results and all information required by the method used. All issued reports shall be retained as technical records.

NOTE 1 For the purposes of this document, test reports and calibration certificates are sometimes referred to as test certificates and calibration reports, respectively.

NOTE 2 Reports can be issued as hard copies or by electronic means, provided that the requirements of this document are met.

7.8.1.3 When agreed with the customer, the results may be reported in a simplified way. Any information listed in 7.8.2 to 7.8.7 that is not reported to the customer shall be readily available.

7.8.2 Common requirements for reports (test, calibration or sampling)

7.8.2.1 Each report shall include at least the following information, unless the laboratory has valid reasons for not doing so, thereby minimizing any possibility of misunderstanding or misuse:

a) a title (e.g. "Test Report", "Calibration Certificate" or "Report of Sampling");

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b) the name and address of the laboratory;

c) the location of performance of the laboratory activities, including when performed at a customer facility or at sites away from the laboratory's permanent facilities, or in associated temporary or mobile facilities;

d) unique identification that all its components are recognized as a portion of a complete report and a clear identification of the end;

e) the name and contact information of the customer;

f) identification of the method used;

g) a description, unambiguous identification, and, when necessary, the condition of the item;

h) the date of receipt of the test or calibration item(s), and the date of sampling, where this is critical to the validity and application of the results;

i) the date(s) of performance of the laboratory activity;

j) the date of issue of the report;

k) reference to the sampling plan and sampling method used by the laboratory or other bodies where these are relevant to the validity or application of the results;

l) a statement to the effect that the results relate only to the items tested, calibrated or sampled;

m) the results with, where appropriate, the units of measurement;

n) additions to, deviations, or exclusions from the method;

o) identification of the person(s) authorizing the report;

p) clear identification when results are from external providers.

NOTE Including a statement specifying that the report shall not be reproduced except in full without approval of the laboratory can provide assurance that parts of a report are not taken out of context.

7.8.2.2 The laboratory shall be responsible for all the information provided in the report, except when information is provided by the customer. Data provided by a customer shall be clearly identified. In addition, a disclaimer shall be put on the report when the information is supplied by the customer and can affect the validity of results. Where the laboratory has not been responsible for the sampling stage (e.g. the sample has been provided by the customer), it shall state in the report that the results apply to the sample as received.

7.8.3 Specific requirements for test reports

7.8.3.1 In addition to the requirements listed in 7.8.2, test reports shall, where necessary for the interpretation of the test results, include the following:

a) information on specific test conditions, such as environmental conditions;

b) where relevant, a statement of conformity with requirements or specifications (see 7.8.6);

c) where applicable, the measurement uncertainty presented in the same unit as that of the measurand or in a term relative to the measurand (e.g. percent) when:

— it is relevant to the validity or application of the test results;

— a customer's instruction so requires, or

— the measurement uncertainty affects conformity to a specification limit;

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d) where appropriate, opinions and interpretations (see 7.8.7);

e) additional information that may be required by specific methods, authorities, customers or groups of customers.

7.8.3.2 Where the laboratory is responsible for the sampling activity, test reports shall meet the requirements listed in 7.8.5 where necessary for the interpretation of test results.

7.8.4 Specific requirements for calibration certificates

7.8.4.1 In addition to the requirements listed in 7.8.2, calibration certificates shall include the following:

a) the measurement uncertainty of the measurement result presented in the same unit as that of the measurand or in a term relative to the measurand (e.g. percent);

NOTE According to ISO/IEC Guide 99, a measurement result is generally expressed as a single measured quantity value including unit of measurement and a measurement uncertainty.

b) the conditions (e.g. environmental) under which the calibrations were made that have an influence on the measurement results;

c) a statement identifying how the measurements are metrologically traceable (see Annex A);

d) the results before and after any adjustment or repair, if available;

e) where relevant, a statement of conformity with requirements or specifications (see 7.8.6);

f) where appropriate, opinions and interpretations (see 7.8.7).

7.8.4.2 Where the laboratory is responsible for the sampling activity, calibration certificates shall meet the requirements listed in 7.8.5 where necessary for the interpretation of calibration results.

7.8.4.3 A calibration certificate or calibration label shall not contain any recommendation on the calibration interval, except where this has been agreed with the customer.

7.8.5 Reporting sampling – specific requirements

Where the laboratory is responsible for the sampling activity, in addition to the requirements listed in 7.8.2, reports shall include the following, where necessary for the interpretation of results:

a) the date of sampling;

b) unique identification of the item or material sampled (including the name of the manufacturer, the model or type of designation and serial numbers, as appropriate);

c) the location of sampling, including any diagrams, sketches or photographs;

d) a reference to the sampling plan and sampling method;

e) details of any environmental conditions during sampling that affect the interpretation of the results;

f) information required to evaluate measurement uncertainty for subsequent testing or calibration.

7.8.6 Reporting statements of conformity

7.8.6.1 When a statement of conformity to a specification or standard is provided, the laboratory shall document the decision rule employed, taking into account the level of risk (such as false accept and false reject and statistical assumptions) associated with the decision rule employed, and apply the decision rule.

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NOTE Where the decision rule is prescribed by the customer, regulations or normative documents, a further consideration of the level of risk is not necessary.

7.8.6.2 The laboratory shall report on the statement of conformity, such that the statement clearly identifies:

a) to which results the statement of conformity applies;

b) which specifications, standards or parts thereof are met or not met;

c) the decision rule applied (unless it is inherent in the requested specification or standard).

NOTE For further information, see ISO/IEC Guide 98-4.

7.8.7 Reporting opinions and interpretations

7.8.7.1 When opinions and interpretations are expressed, the laboratory shall ensure that only personnel authorized for the expression of opinions and interpretations release the respective statement. The laboratory shall document the basis upon which the opinions and interpretations have been made.

NOTE It is important to distinguish opinions and interpretations from statements of inspections and product certifications as intended in ISO/IEC 17020 and ISO/IEC 17065, and from statements of conformity as referred to in 7.8.6.

7.8.7.2 The opinions and interpretations expressed in reports shall be based on the results obtained from the tested or calibrated item and shall be clearly identified as such.

7.8.7.3 When opinions and interpretations are directly communicated by dialogue with the customer, a record of the dialogue shall be retained.

7.8.8 Amendments to reports

7.8.8.1 When an issued report needs to be changed, amended or re-issued, any change of information shall be clearly identified and, where appropriate, the reason for the change included in the report.

7.8.8.2 Amendments to a report after issue shall be made only in the form of a further document, or data transfer, which includes the statement "Amendment to Report, serial number... [or as otherwise identified]", or an equivalent form of wording.

Such amendments shall meet all the requirements of this document.

7.8.8.3 When it is necessary to issue a complete new report, this shall be uniquely identified and shall contain a reference to the original that it replaces.

7.9 Complaints

7.9.1 The laboratory shall have a documented process to receive, evaluate and make decisions on complaints.

7.9.2 A description of the handling process for complaints shall be available to any interested party on request. Upon receipt of a complaint, the laboratory shall confirm whether the complaint relates to laboratory activities that it is responsible for and, if so, shall deal with it. The laboratory shall be responsible for all decisions at all levels of the handling process for complaints.

7.9.3 The process for handling complaints shall include at least the following elements and methods:

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a) description of the process for receiving, validating, investigating the complaint, and deciding what actions are to be taken in response to it;

b) tracking and recording complaints, including actions undertaken to resolve them;

c) ensuring that any appropriate action is taken.

7.9.4 The laboratory receiving the complaint shall be responsible for gathering and verifying all necessary information to validate the complaint.

7.9.5 Whenever possible, the laboratory shall acknowledge receipt of the complaint, and provide the complainant with progress reports and the outcome.

7.9.6 The outcomes to be communicated to the complainant shall be made by, or reviewed and approved by, individual(s) not involved in the original laboratory activities in question.

NOTE This can be performed by external personnel.

7.9.7 Whenever possible, the laboratory shall give formal notice of the end of the complaint handling to the complainant.

7.10 Nonconforming work

7.10.1 The laboratory shall have a procedure that shall be implemented when any aspect of its laboratory activities or results of this work do not conform to its own procedures or the agreed requirements of the customer (e.g. equipment or environmental conditions are out of specified limits, results of monitoring fail to meet specified criteria). The procedure shall ensure that:

a) the responsibilities and authorities for the management of nonconforming work are defined;

b) actions (including halting or repeating of work and withholding of reports, as necessary) are based upon the risk levels established by the laboratory;

c) an evaluation is made of the significance of the nonconforming work, including an impact analysis on previous results;

d) a decision is taken on the acceptability of the nonconforming work;

e) where necessary, the customer is notified and work is recalled;

f) the responsibility for authorizing the resumption of work is defined.

7.10.2 The laboratory shall retain records of nonconforming work and actions as specified in 7.10.1, bullets b) to f).

7.10.3 Where the evaluation indicates that the nonconforming work could recur, or that there is doubt about the conformity of the laboratory's operations with its own management system, the laboratory shall implement corrective action.

7.11 Control of data and information management

7.11.1 The laboratory shall have access to the data and information needed to perform laboratory activities.

7.11.2 The laboratory information management system(s) used for the collection, processing, recording, reporting, storage or retrieval of data shall be validated for functionality, including the proper functioning of interfaces within the laboratory information management system(s) by the laboratory

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before introduction. Whenever there are any changes, including laboratory software configuration or modifications to commercial off-the-shelf software, they shall be authorized, documented and validated before implementation.

NOTE 1 In this document "laboratory information management system(s)" includes the management of data and information contained in both computerized and non-computerized systems. Some of the requirements can be more applicable to computerized systems than to non-computerized systems.

NOTE 2 Commercial off-the-shelf software in general use within its designed application range can be considered to be sufficiently validated.

7.11.3 The laboratory information management system(s) shall:

a) be protected from unauthorized access;

b) be safeguarded against tampering and loss;

c) be operated in an environment that complies with provider or laboratory specifications or, in the case of non-computerized systems, provides conditions which safeguard the accuracy of manual recording and transcription;

d) be maintained in a manner that ensures the integrity of the data and information;

e) include recording system failures and the appropriate immediate and corrective actions.

7.11.4 When a laboratory information management system is managed and maintained off-site or through an external provider, the laboratory shall ensure that the provider or operator of the system complies with all applicable requirements of this document.

7.11.5 The laboratory shall ensure that instructions, manuals and reference data relevant to the laboratory information management system(s) are made readily available to personnel.

7.11.6 Calculations and data transfers shall be checked in an appropriate and systematic manner.

8 Management system requirements

8.1 Options

8.1.1 General

The laboratory shall establish, document, implement and maintain a management system that is capable of supporting and demonstrating the consistent achievement of the requirements of this document and assuring the quality of the laboratory results. In addition to meeting the requirements of Clauses 4 to 7, the laboratory shall implement a management system in accordance with Option A or Option B.

NOTE See Annex B for more information.

8.1.2 Option A

As a minimum, the management system of the laboratory shall address the following:

— management system documentation (see 8.2);

— control of management system documents (see 8.3);

— control of records (see 8.4);

— actions to address risks and opportunities (see 8.5);

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— improvement (see 8.6);

— corrective actions (see 8.7);

— internal audits (see 8.8);

— management reviews (see 8.9).

8.1.3 Option B

A laboratory that has established and maintains a management system, in accordance with the requirements of ISO 9001, and that is capable of supporting and demonstrating the consistent fulfilment of the requirements of Clauses 4 to 7, also fulfils at least the intent of the management system requirements specified in 8.2 to 8.9.

8.2 Management system documentation (Option A)

8.2.1 Laboratory management shall establish, document, and maintain policies and objectives for the fulfilment of the purposes of this document and shall ensure that the policies and objectives are acknowledged and implemented at all levels of the laboratory organization.

8.2.2 The policies and objectives shall address the competence, impartiality and consistent operation of the laboratory.

8.2.3 Laboratory management shall provide evidence of commitment to the development and implementation of the management system and to continually improving its effectiveness.

8.2.4 All documentation, processes, systems, records, related to the fulfilment of the requirements of this document shall be included in, referenced from, or linked to the management system.

8.2.5 All personnel involved in laboratory activities shall have access to the parts of the management system documentation and related information that are applicable to their responsibilities.

8.3 Control of management system documents (Option A)

8.3.1 The laboratory shall control the documents (internal and external) that relate to the fulfilment of this document.

NOTE In this context, "documents" can be policy statements, procedures, specifications, manufacturer's instructions, calibration tables, charts, text books, posters, notices, memoranda, drawings, plans, etc. These can be on various media, such as hard copy or digital.

8.3.2 The laboratory shall ensure that:

a) documents are approved for adequacy prior to issue by authorized personnel;

b) documents are periodically reviewed, and updated as necessary;

c) changes and the current revision status of documents are identified;

d) relevant versions of applicable documents are available at points of use and, where necessary, their distribution is controlled;

e) documents are uniquely identified;

f) the unintended use of obsolete documents is prevented, and suitable identification is applied to them if they are retained for any purpose.

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8.4 Control of records (Option A)

8.4.1 The laboratory shall establish and retain legible records to demonstrate fulfilment of the requirements in this document.

8.4.2 The laboratory shall implement the controls needed for the identification, storage, protection, back-up, archive, retrieval, retention time, and disposal of its records. The laboratory shall retain records for a period consistent with its contractual obligations. Access to these records shall be consistent with the confidentiality commitments, and records shall be readily available.

NOTE Additional requirements regarding technical records are given in 7.5.

8.5 Actions to address risks and opportunities (Option A)

8.5.1 The laboratory shall consider the risks and opportunities associated with the laboratory activities in order to:

a) give assurance that the management system achieves its intended results;

b) enhance opportunities to achieve the purpose and objectives of the laboratory;

c) prevent, or reduce, undesired impacts and potential failures in the laboratory activities;

d) achieve improvement.

8.5.2 The laboratory shall plan:

a) actions to address these risks and opportunities;

b) how to:

— integrate and implement these actions into its management system;

— evaluate the effectiveness of these actions.

NOTE Although this document specifies that the laboratory plans actions to address risks, there is no requirement for formal methods for risk management or a documented risk management process. Laboratories can decide whether or not to develop a more extensive risk management methodology than is required by this document, e.g. through the application of other guidance or standards.

8.5.3 Actions taken to address risks and opportunities shall be proportional to the potential impact on the validity of laboratory results.

NOTE 1 Options to address risks can include identifying and avoiding threats, taking risk in order to pursue an opportunity, eliminating the risk source, changing the likelihood or consequences, sharing the risk, or retaining risk by informed decision.

NOTE 2 Opportunities can lead to expanding the scope of the laboratory activities, addressing new customers, using new technology and other possibilities to address customer needs.

8.6 Improvement (Option A)

8.6.1 The laboratory shall identify and select opportunities for improvement and implement any necessary actions.

NOTE Opportunities for improvement can be identified through the review of the operational procedures, the use of the policies, overall objectives, audit results, corrective actions, management review, suggestions from personnel, risk assessment, analysis of data, and proficiency testing results.

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8.6.2 The laboratory shall seek feedback, both positive and negative, from its customers. The feedback shall be analysed and used to improve the management system, laboratory activities and customer service.

NOTE Examples of the types of feedback include customer satisfaction surveys, communication records and review of reports with customers.

8.7 Corrective actions (Option A)

8.7.1 When a nonconformity occurs, the laboratory shall:

a) react to the nonconformity and, as applicable:

- take action to control and correct it;
- address the consequences;

b) evaluate the need for action to eliminate the cause(s) of the nonconformity, in order that it does not recur or occur elsewhere, by:

- reviewing and analysing the nonconformity;
- determining the causes of the nonconformity;
- determining if similar nonconformities exist, or could potentially occur;

c) implement any action needed;

d) review the effectiveness of any corrective action taken;

e) update risks and opportunities determined during planning, if necessary;

f) make changes to the management system, if necessary.

8.7.2 Corrective actions shall be appropriate to the effects of the nonconformities encountered.

8.7.3 The laboratory shall retain records as evidence of:

a) the nature of the nonconformities, cause(s) and any subsequent actions taken;

b) the results of any corrective action.

8.8 Internal audits (Option A)

8.8.1 The laboratory shall conduct internal audits at planned intervals to provide information on whether the management system:

a) conforms to:

- the laboratory's own requirements for its management system, including the laboratory activities;
- the requirements of this document;

b) is effectively implemented and maintained.

8.8.2 The laboratory shall:

a) plan, establish, implement and maintain an audit programme including the frequency, methods, responsibilities, planning requirements and reporting, which shall take into consideration the

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importance of the laboratory activities concerned, changes affecting the laboratory, and the results of previous audits;

b) define the audit criteria and scope for each audit;

c) ensure that the results of the audits are reported to relevant management;

d) implement appropriate correction and corrective actions without undue delay;

e) retain records as evidence of the implementation of the audit programme and the audit results.

NOTE ISO 19011 provides guidance for internal audits.

8.9 Management reviews (Option A)

8.9.1 The laboratory management shall review its management system at planned intervals, in order to ensure its continuing suitability, adequacy and effectiveness, including the stated policies and objectives related to the fulfilment of this document.

8.9.2 The inputs to management review shall be recorded and shall include information related to the following:

a) changes in internal and external issues that are relevant to the laboratory;

b) fulfilment of objectives;

c) suitability of policies and procedures;

d) status of actions from previous management reviews;

e) outcome of recent internal audits;

f) corrective actions;

g) assessments by external bodies;

h) changes in the volume and type of the work or in the range of laboratory activities;

i) customer and personnel feedback;

j) complaints;

k) effectiveness of any implemented improvements;

l) adequacy of resources;

m) results of risk identification;

n) outcomes of the assurance of the validity of results; and

o) other relevant factors, such as monitoring activities and training.

8.9.3 The outputs from the management review shall record all decisions and actions related to at least:

a) the effectiveness of the management system and its processes;

b) improvement of the laboratory activities related to the fulfilment of the requirements of this document;

c) provision of required resources;

d) any need for change.

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Annex A
(informative)

Metrological traceability

A.1 General

This annex provides additional information on metrological traceability, which is an important concept to ensure comparability of measurement results both nationally and internationally.

A.2 Establishing metrological traceability

A.2.1 Metrological traceability is established by considering, and then ensuring, the following:

a) the specification of the measurand (quantity to be measured);

b) a documented unbroken chain of calibrations going back to stated and appropriate references (appropriate references include national or international standards, and intrinsic standards);

c) that measurement uncertainty for each step in the traceability chain is evaluated according to agreed methods;

d) that each step of the chain is performed in accordance with appropriate methods, with the measurement results and with associated, recorded measurement uncertainties;

e) that the laboratories performing one or more steps in the chain supply evidence for their technical competence.

A.2.2 The systematic measurement error (sometimes called "bias") of the calibrated equipment is taken into account to disseminate metrological traceability to measurement results in the laboratory. There are several mechanisms available to take into account the systematic measurement errors in the dissemination of measurement metrological traceability.

A.2.3 Measurement standards that have reported information from a competent laboratory that includes only a statement of conformity to a specification (omitting the measurement results and associated uncertainties) are sometimes used to disseminate metrological traceability. This approach, in which the specification limits are imported as the source of uncertainty, is dependent upon:

— the use of an appropriate decision rule to establish conformity;

— the specification limits subsequently being treated in a technically appropriate way in the uncertainty budget.

The technical basis for this approach is that the declared conformance to a specification defines a range of measurement values, within which the true value is expected to lie, at a specified level of confidence, which considers both any bias from the true value, as well as the measurement uncertainty.

EXAMPLE The use of OIML R 111 class weights to calibrate a balance.

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A.3 Demonstrating metrological traceability

A.3.1 Laboratories are responsible for establishing metrological traceability in accordance with this document. Calibration results from laboratories conforming to this document provide metrological traceability. Certified values of certified reference materials from reference material producers conforming to ISO 17034 provide metrological traceability. There are various ways to demonstrate conformity with this document: third party recognition (such as an accreditation body), external assessment by customers or self-assessment. Internationally accepted paths include, but are not limited to, the following.

a) Calibration and measurement capabilities provided by national metrology institutes and designated institutes that have been subject to suitable peer-review processes. Such peer-review is conducted under the CIPM MRA (International Committee for Weights and Measures Mutual Recognition Arrangement). Services covered by the CIPM MRA can be viewed in Appendix C of the BIPM KCDB (International Bureau of Weights and Measures Key Comparison Database) which details the range and measurement uncertainty for each listed service.

b) Calibration and measurement capabilities that have been accredited by an accreditation body subject to the ILAC (International Laboratory Accreditation Cooperation) Arrangement or to Regional Arrangements recognized by ILAC have demonstrated metrological traceability. Scopes of accredited laboratories are publicly available from their respective accreditation bodies.

A.3.2 The Joint BIPM, OIML (International Organization of Legal Metrology), ILAC and ISO Declaration on Metrological Traceability provides specific guidance when there is a need to demonstrate international acceptability of the metrological traceability chain.

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Annex B
(informative)

Management system options

B.1 Growth in the use of management systems generally has increased the need to ensure that laboratories can operate a management system that is seen as conforming to ISO 9001, as well as to this document. As a result, this document provides two options for the requirements related to the implementation of a management system.

B.2 Option A (see 8.1.2) lists the minimum requirements for implementation of a management system in a laboratory. Care has been taken to incorporate all those requirements of ISO 9001 that are relevant to the scope of laboratory activities that are covered by the management system. Laboratories that comply with Clauses 4 to 7 and implement Option A of Clause 8 will therefore also operate generally in accordance with the principles of ISO 9001.

B.3 Option B (see 8.1.3) allows laboratories to establish and maintain a management system in accordance with the requirements of ISO 9001, in a manner that supports and demonstrates the consistent fulfilment of Clauses 4 to 7. Laboratories that implement Option B of Clause 8 will therefore also operate in accordance with ISO 9001. Conformity of the management system within which the laboratory operates to the requirements of ISO 9001 does not, in itself, demonstrate the competence of the laboratory to produce technically valid data and results. This is accomplished through compliance with Clauses 4 to 7.

B.4 Both options are intended to achieve the same result in the performance of the management system and compliance with Clauses 4 to 7.

NOTE Documents, data and records are components of documented information as used in ISO 9001 and other management system standards. Control of documents is covered in 8.3. The control of records is covered in 8.4 and 7.5. The control of data related to the laboratory activities is covered in 7.11.

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Figure B.1 illustrates an example of a possible schematic representation of the operational processes of a laboratory, as described in Clause 7.

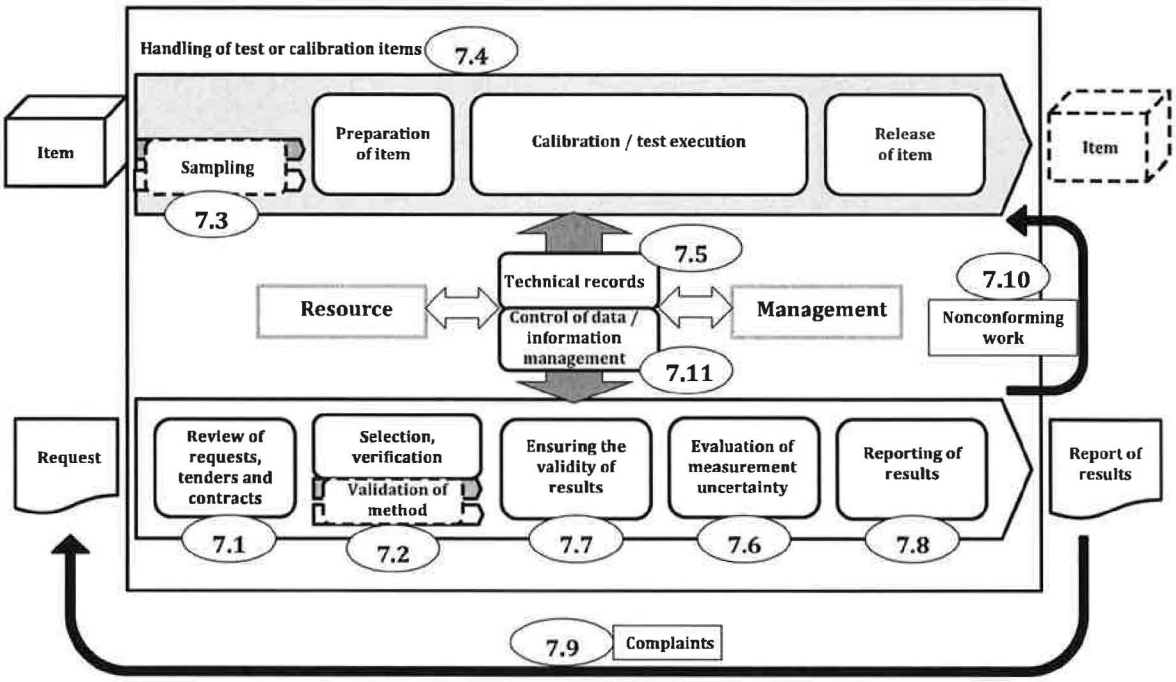

Figure B.1 — Possible schematic representation of the operational processes of a laboratory

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Forensic and Scientific Services CA-99
HSSA | Health Services Support Agency

Initial Request

Stage 1

		Proposal #:	163
Proposed by :	Kylie Rika	**Date:**	01/04/2015
		Due Date:	08/04/2015
Title of Proposal:	Assessment of results obtained from auto-microcon samples		
Project type	☐ Administration ☐ IT/AUSLAB ☐ Laboratory ☑ Data mining/analysis ☐ External Project ☐ Other_____		

Brief Outline of Proposed Change

Currently (and since 19/12/12), any priority 1 or 2 PP21 casework samples that produce a quant value of between 0.00214 ng/uL and 0.0088 ng/uL are sent to microcon as the first step.

It is proposed that an assessment be done on results obtained from these samples to weigh up risk/benefit of implementing "no further action at this time" (or something similar) on samples displaying a quant value between 0.00214 ng/uL and 0.0088 ng/uL.

It has been observed anecdotally that samples which have been sent to microcon as the first step (quant between 0.00214 ng/uL and 0.0088 ng/uL) more often than not, yield a DNA profile result which is unsuitable for interpretation or comparison. In addition, the timeframe involved (from quant to result release) is lengthy, especially if the sample has required an additional amplification to confirm profile result. The current focus for FSS DNA Analysis and QPS is to reduce our turn around time (TAT).

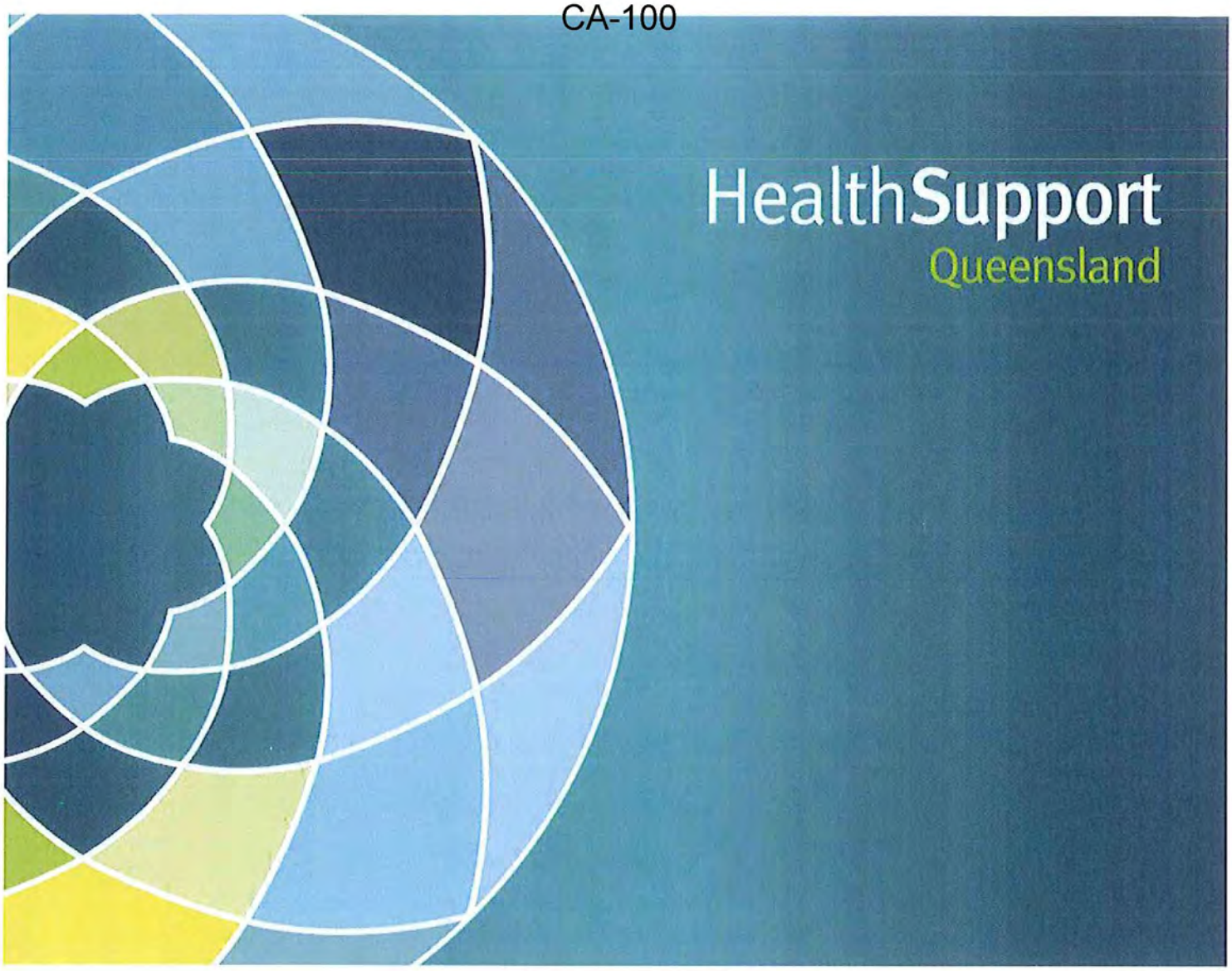
Benefits of the new process could include: Reduction in TAT for samples that have been sent to microcon as the first step, Cost savings in consumables and human resources, Reduction in TAT for all samples (due to more staff processing samples with usable results), Possible reduction in submission of a certain sample type by QPS.

Line Manager :	Justin Howes	**Recommendation:**
Signature:	[redacted]	☐ Proceed to minor change ☑ Proceed to full project plan ☐ Place on hold or abandon Reason:_____

Proposal restarted by:		**Date:**	
Approved By:		**Date:**	
Signature:		**Reason:**	

Please send to Quality Team [redacted] after completion

CA-100



Assessment of results obtained from 'automatic-microcon' samples

Josie Entwistle, Allison Lloyd, Kylie Rika, Thomas Nurthen, Cathie Allen

August 2015

Great state. Great opportunity.

Queensland Government

Assessment of results obtained from 'automatic-microcon' samples

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Forensic DNA Analysis, Department of Health, [redacted]

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Version	Date	Changed by	Description
0.1	11/11/2015	Josie Entwistle	First Draft
0.2	04/12/2015	Josie Entwistle	Second Draft

Document sign off

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Kylie Rika	Senior Scientist Reporting		17/12/2015.

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1. Abstract

Since December 2012, casework samples with the parameters of PowerPlex priority 1 or 2, and have yielded a quantification value between 0.00214 ng/µL and 0.0088 ng/µL have been automatically processed with a Microcon Centrifugal Filter Device concentration step.

An assessment of results from these samples has been conducted.

Relevant data was extracted from AUSLAB, sorted, reconciled and interrogated. Broad categories of informative results and non-informative results were used based on result types that the Queensland Police Service consider informative (including single source and interpretable 2 and 3 person mixtures) and non-informative (complex profiles, no DNA detected, no DNA profile obtained).

From 1001 assessable samples, 184 yielded an informative result, with 79 samples being uploaded to NCIDD.

2. Introduction

Currently (and since 19/12/12), any priority 1 or 2 PowerPlex® 21 (PP21) casework samples that produce DNA extracts with a quantification value of between 0.00214 ng/µL and 0.0088 ng/µL are sent automatically for a concentration step using a Microcon® Centrifugal Filter Device. This concentration step was introduced as part of PP21 implementation in an effort to minimise the stochastic effects observed at these lower quantification values and improve the overall quality of the profile.

It has been observed anecdotally within the laboratory, that samples which have been sent automatically for concentration (quantification between 0.00214 ng/µL and 0.0088 ng/µL) often yield a DNA profile result which is unsuitable for interpretation or comparison (deemed 'non-informative). In addition, the timeframe (from quantification to result release) can be seen to be lengthy, in comparison to other samples types, particularly if the sample has required further amplification/s to enhance or confirm the profile result.

As part of the laboratory's commitment to ongoing quality assessment, and improvement of processes and results released, an assessment of samples processed by automatic-microcon has been conducted. This assessment includes observations of the number of samples processed by automatic-microcon that are deemed 'informative' by QPS and the number of samples that have been nominated for uploading to NCIDD. This assessment also outlines possible process alternatives, including risks and benefits, and taking into consideration the opportunity to improve turn around times, laboratory expenditure, the ability to incorporate the recently introduced Number of Contributors Guidelines to a broader range of suitable samples, and improvement of the quality of profiles and results issued.

3. Materials and Methods

3.1 Materials

The following resources have been required for this data mining project:

Staff

Computers (including applications such as Excel and AUSLAB)

PP21 case work samples that have already been processed within the laboratory via the automatic microcon concentration step

3.2 Methods

Extended enquiries functionality in AUSLAB was used to extract data pertaining to all samples with MCONC1 test codes with received dates from 2012 – March 2015 that have a 'parent' EXH (i.e. not sub-samples). This data dump included the following fields:

Sample ID

QP number

Result type (based on EXH lines released)

NCIDD upload

Original quantification value

Additional quantification values

Additional test codes

Sample type

Case type

A worksheet in Excel was created, containing the data from the data dump. This data was further sorted into columns and refined/filtered to produce only concentrated samples within the laboratory's 'automatic-microcon' quantification range.

Samples with 'no further work required' requests were removed from the data set as these samples couldn't be assessed and would otherwise skew the data.

The data was then interrogated in an attempt to observe any trends that may have suggested proposing changes to current laboratory processing rules and workflow.

4. Results and Discussion

4.1 Results

A data set of 1136 samples that had been concentrated via an automated microcon process was obtained. This was reduced to a data pool of 1001 assessable samples (designated as the assessable data pool), once samples with 'no further work required' requests were excluded.

From this data pool, 817 samples yielded a result that was considered non-informative (complex unsuitable, no DNA profile, no DNA detected). This represents ~82% of the assessable data pool.

184 samples yielded a result that was considered informative (single source, 2 person mixed DNA profile, 3 person mixed DNA profile). This represents ~18% of the assessable data pool.

Of the informative results, 127 samples yielded 2 or 3 person mixed DNA profiles and 57 samples yielded single source DNA profiles. Therefore the mixed DNA profile result samples represented ~12% of the assessable data pool, and ~69% of the informative result pool. The single source DNA profile result samples represented ~5% of the assessable data pool, and ~30% of the informative result pool.

79 samples from the assessable data pool obtained profiles that were uploaded to NCIDD. This represents ~8% of the assessable data pool and ~42% of the informative result pool. Some of the profiles uploaded to NCIDD were from sole samples within a case, and some of these NCIDD uploads resulted in 'cold links'.

	Total from assessable pool	Percentage of total	Percentage of informative
Total assessable results	1001	100%	N/A
Informative	184	18%	N/A
Non-informative	817	82%	N/A
NCIDD	79	8%	42%
Single source DNA profiles	57	5%	30%
Informative mixed DNA profiles	127	12%	69%

Table 1 Automatic-microcon category data

Observations can be made from the assessment of the categories of samples against quantification values.

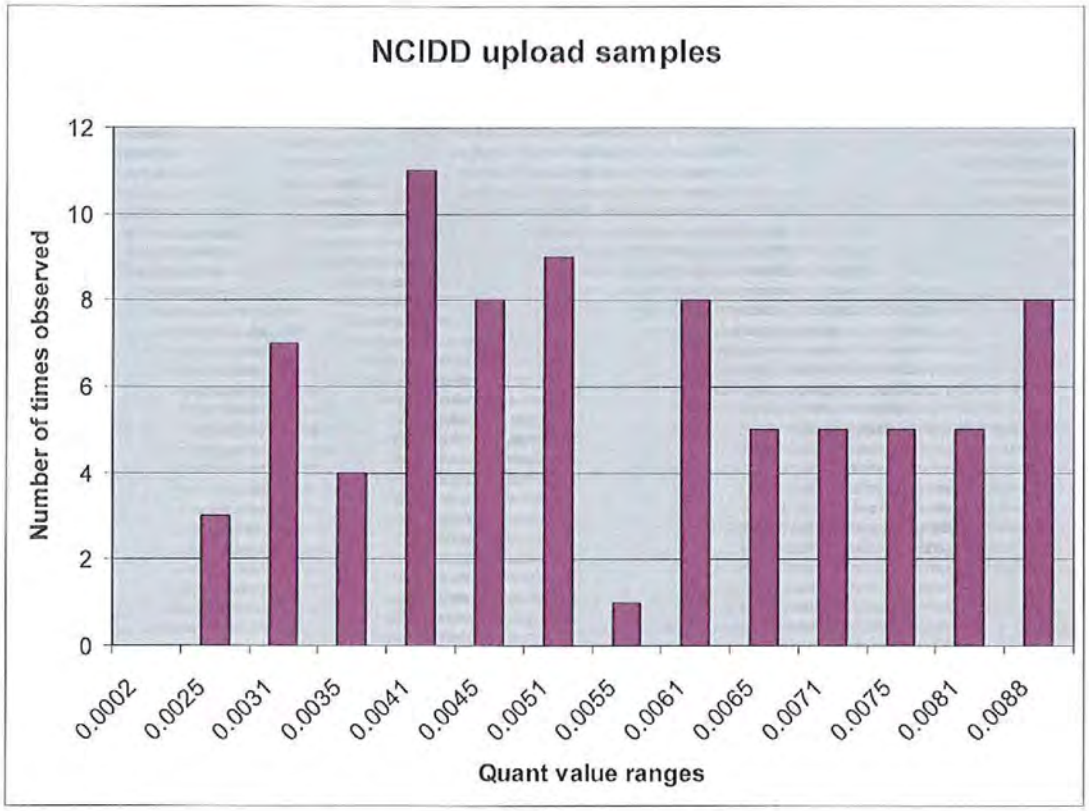

Figure 1 NCIDD upload samples

Automatic-microcon samples uploaded to NCIDD can be observed (see Figure 1) at each of the quant value ranges, with the exception of the range between 0.002 ng/µL and 0.0025 ng/µL and the single NCIDD upload at the quant value range of 0.0055 ng/µL to 0.0061 ng/µL.

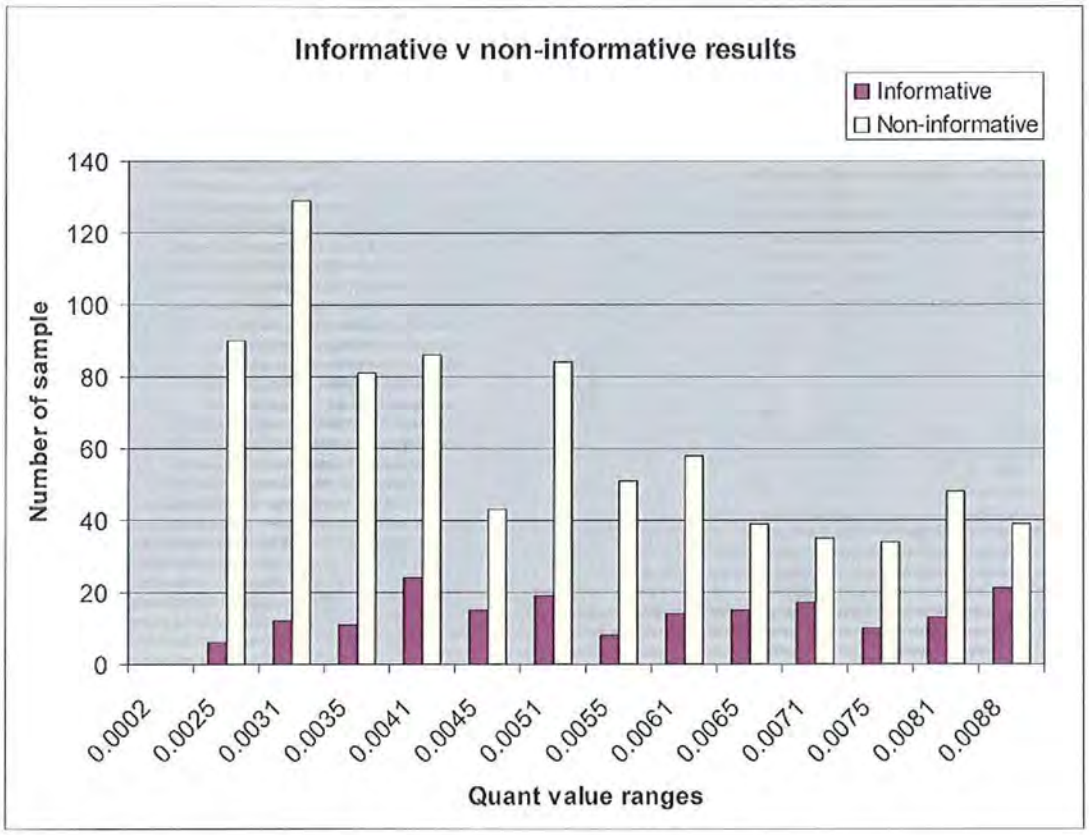

Figure 2 Informative v non-informative results

The number of non-informative results can be observed (see Figure 2) to decrease beyond the quantification value of 0.0035 ng/µL and become closer in occurrence with the numbers observed for informative results.

The number of informative results can be observed to be less than those of non-informative results for the majority of the quantification value ranges and remain fairly consistent across the quantification value ranges.

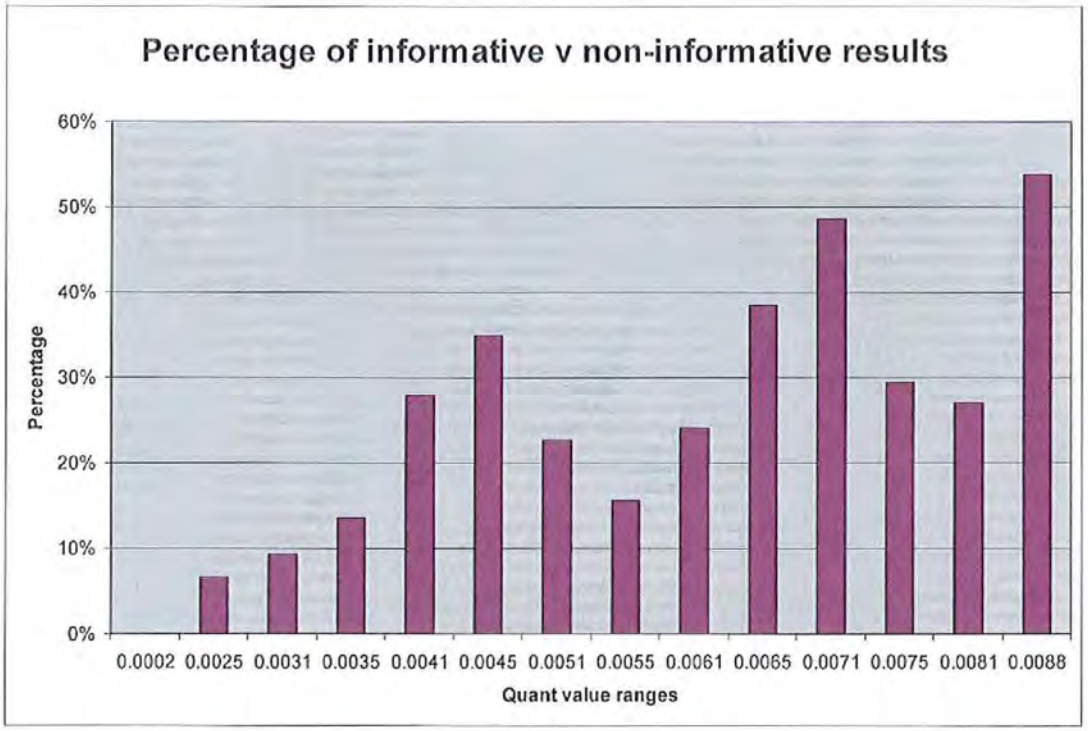

Figure 3 Percentage of informative v non-informative results

The percentage of informative v non-informative results can be observed (see Figure 3) to increase on the whole, with some fluctuation across the quantification value ranges. The lowest percentage of informative v non-informative occurs at the lowest quantification value range and the highest percentage occurs at the highest quantification value range.

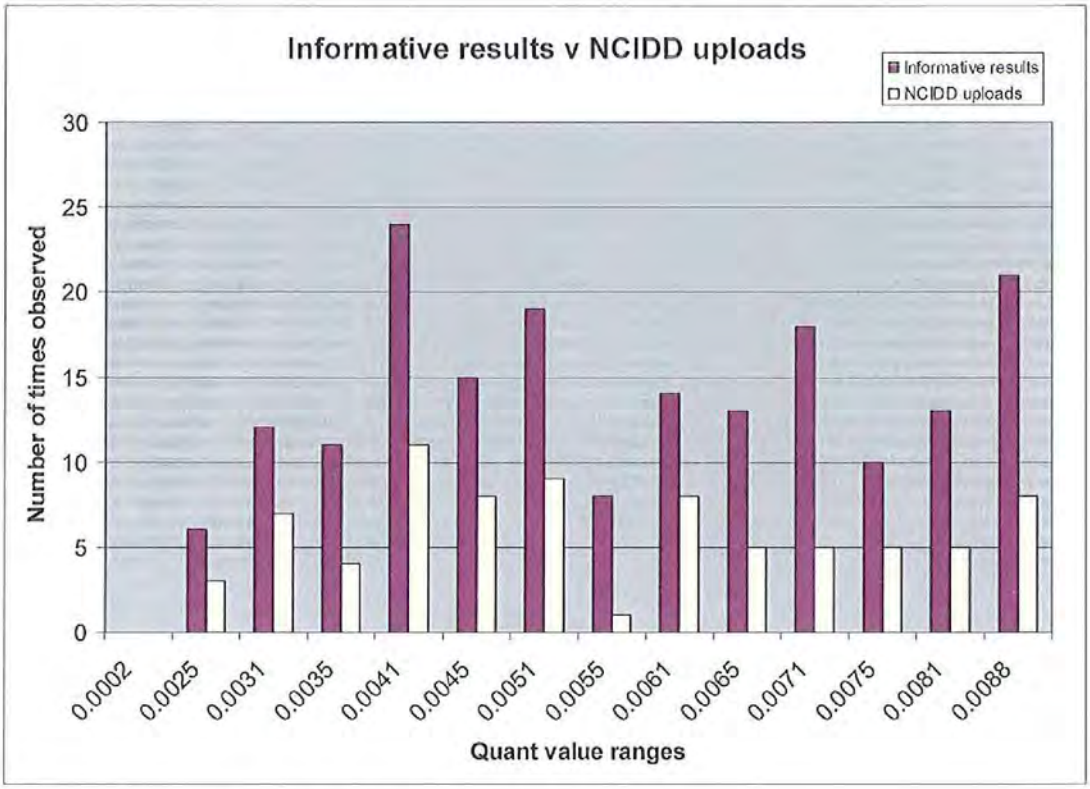

Figure 4 Informative results v NCIDD uploads

The number of samples uploaded to NCIDD can be observed (see Figure 4) to be generally consistent with the informative results and approximately half for each quantification value range. The number of samples uploaded to NCIDD is observed to be highest at the quantification value range of 0.0041 and lowest at the quantification value range of 0.0055 ng/µL.

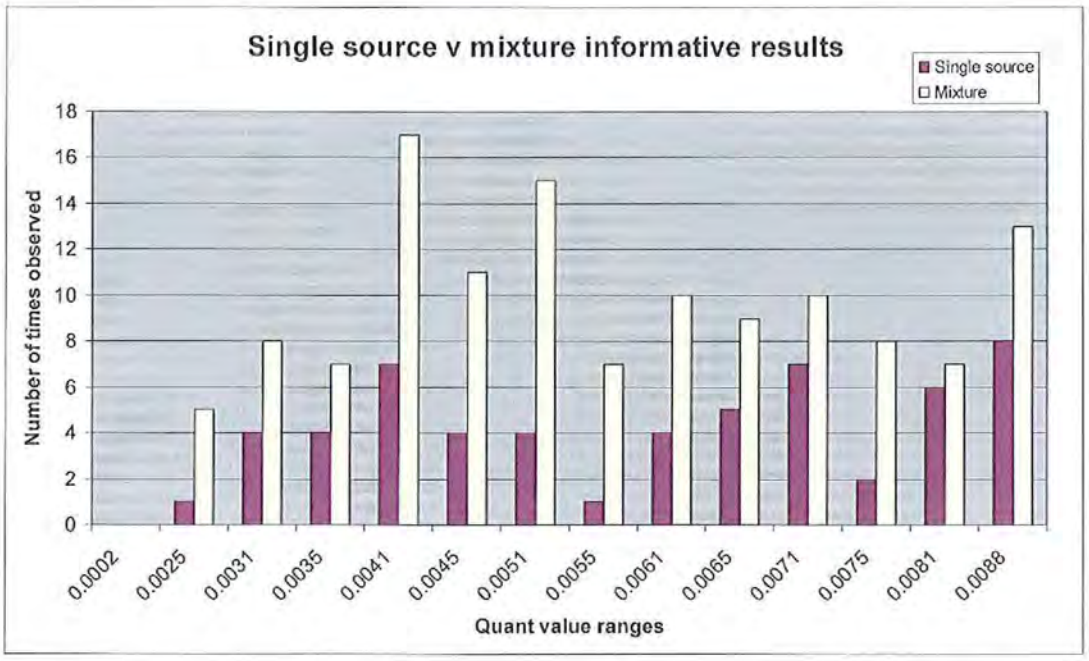

Figure 5 Single source v mixture informative results

The number of mixed DNA profile informative results can be observed (see Figure 5) to be higher than that of single source results. The highest number of informative mixture results can be observed at the quantification value range of 0.0041 ng/µL, and it appears that the bulk of the informative mixed DNA results occur beyond this quantification value range.

The single source informative results can be observed at each of the quantification value ranges and appears to fluctuate across the quantification value ranges.

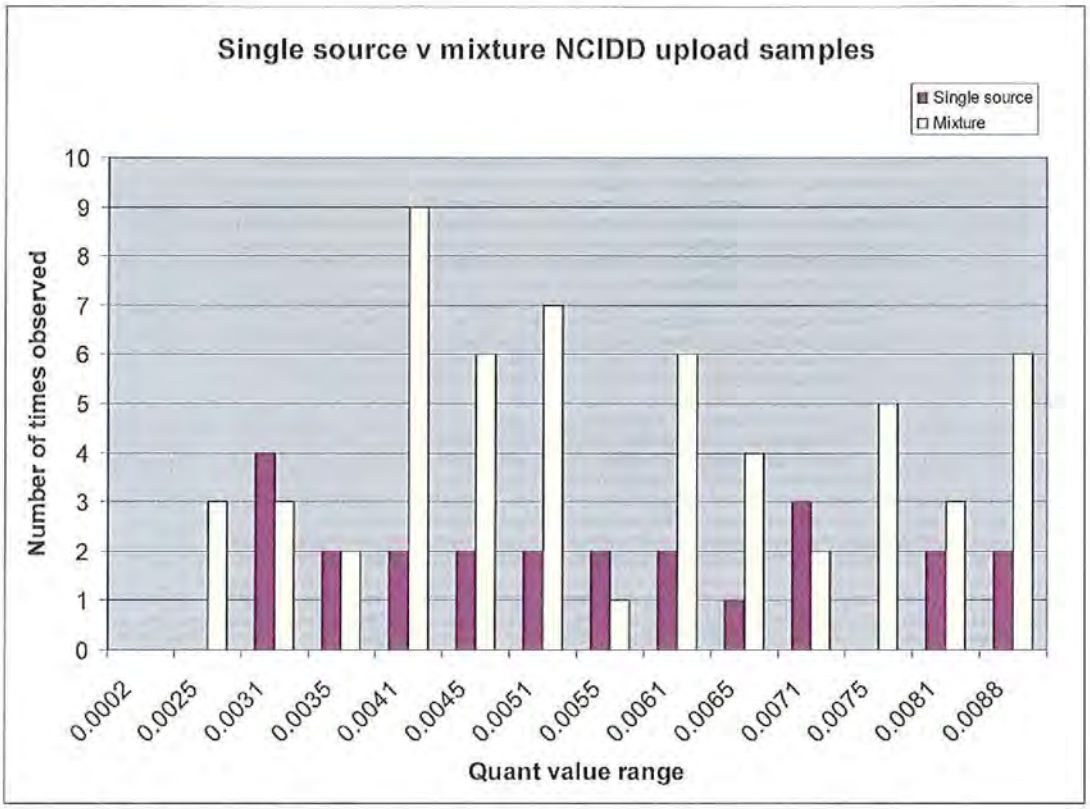

Figure 6 Single source v mixture NCIDD upload samples

The number of mixed DNA profiles uploaded to NCIDD can be observed (see Figure 6) to be highest at the quantification value range of 0.0041 ng/µL and lowest at the quantification value range of 0.0055. It appears that the bulk of uploads from mixed DNA profiles occurs beyond the quantification value range of 0.0041 ng/µL.

The number of NCIDD uploads from single source profiles can be observed to be less than that from mixed DNA profiles and with the exception of no uploads within the quantification value ranges of 0.0025 ng/µL and 0.0081 ng/µL, appears to be fairly consistent within the quantification value ranges.

4.2 Discussion

This data assessment has not been an in-depth study and more detailed statistical analyses was outside the scope, however the data obtained has shown that informative results were obtained across the quantification value ranges within the automatic-microcon process parameters as well as samples uploaded to NCIDD, even at the lowest quantification value ranges.

No real trend was observed for the number of informative results obtained, other than there being informative results and NCIDD uploads across the automatic-microcon quantification range. It appears that across the quantification value ranges, the number of samples loaded for NCIDD was approximately half of the number of informative results obtained and this was generally consistent across the quantification value ranges.

A decline in non-informative results was observed as the quantification value increased. Given the observations in the PP21 validation of greater stochastic effects at lower quantification ranges, this observation is not unexpected.

It was observed that interpretable mixed DNA profiles were obtained and were greater in number than single source results, indicating that not all interpretable results from the automatic-microcon process are single source and that not all mixed DNA profile obtained are non-informative. Additionally, it can be seen that NCIDD uploads were obtained from both single source and mixed DNA results and a higher number of the NCIDD uploads were from mixed DNA profiles than from single source. These observations were consistent across the quantification value ranges.

An important point to note is that there are numerous other variables involved in whether a sample is nominated to upload to NCIDD and therefore, it is difficult to capture the true number of samples suitable for NCIDD uploading from the data pool.

Additionally, there may be a higher significance placed on some of these samples nominated for NCIDD upload, such as a sample being the only sample within the case, the priority and/or case type, and the potential (and actuality) for "cold links" arising from these uploads.

We don't have data from a similar assessment of informative vs non-informative results from samples processed outside the automatic-microcon quantification range to make a comparison. It is possible that what is observed here is similar for all quantification values and therefore these results shouldn't be overstated.

New instruments and processes are soon to be introduced into the laboratory and possibly in the future (Quant Trio, QIAsymphony and Yfiler, for example). These instruments and process may introduce variations to the data observed here and may indicate changes to the processes, irrespective of any possible changes made at this point.

5. Conclusions and Recommendations

This assessment has indicated that there has been value in the automatic-microcon process, with informative results and NCIDD uploads obtained across the quantification value range, including the lowest value ranges, albeit with a high number of non-informative results, which declined as the quantification value increased.

A higher number of informative mixed results were obtained, which also represented the bulk of samples nominated for NCIDD.

NCIDD uploads were obtained across the quantification value ranges and were obtained from both mixed and single source samples and importantly, some of these uploads led to 'cold links' and some were from sole samples within a case.

It is possible that these observations are similar to observations that could be made for samples processed outside of the automatic-microcon process.

Automatic-mirocon process changes, along with introduction of new laboratory instruments may assist in changing the balance of informative to non-informative results.

Based on the analysis of the data, an assessment of current practices and the risks and benefits, two process change options can be considered.

5.1. Process change consideration 1

One possible change to current process could be to submit all samples within the current automatic-microcon quantification range to a half microcon instead of full. Processing as half microcon would provide additional remaining volume to allow for additional amplification runs to enable reproducibility assessments.

Samples falling within this range could be directed to this process step automatically within the Forensic Register.

These samples could then be directed (again by the FR) to a separate CM list, bearing in mind that a large number of these samples may be mixtures and possibly non-informative at first run.

Any samples that can be initially interpreted with a final result could be assessed at this stage, much in the same way that the complex and single source case management lists operate currently.

Profiles that are assessed as requiring additional runs for reproducibility assessments could join the normal CM processing stream after the reworks have been requested.

5.1.1. Benefits

This option seeks to improve upon the already implemented automatic-microcon process, which has shown some success with obtaining informative results and NCIDD uploads from samples within higher stochastic quantification value ranges.

This option presents the least risk with regards to loss of informative results and loss of NCIDD uploads (including cold links).

All samples are given an opportunity for additional processing which may improve the initial result and/or possibly give more confidence with regards to number of contributors present and allowing for interpretation of an informative result.

Additionally, this allows for the use of the newly introduced Number of Contributors Guidelines, being a more consistent approach as with other PP21 samples, as currently the automatic-microcon samples cannot be case managed in this way as there is insufficient remaining volume.

A separate work list for these sample types may result in reduced turn around times for result reporting as some profiles can be reported with final results, with others having their additional runs ordered concurrently at the time of assessment, all from a smaller work list than the general categories in current use.

No additional time awaiting results would be experienced for samples requiring additional runs as both additional runs (XAMP1 and XAMP2) could be requested at the same time as they are likely to be required at full amplification volume.

5.1.2. Risks and disadvantages

The number of samples processed within this category will not be reduced and may in fact, increase with additional runs being requested for reproducibility assessments. The possible additional run (XAMP2) would increase the cost to the laboratory in terms of consumables, staff and time spent on task, including interpretation. This may also increase the turn around time for release of results with the interpretation of an additional profile with a reproducibility calculation.

Additional runs would increase the cost to the laboratory, in terms of staff, consumables and time spent on task (as opposed to other samples).

5.2. Process change consideration 2

An alternative to the above recommendation is to hold all samples within the current automatic-microcon range of 0.002 ng/µL and 0.0088 ng/µL. This would exclude all samples within the automatic-microcon quantification range from processing and case management, with the exception of samples within agreed parameters.

Priority 1 samples and sole samples within a case would be an exception from the hold process and could proceed to a half microcon.

Additionally, there may be an option for held samples to be reactivated if the remainder of samples within the case have yielded non-informative results.

A result line similar to "low DNA" would be sent and either at the discretion of QPS or Forensic DNA Analysis, these samples could be reactivated and proceed to a half microcon with further reworks as required and join the existing case management process.

5.2.1. Benefits

This option would reduce the amount of samples requiring processing (approximately 35 samples per month) and therefore provides the most benefit with regards to turn around times and cost, in terms of consumables, staff and time spent on task.

5.2.2. Risks and disadvantages

Turn around times would increase for reactivated samples, more so than for those requiring additional runs as in Option 1 due to the lag time of reactivation once the initial results have been released and actioned.

This option represents the highest risk for loss of informative results and NCIDD uploads from samples that are not reactivated.

This option gives less of an opportunity for possible improvement of the number of informative results released and uploads to NCIDD as the number of samples being processed by half microcon and with additional runs for reproducibility calculations would be reduced.

Despite the exclusion of Priority 1 samples and sole samples within a case, there remains a risk of possible informative results and NCIDD uploads being lost, with the potential for different informative results and NCIDD uploads not being processed.

Reporting of statements may be affected if reactivation of samples is desired after statement request as there may be limited time for processing and interpretation of samples.

This option represents a higher potential CM burden for analytical staff, with an increased amount of samples requiring validation of "low DNA" results.

5.3. Process change consideration 3

No change to existing process.

5.3.1. Benefits

Samples continue to have an opportunity to have improved results from concentration.

Number of samples requiring this process would not be increased.

No additional cost to the laboratory in terms of staff, time, consumables or funds.

5.3.2. Risks and disadvantages

Number of samples requiring this process wouldn't decrease.

No change in cost to the laboratory in terms of staff, time, consumables or funds.

No opportunity to improve the results for low quant samples.

5.4 Process change consideration 4

Finalise this project at this time, using the concept of this project for an assessment of this process six months post-implementation of the Forensic Register, in conjunction with Quantifiler® Trio DNA Quantification Kit.

5.4.1. Benefits

More effective and efficient use of data with the Forensic Register, with ability to capture additional parameters provided by Quantifiler® Trio DNA Quantification Kit and the Forensic Register including interpretation and Degradation Index.

Data reflective of procedures, instruments and LIMS in use at the time of data capture.

Better opportunity to suggest process improvements conducive to the technology, workflow and LIMS in use at that time.

5.4.2. Risks and disadvantages

Number of samples requiring this process wouldn't decrease for the short-term at least.

No change in cost to the laboratory in terms of staff, time, consumables or funds in the short-term.

No opportunity to improve the results for low quant samples in the short-term.

5.5. General recommendations and considerations

It is recommended that this project be finalised at this point and a new project commence approximately six months after the introduction of the Forensic Register; in conjunction with the use of Quantifiler® Trio DNA Quantification Kit. The concept of this project would be used to guide the new project in terms of a starting point for data mining and parameters of interest.

6. Abbreviations

CM	Case management
DNA	Deoxyribonucleic Acid
NCIDD	National Criminal Investigation DNA Database
QPS	Queensland Police Service
FR	Forensic Register

7. References

1 Nurthen, T, Mathieson, M and Allen, C, *PowerPlex 21 – Amplification of Extracted DNA Validation v2.0.* Forensic DNA Analysis, Forensic & Scientific Serves, 2013

CA-101



A review of the automatic concentration of DNA extracts using Microcon® Centrifugal Filter Devices: Options for QPS consideration.

January 2018

Justin Howes and Cathie Allen

A review of the automatic concentration of DNA extracts using Microcon® Centrifugal Filter Devices: Options for QPS consideration.

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1. Abstract

All casework DNA extracts that underwent a concentration step using the Microcon® process were evaluated and categorised into whether there was meaningful information obtained or not. This evaluation primarily focussed on samples that underwent an 'auto-microcon' process in 2016.

The findings of this evaluation are presented for the Queensland Police Service to advise on whether they would prefer their Priority 2 samples to continue with the 'auto-microcon' process, or to cease this automatic step and notify the laboratory if particular samples are requested to be reworked.

These options relate to Priority 2 (Major Crime) samples only, as the process developed in 2012 for Priority 3 (Volume Crime) samples will be reinstated with the operationally-required move to process these samples using PowerPlex® 21 system (PP21).

2. Definitions

DNA Profile Intelligence: DNA profile information available for interpretation by Forensic DNA practitioners that is able to be provided to clients.

Fail: In this report, this is DNA profile information that was not suitable for comparing to reference DNA profiles and other casework samples. This word was used to filter the data into two possible outcomes (fail/success).

NCIDD: National Criminal Investigation DNA Database.

QPS: Queensland Police Service.

Success: In this report, this is DNA profile information that was obtained that was suitable for comparing to reference DNA profiles and other casework samples. This word was used to filter the data into two possible outcomes (fail/success).

3. Introduction

Microcon® Centrifugal Filter Devices desalt and concentrate macromolecular solutions such as DNA-containing solutions. They employ Amicon's low binding, anisotropic, hydrophilic regenerated cellulose membrane [1].

The use of Microcon® filters to concentrate extract has been a standard post-extraction process within Forensic DNA Analysis to reduce the volume of

extract from approximately 100uL to ≤35µL for amplification with PowerPlex® 21 system.

Since the implementation of PP21 amplification kit within Forensic DNA Analysis for casework samples in December 2012, extracts with low Quantification values were recommended to be concentrated. Templates of <0.132ng (Quantification <0.0088ng/uL) were found to exhibit marked stochastic effects after amplification [2]. Consequently, a workflow that directed extracts automatically to a concentration step based on Quantification value was implemented ('auto-microcon' process) for Priority 2 samples.

A workflow for Priority 3 samples remained within active Standard Operating Procedures to have the DNA extracts not amplified, nor automatically concentrated with Microcon® filters, but to be held after Quantification and QPS informed that low levels of DNA were obtained that were insufficient for further processing at that stage [3][4].

Anecdotally, the suitability to provide QPS with DNA profile Intelligence from extracts that have been concentrated has been noted to be limited, and added to scientist's time and availability to direct resources to samples with more DNA detected.

4. Data interrogation

The 'auto-microcon' data was interrogated by assessing the DNA profile outcome results reported as Exhibit Report lines as a function of the Quantification value.

The Exhibit lines were interrogated and grouped into two interpretation outcomes as follows:

1. 'Fail': DNA profile interpretation outcomes of 'Complex unsuitable for interpretation', 'No DNA profile', 'Partial unsuitable for interpretation', 'No DNA Detected';

2. 'Success': All other DNA profile outcomes including single source DNA profiles matching assumed known contributors or different reference DNA profiles, mixtures that were suitable for comparison to reference DNA profiles, DNA profiles that were suitable for loading to NCIDD.

NB. These descriptions were used to filter the data. A 'fail' does not mean there was a Quality failure in the process; a 'success' does not necessarily mean a DNA match.

5. Assessment of 'auto-microcon' results

Intent
Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 through the 'auto-microcon' workflow.

Data Analysis
The samples applicable to this experiment had Quantification values in the range 0.001ng/μL to 0.0088ng/μL, and a total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value. A percentage of samples that fell into these categories was determined.

The 'auto-microcon' data could be expressed as a function of Quantification value.

The percentage of samples that had an 'auto-microcon' process and led to an NCIDD upload was obtained. This data could be filtered further into the outcome from the NCIDD load, at the time of data collection.

6. Datamine of the difference in pre- and post- Microcon® Quantification values

Intent
Evaluate the difference between the Quantification values obtained for samples prior to the 'auto-microcon' step, and then after the 'auto-microcon' process. This is to assess, through the Quantification data, the effectiveness of the Microcon® step in concentrating the DNA extract.

As this is purely a datamining experiment, only the samples that yielded a result of 'success' were examined.

Data Analysis

The samples applicable to this experiment had Quantification values above 0.001ng/μL and less than 0.015ng/μL where the final result was 'success'.

This range was considered by the author to be able to provide a sufficient demonstration of the trend of the data (N=278 samples).

7. Results and Discussion

7.1 Assessment of 'auto-microcon' results

There were N=1449 samples in the 'auto-microcon' Quantification range, excluding certain samples as per Section 5.

The percentage of samples that resulted in a determination of 'fail' was 89.4% (Fig 1). As expected, the number of 'fails' increased when the Quantification decreased and approached the Limit of Detection of Quantification ie. 0.001ng/μL (Fig 2). This was considered to be due to there being less DNA detected in the extract, and therefore less DNA to concentrate.

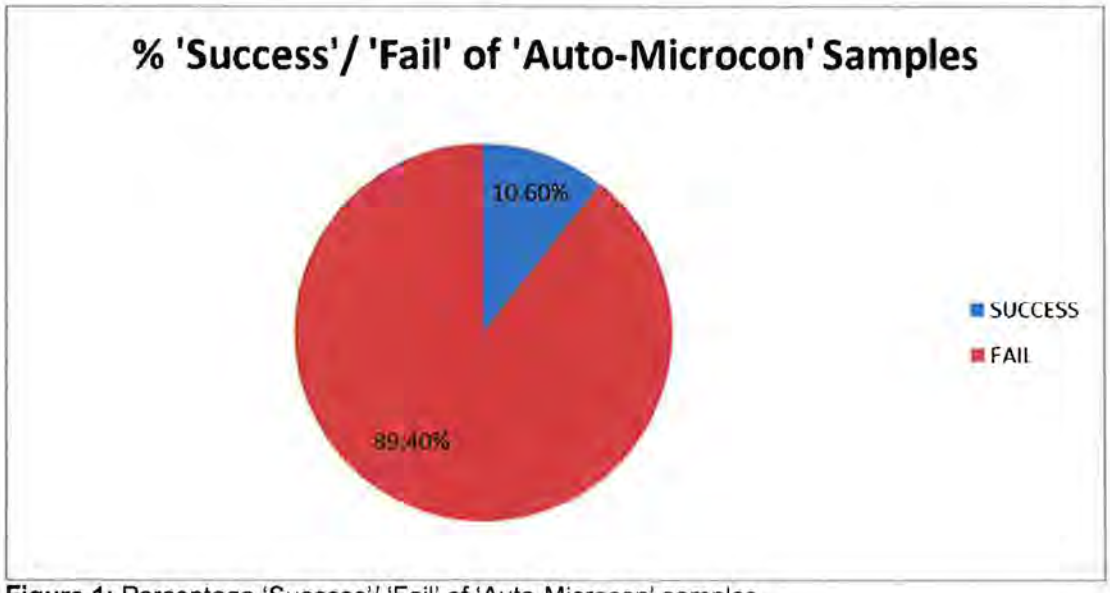

Figure 1: Percentage 'Success'/ 'Fail' of 'Auto-Microcon' samples.

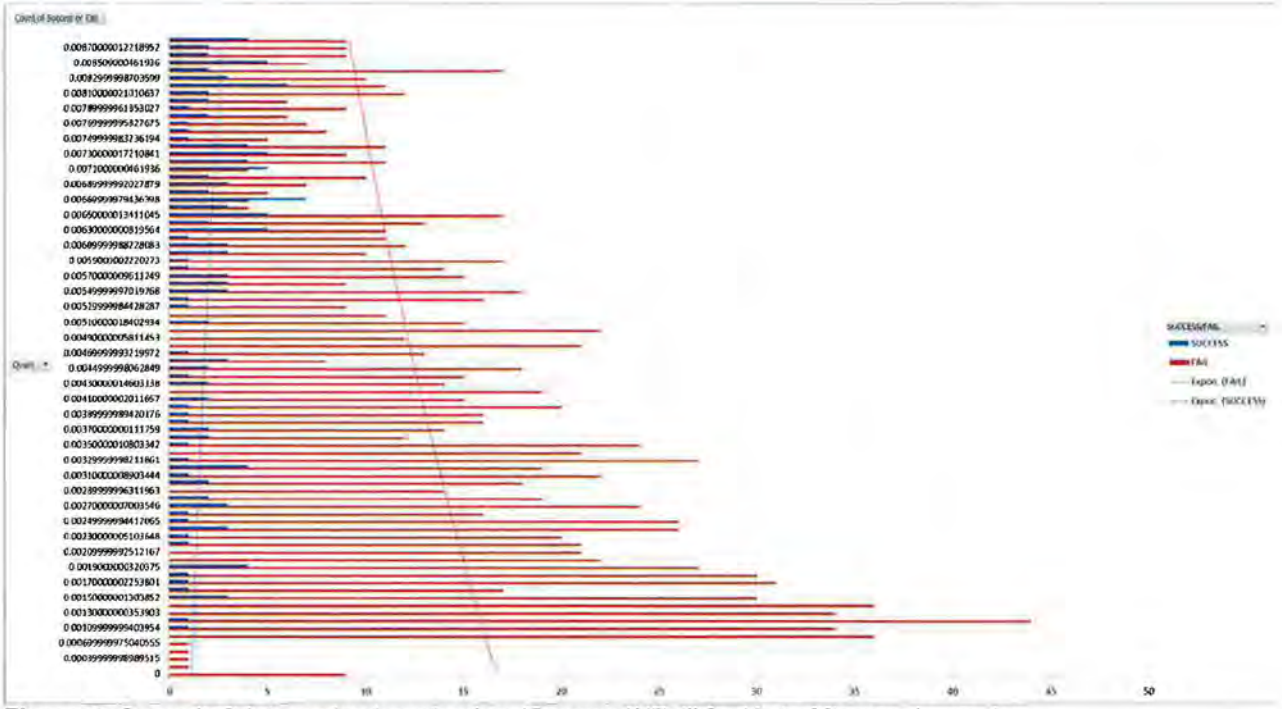

Figure 2: Spread of data and categorised as 'Success'/ 'Fail' for 'Auto-Microcon' samples.

If samples were not processed through the 'auto-microcon' process, what DNA Intelligence would the client miss out on? To evaluate this, the 'success' data was drilled down to the samples that had some NCIDD interaction and in particular, where they were the only samples in the case that were NCIDD-suitable for that particular profile. This represented 1.86% of all 'auto-microcon' samples. In looking at samples that provide *new* Intelligence, that is DNA information available for future linking, or has provided a cold-link, this equated to 1.45% of all 'auto-microcon' samples (Fig 3)..

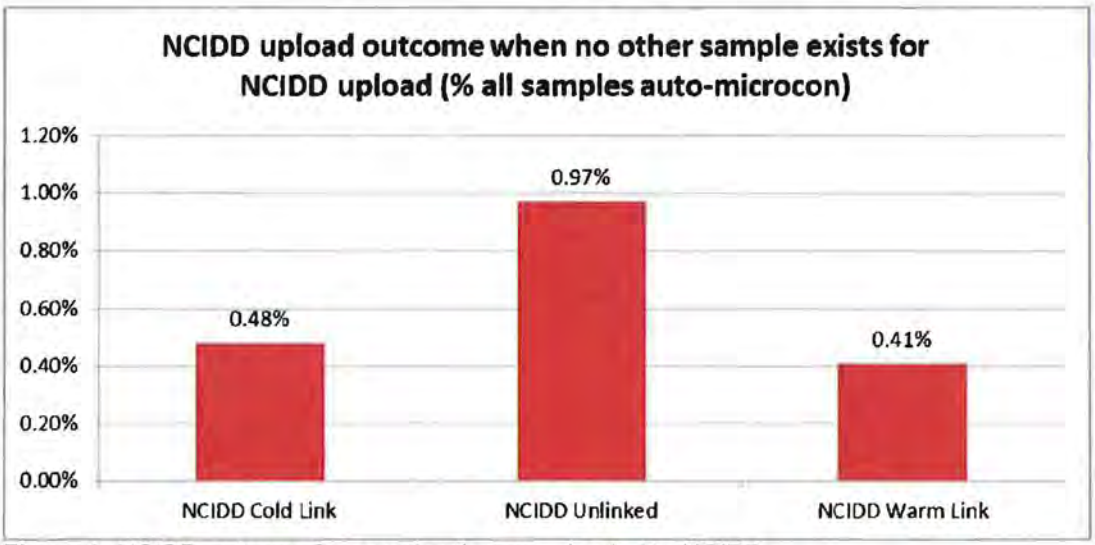

Figure 3: NCIDD outcome for samples that were loaded to NCIDD

This 1.45% of 'auto-microcon' samples is considered to be the pertinent value for the client to assess if the 'auto-microcon' process was not performed.

7.2 Datamine of the difference in pre- and post- Microcon® Quantification values

The samples applicable to this experiment had Quantification values above 0.001ng/μL where the final result was 'success'.

As the Microcon® process concentrates the DNA extract from approximately 100uL to approximately 35μL, in theory it would be a reasonable expectation to obtain approximately two to three-fold increases in DNA Quantification after concentration. Figure 4 shows the plot of the differences found for samples that resulted in 'success'.

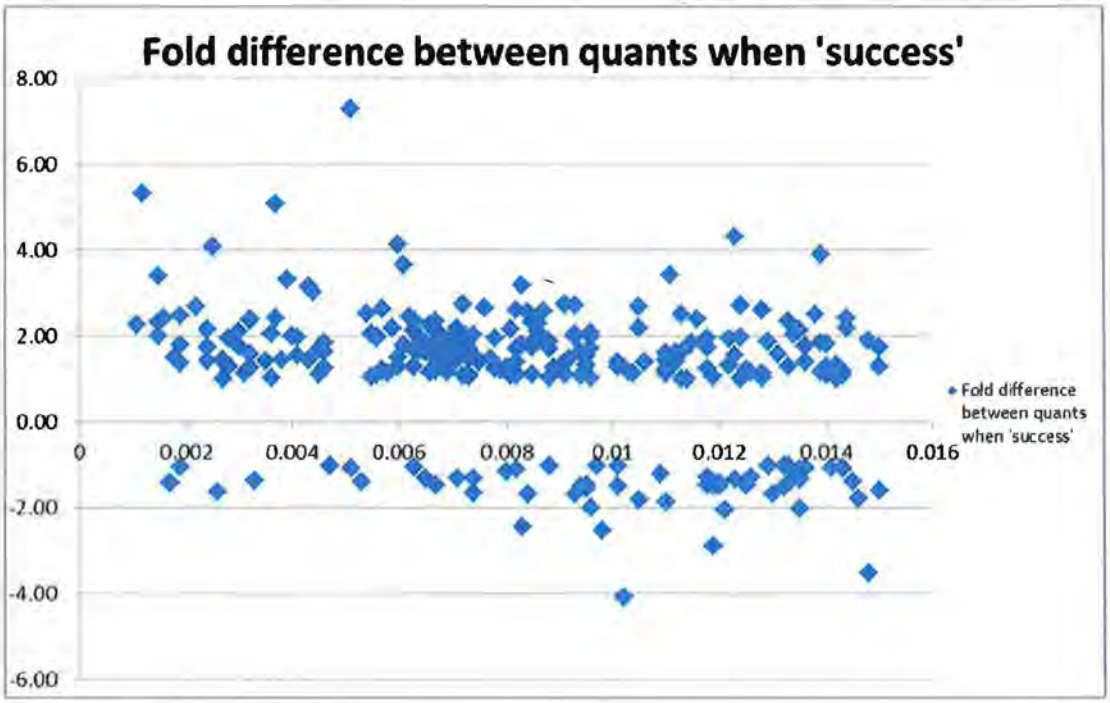

Figure 4: Quantification differences pre and post concentration

The findings are not unexpected as the scatter focusses mostly around two-fold increases in Quantification. It was also not unexpected to observe the variable results. Anecdotally, variability in success rates is found at profile management stage when assessing results of samples that have had this concentration step.

DNA can be lost in the process as seen in Fig 4 where the Quantification values decreased after concentration (below the horizontal axis). Variability in results could be attributed to a number of things, including but not limited to the slight

differences between operators and instrumentation, the differences in substrate type and level of degradation, and the variability in Quantification result.

8. Options for consideration

The options to consider are:

1. Continue with 'auto-microcon' process for Priority 2 (Major Crime) casework; or,

2. Cease the 'auto-microcon' process for Priority 2 (Major Crime) casework and report the exhibit result of 'DNA insufficient for further processing' based on Quantification result.

    a. Priority 1 samples could proceed with the 'auto-microcon' process. If a DNA concentration rework is required, the Microcon® process can be ordered manually by the scientist.

In considering continuing or discontinuing the automatic concentration of DNA extracts for Priority 2 (Major Crime) samples, some key elements to consider include, but are not limited to:

- The opportunity to link DNA profiles on NCIDD would not be initially possible (without automatic concentration) for approximately 1.45% of samples that would qualify for this process. Of the 'auto-microcon' data set (N=1449 samples) evaluated, 1.45% equates to 21 samples;

- Time and cost for processing all samples in the 'auto-microcon' range, including batch preparation, Quality checking and control;

- Time and cost for processing these samples further with additional rework options, as one would expect with low levels of DNA detected initially;

- The ability to potentially reallocate staff time currently allocated to processing, interpreting and reporting 'auto-microcon' samples, to samples with higher DNA yield, thus improving the turnaround time for results on these samples;

- The opportunity to conserve DNA extract for further processing with other technologies should that be considered (eg. Y-STR analysis, Low Copy Number analysis);

- The improved ability to provide quick results to QPS (using the Forensic Register at Quantification stage) indicating low levels of DNA detected, thus enabling QPS to employ further strategies at their discretion (eg. further sampling of items, request the rework);

- The continued ability to process the DNA extract upon client request or depending on priority (eg Priority 1 – Critical Priority).

9. References

[1] QIS 19544v11 – Concentration of DNA Extracts Using Microcon Centrifugal Filter Devices

[2] PowerPlex® 21– Amplification of Extracted DNA Validation. Megan Mathieson, Thomas Nurthen, Cathie Allen. December 2012. Forensic DNA Analysis.

[3] QIS 23008v15 – Explanation of EXR/EXH Results

[4] QIS 24012v13 – Miscellaneous Analytical Section Tasks

CA-102



Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

November 2017

Justin Howes and Cathie Allen

Great state. Great opportunity.

Queensland Government

Project Proposal #184 Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

Published by the State of Queensland (Queensland Health), November 2017

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1. Abstract

All samples that underwent a Microcon® process were evaluated and categorised into whether there was meaningful information obtained or not. This evaluation focussed primarily on samples processed in 2016 that underwent an 'auto-microcon' process. Arguably minimal value in proceeding (define value? For whom/what? If simply looking at success rates from a numbers perspective only, agree minimal value for us and the client. If looking at value from a sample/case perspective, then the 10% successes could potentially be very valuable to the client?) with this automatic processing step was found. Given this, further workflow streamlining processes could be implemented that would provide significant processing efficiencies, and cost and time savings such that these efforts could be better placed in processing higher DNA-yielding samples.

~~3.~~2. Introduction

Microcon® Centrifugal Filter Devices desalt and concentrate macromolecular solutions such as DNA-containing solutions. They employ Amicon's low binding, anisotropic, hydrophilic regenerated cellulose membrane [1].

The use of Microcon® filters to concentrate extract has been a standard post-extraction process within Forensic DNA Analysis to reduce the volume of extract from approximately 100uL to ≤20µL for amplification with AmpFℓSTR® Profiler Plus®, and to ≤35µL for amplification with PowerPlex® 21 system (PP21).

Since the implementation of PP21 amplification kit within Forensic DNA Analysis for casework samples in December 2012, extracts with low Quantification values were recommended to be concentrated. Templates of <0.132ng were found to exhibit marked stochastic effects after amplification [2]. Consequently, a workflow that directed extracts automatically to a concentration step based on Quantification value was implemented ('auto-microcon' process).

Anecdotally, the suitability to provide the Queensland Police Service (QPS) with DNA profile Intelligence from extracts that have been concentrated has been noted to be limited. Furthermore, extracts that are of low quant value that have been automatically concentrated have been observed to rarely yield DNA information for QPS.

NB. Project #163 – *Assessment of results obtained from 'automatic-microcon' samples* [3] was conducted to evaluate the results of samples that were processed with the 'auto-microcon' process. A recommendation of this project

was to re-evaluate after the introduction of the Forensic Register in conjunction with the use of Quantifiler® Trio DNA Quantification Kit.

This recommendation was based on the perceived ease of retrieving data from the FR as opposed to AUSLAB, and with the thought that the FR would soon be implemented. For the purposes of this project, it is not considered essential to have the FR implemented if the data can be retrieved from AUSLAB. However, it is considered important that the data be spanning a sufficient period of processing, and be based on the same Quantification system namely the Quantifiler® Trio DNA Quantification Kit.

The purpose of this project is to evaluate the suitability for interpretation (this is your measure of success, then?) of DNA profiles that may be obtained after the post-extraction concentration step using the Microcon® centrifugal filter devices. This evaluation includes an assessment of those samples that underwent the 'auto-microcon' process. This evaluation is based on a data mine of extracts in the year 2016 that were concentrated with Microcon® centrifugal filter devices, and assesses the 'suitability' of PP21 profile outcomes as a function of quant values obtained from using the Quantifiler® Trio DNA Quantification Kit.

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This evaluation looks at two data sets as a function of the Quantification value:

1. PP21 DNA profile outcomes from extracts that were processed through the 'auto-microcon' process;

2. PP21 DNA profile outcomes from all extracts that were concentrated with the Microcon® filter devices.

~~4.~~3. Resources

The following resources were required for this validation/project:

Forensic DNA Analysis staff and computer time to retrieve data from AUSLAB and to use Microsoft Excel.

~~5.~~4. Methods

~~5.1.~~4.1. Data retrieval from AUSLAB (LIMS)

Data was retrieved from AUSLAB using Extended Enquiries. Data was searched for samples that had a testcode of 'XPLEX' and 'MCONC1' ordered in the year 2016 in Forensic DNA Analysis. Samples with the XPLEX (both testcodes?) testcode were High Priority (P2) samples.

The data was output with the corresponding Quantification value and the reported DNA profile interpretation (Exhibit Report Line in the Exhibit Report (EXH)) for that particular barcode. If the barcode was a sub-sample, the corresponding EXH line for the sub-sample was output.

For ease of data interrogation, the RAW data (I:\Change Management\Proposal#184 - Evaluation of the efficacy of Microcons\Data\RAW Data from AUSLAB) had a column added to describe whether the sample underwent the 'auto-microcon' process ('AUTO' = 0.001ng/μL<Quant <0.0088ng/μL) or not ('MANUAL' = Quant >0.0088ng/μL). Another column was added to describe whether there was a Quantification value returned in the data collation ('TRUE' = Quant value obtained), or not ('FALSE' = no Quant value obtained (ie. 0 ng/μL).

The data excluded samples that had not returned a DNA profile result, Quality samples (including environmental monitoring samples), have no quant value in the data export, or have quality issues noted.

~~5.2.4.~~2. Data interrogation

The data was interrogated by assessing the DNA profile outcome results reported as Exhibit Report lines as a function of the Quantification value.

The Exhibit lines were interrogated and grouped into two interpretation outcomes as follows:

1. 'Fail': DNA profile interpretation outcomes of 'Complex unsuitable for interpretation', 'No DNA profile', 'Partial unsuitable for interpretation', 'No DNA Detected';

2. 'Success': All other DNA profile outcomes. I think you need to be specific here, especially if you are going to go on to make further decisions with respect to 'value' of these success – ie NCIDD load

Perhaps accept and reject rather than success and fail for the first stage, where you are simply deciding which data to include?

Then perhaps redefine 'success' for each progressive section

~~6.~~5. Experimental Design

~~6.1.~~5.1. Experiment 1: Assessment of 'auto-microcon' results

Intent
Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 through the 'auto-microcon' workflow.

Data Analysis
The samples applicable to this experiment had Quantification values in the range 0.001ng/μL to 0.0088ng/μL, and a total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value. A percentage of samples that fell into these categories was determined.

The 'auto-microcon' data could be expressed as a function of Quantification value.

Of the DNA profile interpretation outcomes of 'success', the data was broken down further to determine the percentage of samples that were reworked prior to the DNA profile outcome of 'success'.

The percentage of samples that had an 'auto-microcon' process and led to an NCIDD upload was obtained. This data could be filtered further into the outcome from the NCIDD load, at the time of data collection.

~~6.2.~~5.2. Experiment 2: Assessment of all DNA profile results from extracts that have had a concentration step.

Intent
Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 and underwent a post-extraction concentration step using Microcon® centrifugal filter devices.

Data Analysis

The samples that were applicable to this experiment had Quantification values above 0.001ng/μL, and underwent the Microcon® process. This included the 'auto-microcon' samples, and those that had a Microcon® rework performed (termed 'manual'). This combination of data was termed 'combined data'.

A total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value.

The percentage of samples that fell into these categories ('manual' and 'combined') was determined. 'Manual' referred to the samples beyond the 'auto-microcon' range that were reworked with the Microcon® process, and 'combined' referred to all samples ('auto-microcon' and 'manual').

There was a point where the number of 'success' samples was approximately the same as the number of 'fail' samples when the Microcon® process was performed. This appeared to be approximately Quant = 0.02ng/uL. Therefore, the data was interrogated further at a Quantification value lower than this mark to determine what percentage of samples in certain ranges led to DNA profile interpretation outcomes of 'success'.

From this data, a sub-section of samples was interrogated further to evaluate the effect on DNA Intelligence (is this defined somewhere?) that was obtained. A range of samples with Quantification range up to 0.015ng/uL was chosen and a total number of samples was determined. This Quantification value was chosen as it was the approximate value where all samples below this value that underwent a Microcon® process, led to an approximate, round figure of 85% 'failure'.

With this Quantification value chosen, the data was interrogated further. The percentage of samples in this range that were determined to be a 'success' and were reworked further was determined.

The percentage of samples that were in this Quantification range and led to an NCIDD upload was determined. This data could be filtered further into the outcome from the NCIDD load. Changing or developing 'success/value' This data could then be used to evaluate the potential for samples to not provide meaningful DNA Intelligence what is meaningful DNA intelligence? to QPS if the Microcon® process was re-defined in some way.

5.3. Experiment 3: Datamine of the difference in pre- and post-Microcon® Quantification values

Intent
Evaluate the difference between the values obtained from the Quantification process in samples that have had a Microcon® concentration step applied.

As this is purely a datamining experiment, only the samples that have yielded a result of 'success' was examined. Is 'success' in experiment the updated version? ie NCIDD upload/outcome

Data Analysis

The samples applicable to this experiment had Quantification values above 0.001ng/µL where the final result was 'success'.

The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/µL and 0.015ng/µL were examined.

This range was considered by the author to be able to provide a sufficient demonstration of the trend of the data.

~~7.~~6. Results and Discussion

6.1 Assessment of 'auto-microcon' results

For samples in the 'auto-microcon' Quantification range, the total number of samples that were processed this way (excluding certain samples as per Section 5.1) was N= 1449 samples.

The percentage of samples that resulted in a determination of 'fail' was 89.4% (Fig 1). As expected, the number of 'fails' increased when the Quantification decreased and approached the Limit of Detection of Quantification ie. 0.001ng/uL (Fig 2). This was considered to be due to there being less DNA detected in the extract, and therefore less DNA to concentrate.

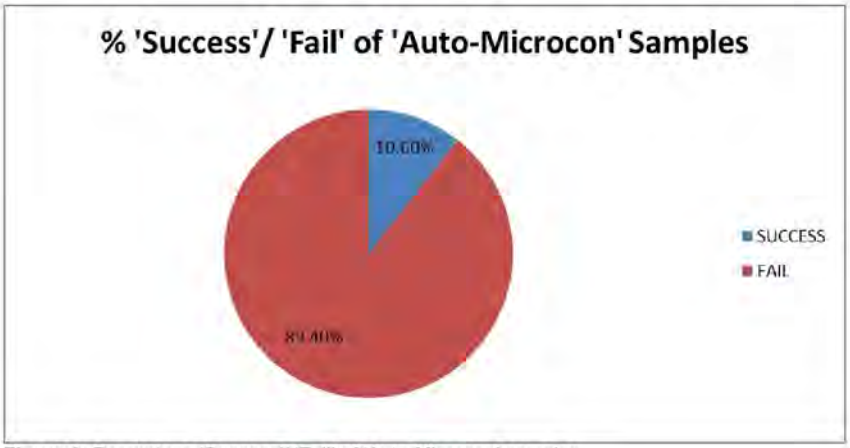

Figure 1: Percentage 'Success'/ 'Fail' of 'Auto-Microcon' samples.

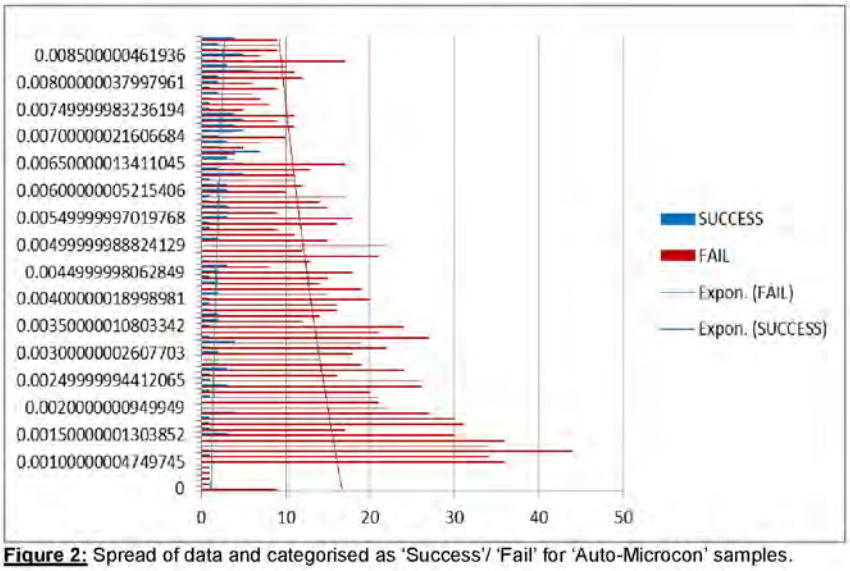

Figure 2: Spread of data and categorised as 'Success'/ 'Fail' for 'Auto-Microcon' samples.

In order to reach a DNA profile interpretation outcome of 'success', it was found that 74.7% of samples had an additional rework to the Microcon® process (Fig 3). Is this because of number of contributors, considering these samples are all P2? (so might not necessarily reflect profile quality or lack thereof, per se) How relevant is this?

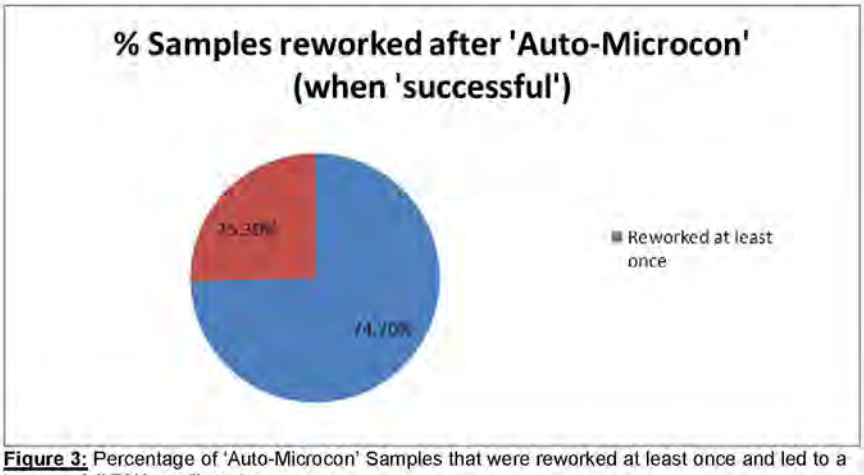

Figure 3: Percentage of 'Auto-Microcon' Samples that were reworked at least once and led to a 'successful' DNA profile outcome.

In putting the data behind Figures 2 and 3 together, if an 'auto-microcon' process was not conducted and was subsequently requested by the client for samples in this Quantification range, there would be approximately a 10% chance of obtaining a 'successful' DNA profile interpretation. Furthermore, in order to achieve that outcome, approximately 75% of these 'successful' samples would have needed a further rework. This means, for these samples, there would be a turnaround time factor for the client to consider, and in a potential fee-for-service model with requesting clients, being prepared to have increased processing costs associated with these low-quant samples would be a client consideration. I am not sure you can put these together in this way? Remember, you are using P2 samples (that require repro for STRmix)

If samples were not processed through the 'auto-microcon' process, what DNA Intelligence would the client miss out on? To evaluate this, the 'success' data was drilled down to the samples that had some NCIDD interaction and in particular, where they were the only samples in the case that were NCIDD-suitable for that particular profile (Fig 4). This is a bit too vague for me This represented 1.86% of all 'auto-microcon' samples. In looking at samples that provide *new* Intelligence, that is DNA information available for future linking, or has provided a cold-link, this equated to 1.45% of all 'auto-microcon' samples.

This 1.45% of samples would be the pertinent value for the client to consider if the 'auto-microcon' process was not performed – this samples are our RISK if

we decide to remove this process – in removing this process we are also removing 1.45% of samples that do provide our client with 'success'. In considering this, it would be important to evaluate the time and cost for processing, and the opportunity to concentrate efforts on other higher yielding samples. In saying this, with the ease of communication through the Forensic Register, these samples could processed if the client has no other forensic Intelligence assisting the matter, or if the item is considered to be of critical priority.

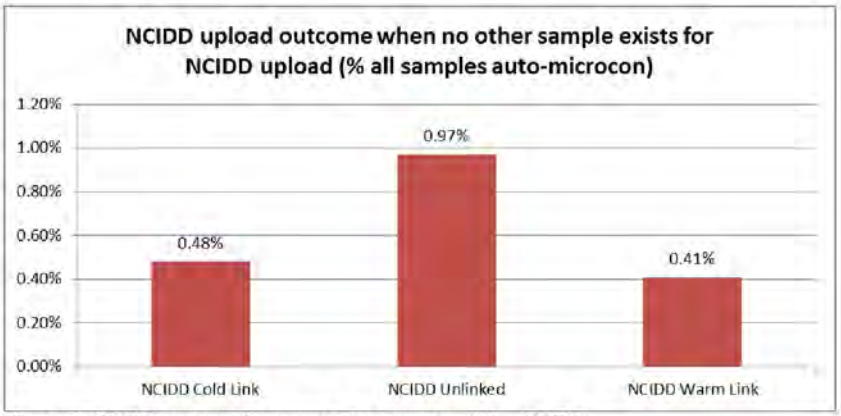

Figure 4: NCIDD outcome for samples that were loaded to NCIDD

Ultimately, this data means that for approximately 90% of samples that underwent an 'auto-microcon' process, there is arguably negligible DNA profile Intelligence for the client. If the 'auto-microcon' was not applied, there would be the following advantages, including but not limited to:

-the potential to make available at least 1449 processing positions for other samples including further available positions that would have been used for reworks,

-the lack of a need for the considerable efforts required to prepare and process Microcon® (and further rework) batches for this number of samples,

-consumable and labour savings in the end-to-end processing of these samples, and

-time and effort could be redirected in the laboratory workflow to other activities including service extensions like Y-STR profiling.

This is good, but for the argument to be presented in a balanced and transparent fashion perhaps you should include the perceived risks and impacts too? Maybe a table? This is particularly important for the 'success' samples – if you are going to remove a process that gives any 'success' then you need to

know what the impact will be and perhaps offer a mitigation strategy. For example, examine the 1.45% identified risk for QPS to see if there are any trends that predict success (ie sample type, substrate, collection location) that could be used to provide advice to QPS about which samples to request m'con on?

6.2 Assessment of all DNA profile results from extracts that have had a concentration step.

All samples from 2016 that had a Microcon® process were determined. The total number of samples was N= 2201 samples, excluding certain samples as per Section 5.1.

The percentage of samples that resulted in a determination of 'fail' was 78.5% (see Fig 5). As expected, in looking at the spread of the 'combined' data, the number of 'successes' increased when the Quantification increased (Fig 6).

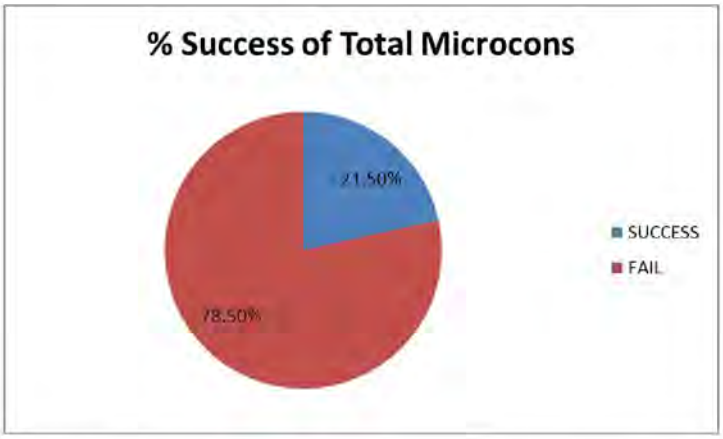

Figure 5: Percentage 'Success'/ 'Fail' of all Microcon® samples ('combined' data).

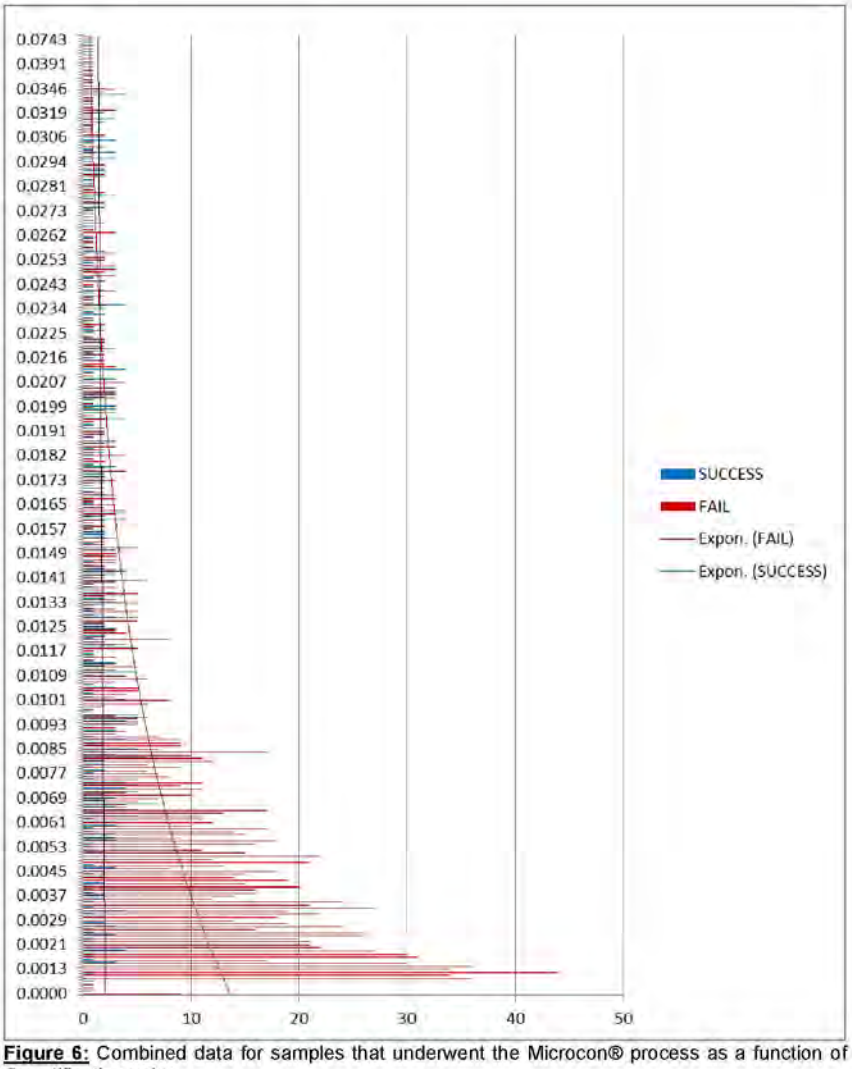

Figure 6: Combined data for samples that underwent the Microcon® process as a function of Quantification value.

As mentioned in Section 5.2, the Quantification value where there was roughly the same number of 'success' and 'fail' samples was approximately 0.02ng/uL. It must be noted that this is a rough estimate *at this* particular Quantification value, and it is based on limited samples that returned that Quantification value. It can be argued that taking a range of Quantification values to look at the overall success/fail percentages could provide the client with approximate likelihoods of obtaining meaningful DNA Intelligence.

A number of ranges were looked at to determine the percentage 'success' of samples with Quantification values in various ranges (Fig 7). The ranges were established up to the highest Quantification value of 0.02ng/uL. As expected, the percentage 'success' increased as the Quantification increased due to the higher amount of DNA in the extract available to be concentrated.

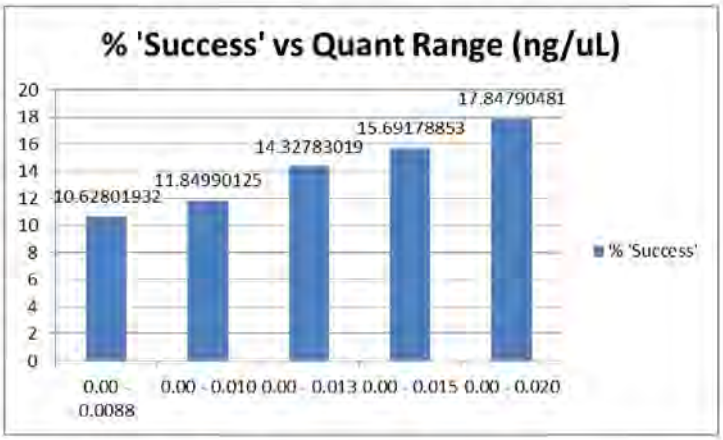

Figure 7: Percentage 'success' for samples that underwent a Microcon® process

In viewing the data in Fig 7, a limitation is that all samples that fell in the 'auto-microcon' range, had a Microcon® process performed, whereas there are samples that are in higher Quantification ranges that might not have required a Microcon® concentration rework step to yield useful DNA profiles. These samples were not evaluated.

A lower Quantification value to where the number of 'successes' roughly equalled the 'failures' was chosen to be the upper end of data ranges that were evaluated further. The value chosen was 0.015ng/uL. Table 1 and Figure 8 describe the risk to NCIDD upload for samples in these ranges if Microcon® concentration steps were not performed.

Table 1: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

	% No other samples to Upload in Quantification ranges (Q)		
	Q = 0.00ng/uL to 0.01ng/uL (total samples in range = 1519)	Q = 0.00ng/uL to 0.0133ng/uL (total samples in range = 1696)	Q = 0.00ng/uL to 0.015ng/uL (total samples in range = 1778)
NCIDD Cold link	0.92	0.88	1.01
NCIDD Unlinked	0.53	0.77	1.24
NCIDD Warm Link	0.46	0.83	0.90

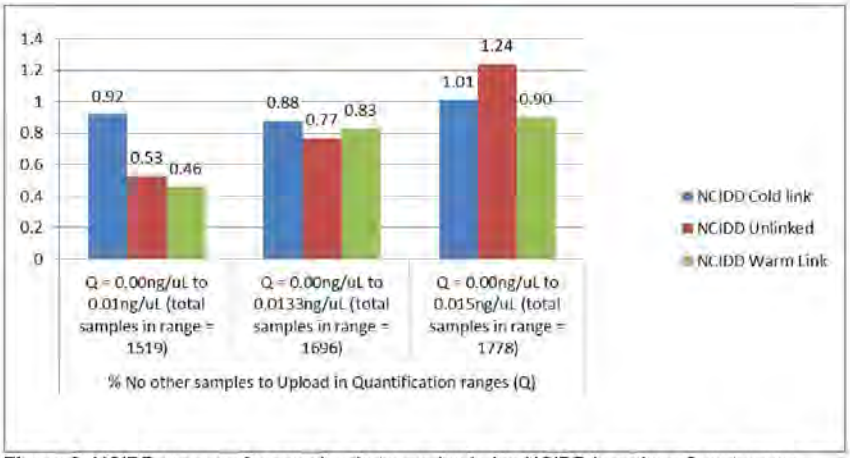

Figure 8: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

Approximately 1.45% of samples in the Quantification range up to 0.01ng/uL resulted in 'new' DNA Intelligence. This percentage is the same as that found in the 'auto-microcon' range. This percentage increased to 1.65% and 2.25% for the Quantification ranges up to 0.0133ng/uL and 0.015ng/uL respectively.

The number of further reworks required to obtain 'success' outcomes decreased as the Quantification increased. This is not unexpected given higher DNA yields detected would not necessarily require as many reworks in order to yield DNA profiles.

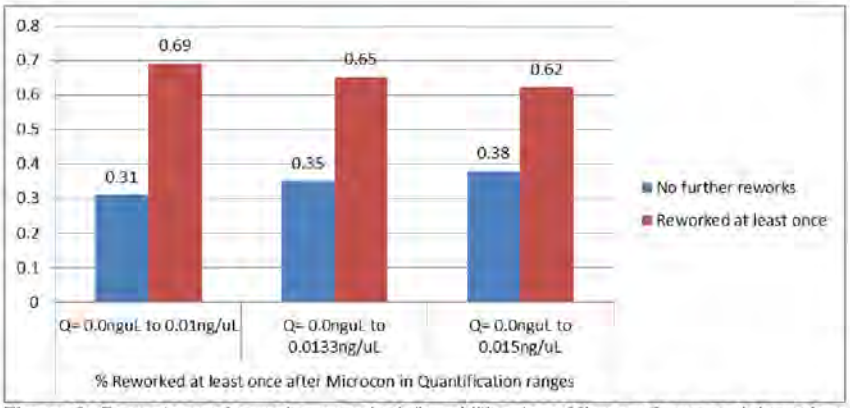

Figure 9: Percentage of samples reworked (in addition to a Microcon® process) in various Quantification ranges.

6.3 Datamine of the difference in pre- and post- Microcon® Quantification values

The samples applicable to this experiment had Quantification values above 0.001ng/μL where the final result was 'success'. The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/μL and 0.015ng/μL were examined.

As the Microcon® process concentrates the DNA extract from approximately 100uL to approximately 35uL, in theory it would be a reasonable expectation to obtain approximately two to three-fold increases in DNA Quantification after concentration. Figure 10 shows the plot of the differences found for samples that resulted in 'success'.

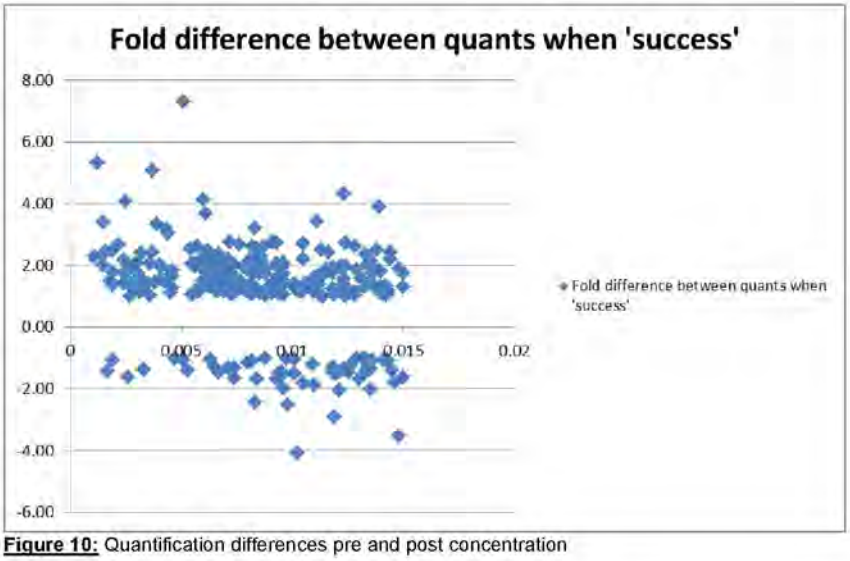

Figure 10: Quantification differences pre and post concentration

The findings are not unexpected as the scatter focusses mostly around two-fold increases in Quantification. It was also not unexpected to observe the variable results – we know that quant step itself has inherent variability. Anecdotally, variability in success rates is found at profile management stage when assessing results of samples that have had this concentration step.

DNA can be lost in the process as seen in Fig 10 where the Quantification values decreased after concentration. Variability in results could be attributed to a number of things, including but not limited to the slight differences between operators and instrumentation, the differences in substrate type and level of degradation, and the variability in Quantification result.

8.7. Conclusion and Recommendations

The data analysis demonstrated that there was arguably minimal value in performing the 'auto-microcon' concentration step. This opinion was formed by analysing the data from 2016 where it was found that for all samples that underwent the 'auto-microcon' step, 89% did not yield meaningful results.

It was found that in considering all samples that underwent a Microcon® step at some stage in 2016, 78.5% did not yield meaningful results (what does this mean? They are fails? Or they didn't give new intel?). As expected, when the Quantification value increased, the percentage of meaningful results increased. However, it was also demonstrated in the data analysis that the Quantification values did not always improve after Microcon®, but where they did, the magnitude of change was roughly equivalent to the change in volume (from neat to concentrated sample).

Based on the data analysis, the following recommendations are offered:

1. Cease 'auto-microcon' processing with the following exceptions:
   a. Priority 1 samples (Critical Priority); and

   b. Coronial/DVI samples where profiles are mostly single-source and quite often incomplete profiles may be enough to provide Intelligence on possible identity.

2. Cease processing all Priority 3 samples up to the Quantification value of 0.0133ng/uL (template of 200ng). Maybe this, and reworks, could form a part B to this project?

3. For samples in the range described in Recommendation 2, automatically send result information via the Forensic Register to QPS at Quantification stage. This result information is recommended to be the exhibit result line of 'DNA Insufficient for Further Processing'. This recommendation is an extension to the current 'No DNA Detected' process, which looks at Priority 2 samples yielding Quantification results of less than the Limit of Detection.

4. Re-analyse Priority 2 samples in the range 0.0088ng/uL to 0.0133ng/uL after a six month period of processing to evaluate whether Recommendation 2 can be extended to Priority 2 samples.

5. Communicate the change in process to QPS and ensure that QPS are aware that for samples in the ranges mentioned in Recommendations 1 and 2, that they could be requested for Microcon® concentration steps at any point in time. This request can be made via the Forensic Register after they have received the 'DNA insufficient...' result line.

~~7.~~8. References

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[1] QIS 19544v11 – Concentration of DNA Extracts Using Microcon Centrifugal Filter Devices

[2] PowerPlex® 21– Amplification of Extracted DNA Validation. Megan Mathieson, Thomas Nurthen, Cathie Allen. December 2012. Forensic DNA Analysis.

[3] Project #163 - Assessment of results obtained from 'automatic-microcon' samples. Josie Entwistle, Allison Lloyd, Kylie Rika, Thomas Nurthen, Cathie Allen. August 2015. Forensic DNA Analysis.



Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

November 2017

Justin Howes and Cathie Allen

Great state. Great opportunity.

Queensland Government

Project Proposal #184 Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

Published by the State of Queensland (Queensland Health), November 2017

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Document Details

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1. Abstract

All samples that underwent a Microcon® process were evaluated and categorised into whether there was meaningful information obtained or not. This evaluation focussed primarily on samples processed in 2016 that underwent an 'auto-microcon' process. Arguably minimal value in proceeding (define value? For whom/what? If simply looking at success rates from a numbers perspective only, agree minimal value for us and the client. If looking at value from a sample/case perspective, then the 10% successes could potentially be very valuable to the client?) with this automatic processing step was found. Given this, further workflow streamlining processes could be implemented that would provide significant processing efficiencies, and cost and time savings such that these efforts could be better placed in processing higher DNA-yielding samples.

Abstract to be re-written.

~~3.~~2. Introduction

Microcon® Centrifugal Filter Devices desalt and concentrate macromolecular solutions such as DNA-containing solutions. They employ Amicon's low binding, anisotropic, hydrophilic regenerated cellulose membrane [1].

The use of Microcon® filters to concentrate extract has been a standard post-extraction process within Forensic DNA Analysis to reduce the volume of extract from approximately 100uL to ≤20µL for amplification with AmpFℓSTR® Profiler Plus®, and to ≤35µL for amplification with PowerPlex® 21 system (PP21).

Since the implementation of PP21 amplification kit within Forensic DNA Analysis for casework samples in December 2012, extracts with low Quantification values were recommended to be concentrated. Templates of <0.132ng were found to exhibit marked stochastic effects after amplification [2]. Consequently, a workflow that directed extracts automatically to a concentration step based on Quantification value was implemented ('auto-microcon' process).

Anecdotally, the suitability to provide the Queensland Police Service (QPS) with DNA profile Intelligence from extracts that have been concentrated has been noted to be limited. Furthermore, extracts that are of low quant value that have been automatically concentrated have been observed to rarely yield DNA information for QPS.

NB. Project #163 – *Assessment of results obtained from 'automatic-microcon' samples* [3] was conducted to evaluate the results of samples that were processed with the 'auto-microcon' process. A recommendation of this project

was to re-evaluate after the introduction of the Forensic Register in conjunction with the use of Quantifiler® Trio DNA Quantification Kit.

This recommendation was based on the perceived ease of retrieving data from the FR as opposed to AUSLAB, and with the thought that the FR would soon be implemented. For the purposes of this project, it is not considered essential to have the FR implemented if the data can be retrieved from AUSLAB. However, it is considered important that the data be spanning a sufficient period of processing, and be based on the same Quantification system namely the Quantifiler® Trio DNA Quantification Kit.

The purpose of this project is to evaluate the suitability for interpretation (this is your measure of success, then?) Definitions to be added of DNA profiles that may be obtained after the post-extraction concentration step using the Microcon® centrifugal filter devices. This evaluation includes an assessment of those samples that underwent the 'auto-microcon' process. This evaluation is based on a data mine of extracts in the year 2016 that were concentrated with Microcon® centrifugal filter devices, and assesses the 'suitability' of PP21 profile outcomes as a function of quant values obtained from using the Quantifiler® Trio DNA Quantification Kit.

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This evaluation looks at two data sets as a function of the Quantification value:

1. PP21 DNA profile outcomes from extracts that were processed through the 'auto-microcon' process;

2. PP21 DNA profile outcomes from all extracts that were concentrated with the Microcon® filter devices.

~~4.~~3. Resources

The following resources were required for this validation/project:

Forensic DNA Analysis staff and computer time to retrieve data from AUSLAB and to use Microsoft Excel.

~~5.~~4. Methods

~~5.1.~~4.1. Data retrieval from AUSLAB (LIMS)

Data was retrieved from AUSLAB using Extended Enquiries. Data was searched for samples that had a testcode of 'XPLEX' and 'MCONC1' ordered in

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The data excluded samples that had not returned a DNA profile result, Quality samples (including environmental monitoring samples), have no quant value in the data export, or have quality issues noted.

~~5.2.~~4.2. Data interrogation

The data was interrogated by assessing the DNA profile outcome results reported as Exhibit Report lines as a function of the Quantification value.

The Exhibit lines were interrogated and grouped into two interpretation outcomes as follows:

1. 'Fail': DNA profile interpretation outcomes of 'Complex unsuitable for interpretation', 'No DNA profile', 'Partial unsuitable for interpretation', 'No DNA Detected';

2. 'Success': All other DNA profile outcomes. I think you need to be specific here, especially if you are going to go on to make further decisions with respect to 'value' of these success – ie NCIDD load

Perhaps accept and reject rather than success and fail for the first stage, where you are simply deciding which data to include?

Then perhaps redefine 'success' for each progressive section

Definitions to be added.

~~6.~~5. Experimental Design

~~6.1.~~5.1. Experiment 1: Assessment of 'auto-microcon' results

Intent
Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 through the 'auto-microcon' workflow.

Data Analysis
The samples applicable to this experiment had Quantification values in the range 0.001ng/μL to 0.0088ng/μL, and a total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value. A percentage of samples that fell into these categories was determined.

The 'auto-microcon' data could be expressed as a function of Quantification value.

Of the DNA profile interpretation outcomes of 'success', the data was broken down further to determine the percentage of samples that were reworked prior to the DNA profile outcome of 'success'.

The percentage of samples that had an 'auto-microcon' process and led to an NCIDD upload was obtained. This data could be filtered further into the outcome from the NCIDD load, at the time of data collection.

~~6.2.~~5.2. Experiment 2: Assessment of all DNA profile results from extracts that have had a concentration step.

Intent
Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 and underwent a post-extraction concentration step using Microcon® centrifugal filter devices.

Data Analysis

The samples that were applicable to this experiment had Quantification values above 0.001ng/μL, and underwent the Microcon® process. This included the 'auto-microcon' samples, and those that had a Microcon® rework performed (termed 'manual'). This combination of data was termed 'combined data'.

A total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value.

The percentage of samples that fell into these categories ('manual' and 'combined') was determined. 'Manual' referred to the samples beyond the 'auto-microcon' range that were reworked with the Microcon® process, and 'combined' referred to all samples ('auto-microcon' and 'manual').

There was a point where the number of 'success' samples was approximately the same as the number of 'fail' samples when the Microcon® process was performed. This appeared to be approximately Quant = 0.02ng/uL. Therefore, the data was interrogated further at a Quantification value lower than this mark to determine what percentage of samples in certain ranges led to DNA profile interpretation outcomes of 'success'.

From this data, a sub-section of samples was interrogated further to evaluate the effect on DNA Intelligence (is this defined somewhere?) Definitions to be added that was obtained. A range of samples with Quantification range up to 0.015ng/uL was chosen and a total number of samples was determined. This Quantification value was chosen as it was the approximate value where all samples below this value that underwent a Microcon® process, led to an approximate, round figure of 85% 'failure'.

With this Quantification value chosen, the data was interrogated further. The percentage of samples in this range that were determined to be a 'success' and were reworked further was determined.

The percentage of samples that were in this Quantification range and led to an NCIDD upload was determined. This data could be filtered further into the outcome from the NCIDD load. Changing or developing 'success/value' Definitions to be added This data could then be used to evaluate the potential for samples to not provide meaningful DNA Intelligence what is meaningful DNA intelligence? Definitions to be added to QPS if the Microcon® process was re-defined in some way.

5.3. Experiment 3: Datamine of the difference in pre- and post-Microcon® Quantification values

Intent
Evaluate the difference between the values obtained from the Quantification process in samples that have had a Microcon® concentration step applied.

As this is purely a datamining experiment, only the samples that have yielded a result of 'success' was examined. Is 'success' in experiment the updated version? ie NCIDD upload/outcome to be clarified.

Data Analysis

The samples applicable to this experiment had Quantification values above 0.001ng/µL where the final result was 'success'.

The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/µL and 0.015ng/µL were examined.

This range was considered by the author to be able to provide a sufficient demonstration of the trend of the data.

~~7.~~6. Results and Discussion

6.1 Assessment of 'auto-microcon' results

For samples in the 'auto-microcon' Quantification range, the total number of samples that were processed this way (excluding certain samples as per Section 5.1) was N= 1449 samples.

The percentage of samples that resulted in a determination of 'fail' was 89.4% (Fig 1). As expected, the number of 'fails' increased when the Quantification decreased and approached the Limit of Detection of Quantification ie. 0.001ng/uL (Fig 2). This was considered to be due to there being less DNA detected in the extract, and therefore less DNA to concentrate.

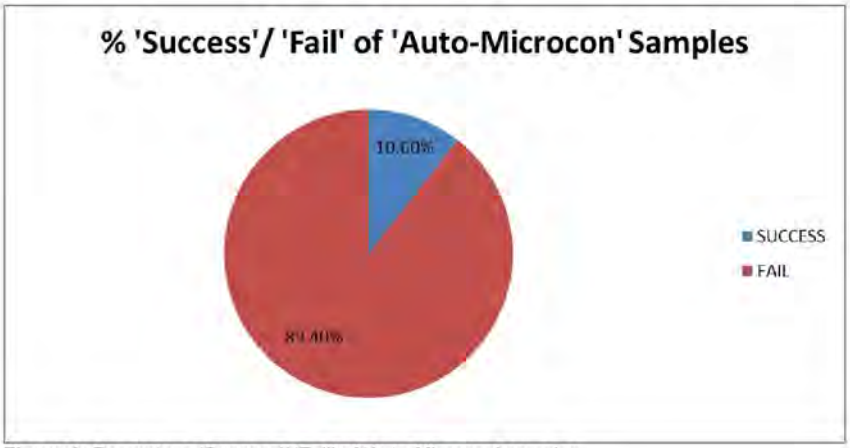

Figure 1: Percentage 'Success'/ 'Fail' of 'Auto-Microcon' samples.

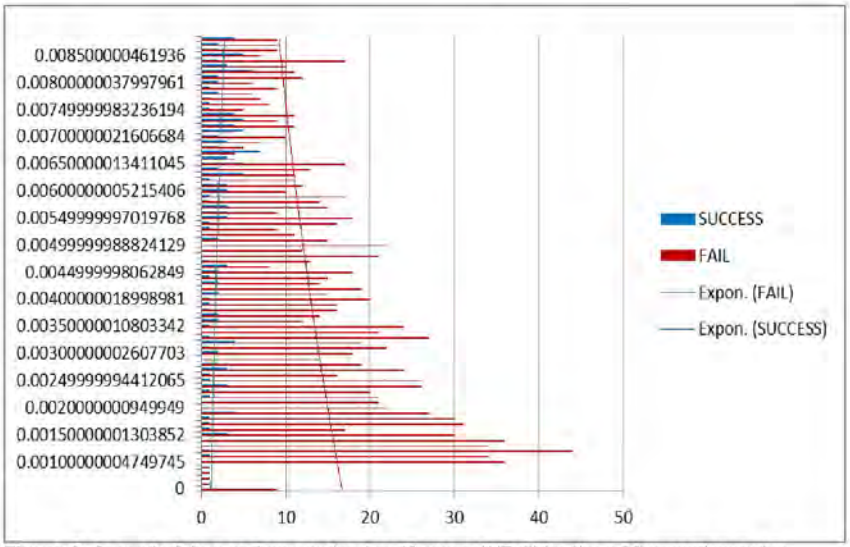

Figure 2: Spread of data and categorised as 'Success'/ 'Fail' for 'Auto-Microcon' samples.

In order to reach a DNA profile interpretation outcome of 'success', it was found that 74.7% of samples had an additional rework to the Microcon® process (Fig 3). Is this because of number of contributors, considering these samples are all P2? (so might not necessarily reflect profile quality or lack thereof, per se) How relevant is this? Reworks to be removed. No, contributs guidelines don't work for auto-mic sample.

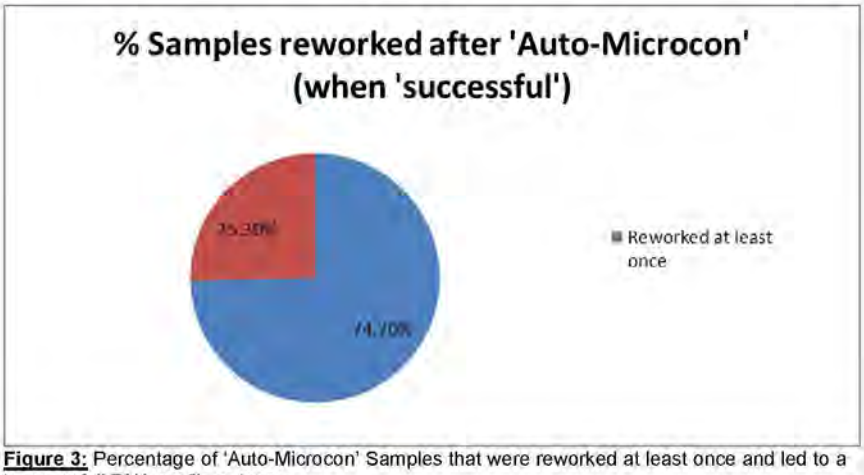

Figure 3: Percentage of 'Auto-Microcon' Samples that were reworked at least once and led to a 'successful' DNA profile outcome.

In putting the data behind Figures 2 and 3 together, if an 'auto-microcon' process was not conducted and was subsequently requested by the client for samples in this Quantification range, there would be approximately a 10% chance of obtaining a 'successful' DNA profile interpretation. Furthermore, in order to achieve that outcome, approximately 75% of these 'successful' samples would have needed a further rework. This means, for these samples, there would be a turnaround time factor for the client to consider, and in a potential fee-for-service model with requesting clients, being prepared to have increased processing costs associated with these low-quant samples would be a client consideration. I am not sure you can put these together in this way? Remember, you are using P2 samples (that require repro for STRmix) Repro/no contr doesn't work for auto-mics, but reworking discussion point to be removed anyway.

If samples were not processed through the 'auto-microcon' process, what DNA Intelligence would the client miss out on? To evaluate this, the 'success' data was drilled down to the samples that had some NCIDD interaction and in particular, where they were the only samples in the case that were NCIDD-suitable for that particular profile (Fig 4). This is a bit too vague for me This represented 1.86% of all 'auto-microcon' samples. In looking at samples that provide *new* Intelligence, that is DNA information available for future linking, or has provided a cold-link, this equated to 1.45% of all 'auto-microcon' samples.

This 1.45% of samples would be the pertinent value for the client to consider if the 'auto-microcon' process was not performed – this samples are our RISK if we decide to remove this process – in removing this process we are also removing 1.45% of samples that do provide our client with 'success'. Yes In considering this, it would be important to evaluate the time and cost for processing, and the opportunity to concentrate efforts on other higher yielding samples. In saying this, with the ease of communication through the Forensic Register, these samples could processed if the client has no other forensic Intelligence assisting the matter, or if the item is considered to be of critical priority.

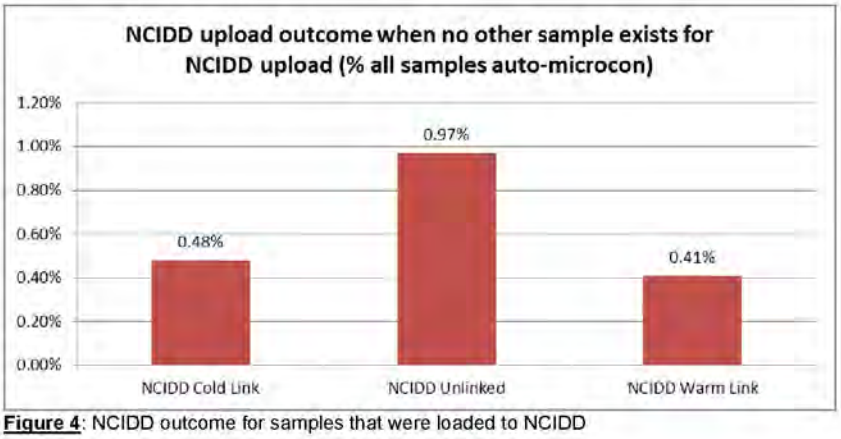

Figure 4: NCIDD outcome for samples that were loaded to NCIDD

Ultimately, this data means that for approximately 90% of samples that underwent an 'auto-microcon' process, there is arguably negligible DNA profile Intelligence for the client. If the 'auto-microcon' was not applied, there would be the following advantages, including but not limited to:

-the potential to make available at least 1449 processing positions for other samples including further available positions that would have been used for reworks,

-the lack of a need for the considerable efforts required to prepare and process Microcon® (and further rework) batches for this number of samples,

-consumable and labour savings in the end-to-end processing of these samples, and

-time and effort could be redirected in the laboratory workflow to other activities including service extensions like Y-STR profiling.

This is good, but for the argument to be presented in a balanced and transparent fashion perhaps you should include the perceived risks and impacts

too? Maybe a table? This is particularly important for the 'success' samples – if you are going to remove a process that gives any 'success' then you need to know what the impact will be and perhaps offer a mitigation strategy. For example, examine the 1.45% identified risk for QPS to see if there are any trends that predict success (ie sample type, substrate, collection location) that could be used to provide advice to QPS about which samples to request m'con on? These are all samples that were low quant first time round (hence the automic), and all samples are available for QPS to request rework on. Can add some details from items in this 'success' category.

6.2 Assessment of all DNA profile results from extracts that have had a concentration step.

All samples from 2016 that had a Microcon® process were determined. The total number of samples was N= 2201 samples, excluding certain samples as per Section 5.1.

The percentage of samples that resulted in a determination of 'fail' was 78.5% (see Fig 5). As expected, in looking at the spread of the 'combined' data, the number of 'successes' increased when the Quantification increased (Fig 6).

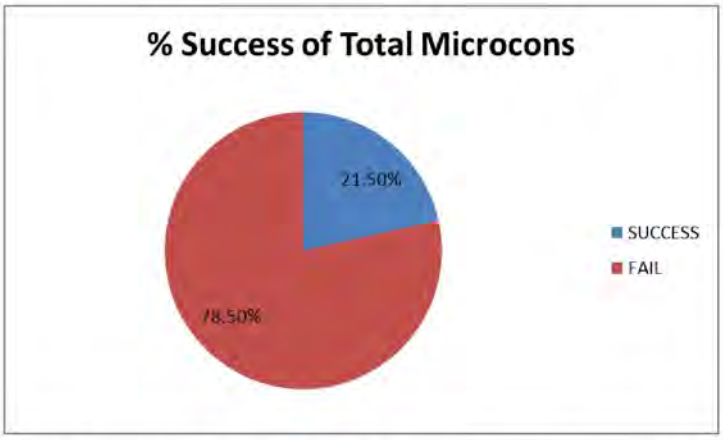

Figure 5: Percentage 'Success'/ 'Fail' of all Microcon® samples ('combined' data).

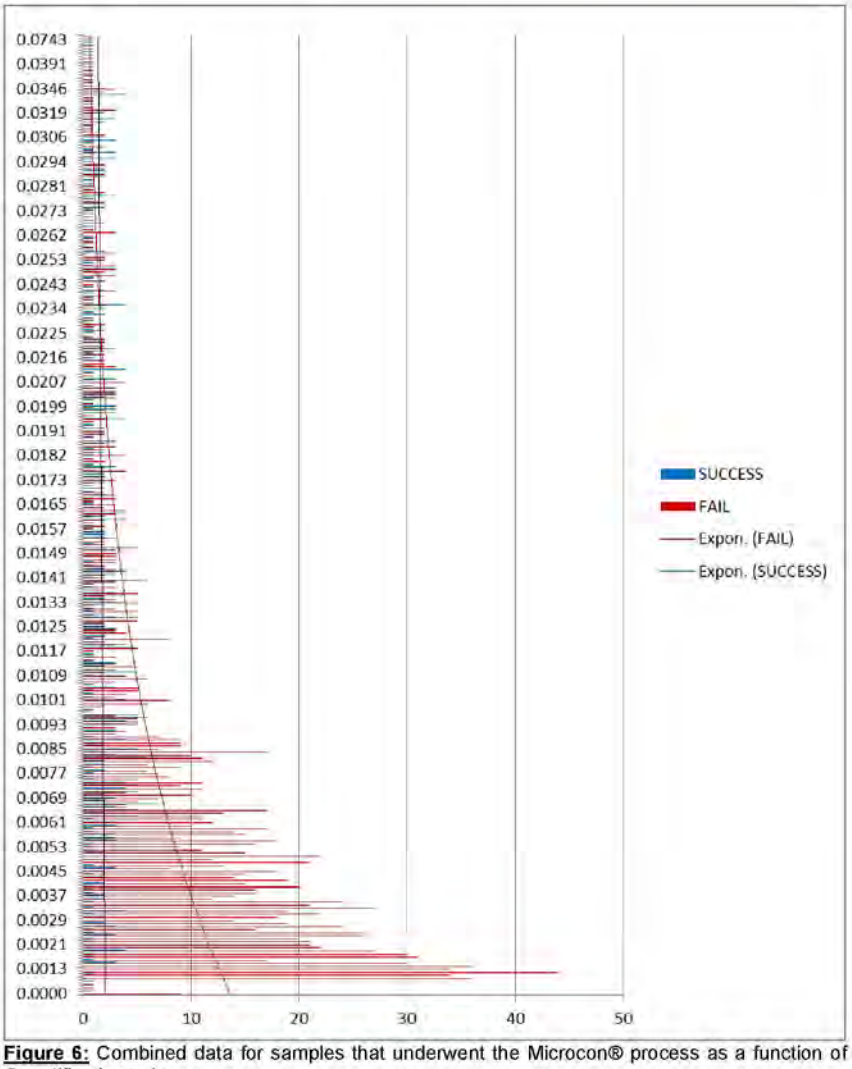

Figure 6: Combined data for samples that underwent the Microcon® process as a function of Quantification value.

As mentioned in Section 5.2, the Quantification value where there was roughly the same number of 'success' and 'fail' samples was approximately 0.02ng/uL. It must be noted that this is a rough estimate *at this* particular Quantification value, and it is based on limited samples that returned that Quantification value. It can be argued that taking a range of Quantification values to look at the overall success/fail percentages could provide the client with approximate likelihoods of obtaining meaningful DNA Intelligence.

A number of ranges were looked at to determine the percentage 'success' of samples with Quantification values in various ranges (Fig 7). The ranges were established up to the highest Quantification value of 0.02ng/uL. As expected, the percentage 'success' increased as the Quantification increased due to the higher amount of DNA in the extract available to be concentrated.

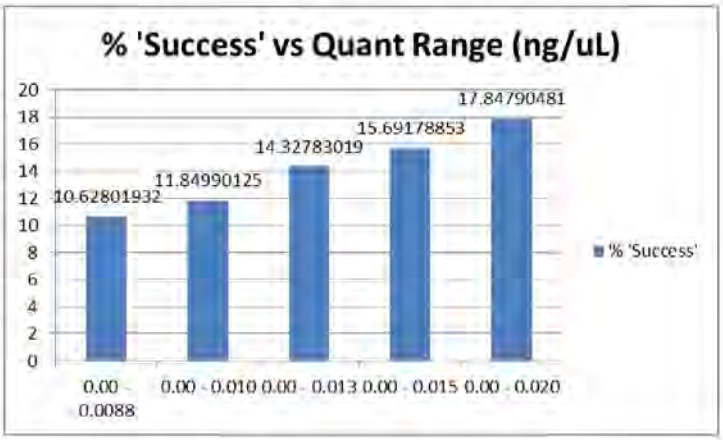

Figure 7: Percentage 'success' for samples that underwent a Microcon® process

In viewing the data in Fig 7, a limitation is that all samples that fell in the 'auto-microcon' range, had a Microcon® process performed, whereas there are samples that are in higher Quantification ranges that might not have required a Microcon® concentration rework step to yield useful DNA profiles. These samples were not evaluated.

A lower Quantification value to where the number of 'successes' roughly equalled the 'failures' was chosen to be the upper end of data ranges that were evaluated further. The value chosen was 0.015ng/uL. Table 1 and Figure 8 describe the risk to NCIDD upload for samples in these ranges if Microcon® concentration steps were not performed.

Table 1: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

	% No other samples to Upload in Quantification ranges (Q)		
	Q = 0.00ng/uL to 0.01ng/uL (total samples in range = 1519)	Q = 0.00ng/uL to 0.0133ng/uL (total samples in range = 1696)	Q = 0.00ng/uL to 0.015ng/uL (total samples in range = 1778)
NCIDD Cold link	0.92	0.88	1.01
NCIDD Unlinked	0.53	0.77	1.24
NCIDD Warm Link	0.46	0.83	0.90

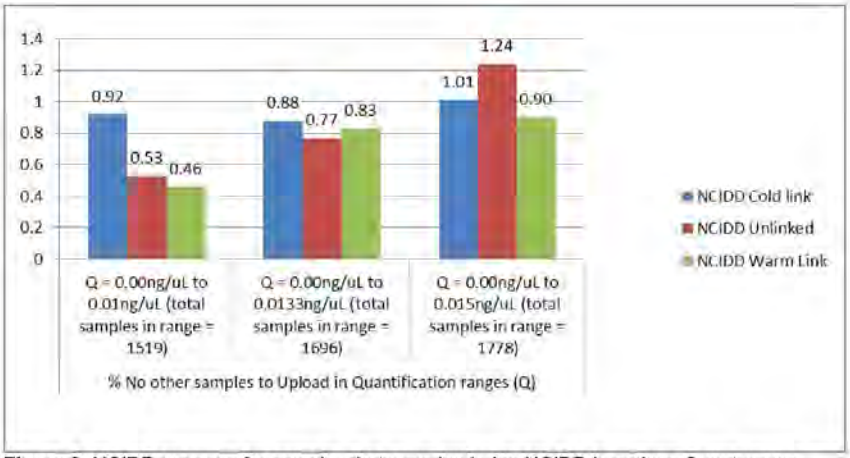

Figure 8: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

Approximately 1.45% of samples in the Quantification range up to 0.01ng/uL resulted in 'new' DNA Intelligence. This percentage is the same as that found in the 'auto-microcon' range. This percentage increased to 1.65% and 2.25% for the Quantification ranges up to 0.0133ng/uL and 0.015ng/uL respectively.

The number of further reworks required to obtain 'success' outcomes decreased as the Quantification increased. This is not unexpected given higher DNA yields detected would not necessarily require as many reworks in order to yield DNA profiles.

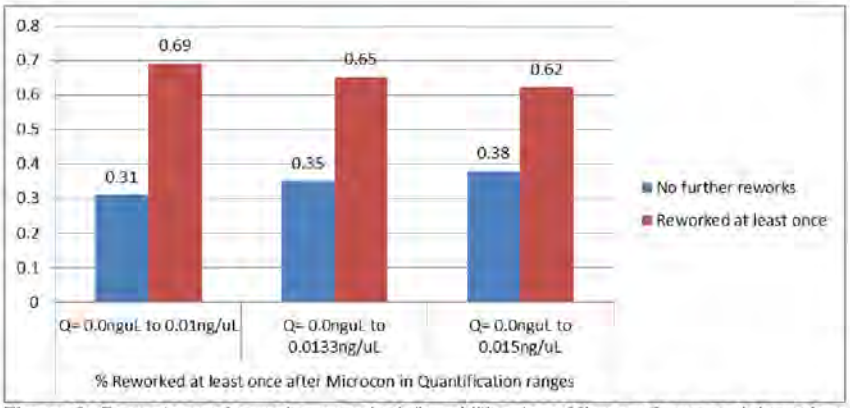

Figure 9: Percentage of samples reworked (in addition to a Microcon® process) in various Quantification ranges.

6.3 Datamine of the difference in pre- and post- Microcon® Quantification values

The samples applicable to this experiment had Quantification values above 0.001ng/μL where the final result was 'success'. The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/μL and 0.015ng/μL were examined.

As the Microcon® process concentrates the DNA extract from approximately 100uL to approximately 35uL, in theory it would be a reasonable expectation to obtain approximately two to three-fold increases in DNA Quantification after concentration. Figure 10 shows the plot of the differences found for samples that resulted in 'success'.

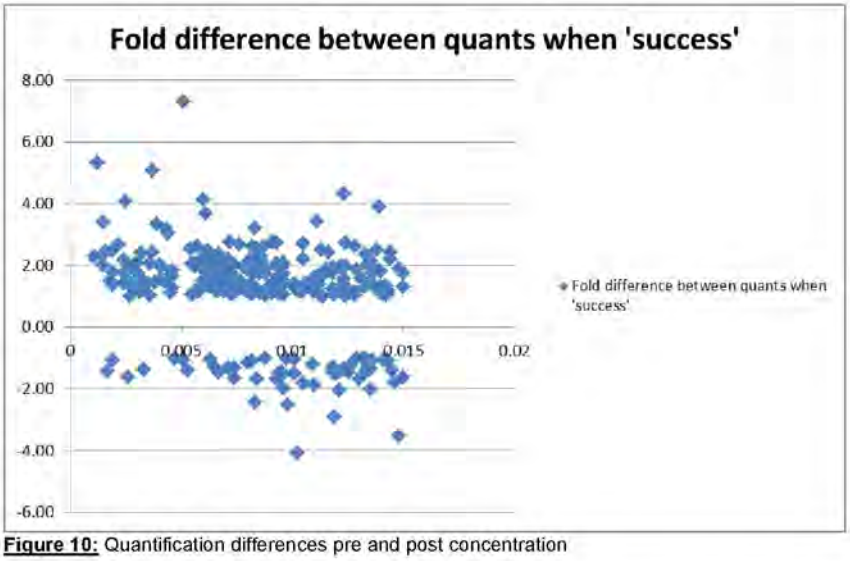

Figure 10: Quantification differences pre and post concentration

The findings are not unexpected as the scatter focusses mostly around two-fold increases in Quantification. It was also not unexpected to observe the variable results – we know that quant step itself has inherent variability. Can add more words around this as variability in all steps. Anecdotally, variability in success rates is found at profile management stage when assessing results of samples that have had this concentration step.

DNA can be lost in the process as seen in Fig 10 where the Quantification values decreased after concentration. Variability in results could be attributed to a number of things, including but not limited to the slight differences between operators and instrumentation, the differences in substrate type and level of degradation, and the variability in Quantification result.

8.7. Conclusion and Recommendations

The data analysis demonstrated that there was arguably minimal value in performing the 'auto-microcon' concentration step. This opinion was formed by analysing the data from 2016 where it was found that for all samples that underwent the 'auto-microcon' step, 89% did not yield meaningful results.

It was found that in considering all samples that underwent a Microcon® step at some stage in 2016, 78.5% did not yield meaningful results (what does this mean? They are fails? Or they didn't give new Intel?). Definitions to be added.As expected, when the Quantification value increased, the percentage of meaningful results increased. However, it was also demonstrated in the data analysis that the Quantification values did not always improve after Microcon®, but where they did, the magnitude of change was roughly equivalent to the change in volume (from neat to concentrated sample).

Based on the data analysis, the following recommendations are offered:Recommendations to be revised as will keep simple/sample values for implementation, and revise further on as samples may get reworked where Q value is greater than 0.0088ng/uL.

1. Cease 'auto-microcon' processing with the following exceptions:
   a. Priority 1 samples (Critical Priority); and

   b. Coronial/DVI samples where profiles are mostly single-source and quite often incomplete profiles may be enough to provide Intelligence on possible identity.

2. Cease processing all Priority 3 samples up to the Quantification value of 0.0133ng/uL (template of 200ng). Maybe this, and reworks, could form a part B to this project?

3. For samples in the range described in Recommendation 2, automatically send result information via the Forensic Register to QPS at Quantification stage. This result information is recommended to be the exhibit result line of 'DNA Insufficient for Further Processing'. This recommendation is an extension to the current 'No DNA Detected' process, which looks at Priority 2 samples yielding Quantification results of less than the Limit of Detection.

4. Re-analyse Priority 2 samples in the range 0.0088ng/uL to 0.0133ng/uL after a six month period of processing to evaluate whether Recommendation 2 can be extended to Priority 2 samples.

5. Communicate the change in process to QPS and ensure that QPS are aware that for samples in the ranges mentioned in Recommendations 1 and 2, that they could be requested for Microcon® concentration steps at any point in time. This request can be made via the Forensic Register after they have received the 'DNA insufficient...' result line.

~~7.~~8. References

Formatted: Bullets and Numbering

[1] QIS 19544v11 – Concentration of DNA Extracts Using Microcon Centrifugal Filter Devices

[2] PowerPlex® 21– Amplification of Extracted DNA Validation. Megan Mathieson, Thomas Nurthen, Cathie Allen. December 2012. Forensic DNA Analysis.

[3] Project #163 - Assessment of results obtained from 'automatic-microcon' samples. Josie Entwistle, Allison Lloyd, Kylie Rika, Thomas Nurthen, Cathie Allen. August 2015. Forensic DNA Analysis.



Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

November 2017

Justin Howes and Cathie Allen

Great state. Great opportunity.

Queensland Government

Project Proposal #184 Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

Published by the State of Queensland (Queensland Health), November 2017

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Document Details

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1. Abstract

All samples that underwent a Microcon® process were evaluated and categorised into whether there was meaningful information obtained or not. This evaluation focussed primarily on samples processed in 2016 that underwent an 'auto-microcon' process. Arguably minimal value in proceeding with this automatic processing step was found. Given this, further workflow streamlining processes could be implemented that would provide significant processing efficiencies, and cost and time savings such that these efforts could be better placed in processing higher DNA-yielding samples.

2. Introduction

Microcon® Centrifugal Filter Devices desalt and concentrate macromolecular solutions such as DNA-containing solutions. They employ Amicon's low binding, anisotropic, hydrophilic regenerated cellulose membrane [1].

The use of Microcon® filters to concentrate extract has been a standard post-extraction process within Forensic DNA Analysis to reduce the volume of extract from approximately 100uL to ≤20µL for amplification with AmpFℓSTR® Profiler Plus®, and to ≤35µL for amplification with PowerPlex® 21 system (PP21).

Since the implementation of PP21 amplification kit within Forensic DNA Analysis for casework samples in December 2012, extracts with low Quantification values were recommended to be concentrated. Templates of <0.132ng were found to exhibit marked stochastic effects after amplification [2]. Consequently, a workflow that directed extracts automatically to a concentration step based on Quantification value was implemented ('auto-microcon' process).

Anecdotally, the suitability to provide the Queensland Police Service (QPS) with DNA profile Intelligence from extracts that have been concentrated has been noted to be limited. Furthermore, extracts that are of low quant value that have been automatically concentrated have been observed to rarely yield DNA information for QPS.

NB. Project #163 – *Assessment of results obtained from 'automatic-microcon' samples* [3] was conducted to evaluate the results of samples that were processed with the 'auto-microcon' process. A recommendation of this project was to re-evaluate after the introduction of the Forensic Register in conjunction with the use of Quantifiler® Trio DNA Quantification Kit.

This recommendation was based on the perceived ease of retrieving data from the FR as opposed to AUSLAB, and with the thought that the FR would soon be implemented. For the purposes of this project, it is not considered essential to have the FR implemented if the data can be retrieved from AUSLAB. However, it is considered important that the data be spanning a sufficient period of processing, and be based on the same Quantification system namely the Quantifiler® Trio DNA Quantification Kit.

The purpose of this project is to evaluate the suitability for interpretation of DNA profiles that may be obtained after the post-extraction concentration step using the Microcon® centrifugal filter devices. This evaluation includes an assessment of those samples that underwent the 'auto-microcon' process. This evaluation is based on a data mine of extracts in the year 2016 that were concentrated with Microcon® centrifugal filter devices, and assesses the 'suitability' of PP21 profile outcomes as a function of quant values obtained from using the Quantifiler® Trio DNA Quantification Kit.

This evaluation looks at two data sets as a function of the Quantification value:

1. PP21 DNA profile outcomes from extracts that were processed through the 'auto-microcon' process;

2. PP21 DNA profile outcomes from all extracts that were concentrated with the Microcon® filter devices.

3. Resources

The following resources were required for this validation/project:

Forensic DNA Analysis staff and computer time to retrieve data from AUSLAB and to use Microsoft Excel.

4. Methods

4.1. Data retrieval from AUSLAB (LIMS)

Data was retrieved from AUSLAB using Extended Enquiries. Data was searched for samples that had a testcode of 'XPLEX' and 'MCONC1' ordered in the year 2016 in Forensic DNA Analysis. Samples with the XPLEX testcode were High Priority (P2) samples.

The data was output with the corresponding Quantification value and the reported DNA profile interpretation (Exhibit Report Line in the Exhibit Report

(EXH)) for that particular barcode. If the barcode was a sub-sample, the corresponding EXH line for the sub-sample was output.

For ease of data interrogation, the RAW data (I:\Change Management\Proposal#184 - Evaluation of the efficacy of Microcons\Data\RAW Data from AUSLAB) had a column added to describe whether the sample underwent the 'auto-microcon' process ('AUTO' = 0.001ng/μL<Quant <0.0088ng/μL) or not ('MANUAL' = Quant >0.0088ng/μL). Another column was added to describe whether there was a Quantification value returned in the data collation ('TRUE' = Quant value obtained), or not ('FALSE' = no Quant value obtained (ie. 0 ng/μL).

The data excluded samples that had not returned a DNA profile result, Quality samples (including environmental monitoring samples), have no quant value in the data export, or have quality issues noted.

4.2. Data interrogation

The data was interrogated by assessing the DNA profile outcome results reported as Exhibit Report lines as a function of the Quantification value.

The Exhibit lines were interrogated and grouped into two interpretation outcomes as follows:

1. 'Fail': DNA profile interpretation outcomes of 'Complex unsuitable for interpretation', 'No DNA profile', 'Partial unsuitable for interpretation', 'No DNA Detected';

2. 'Success': All other DNA profile outcomes.

~~6.~~5. Experimental Design

~~6.1.~~5.1. Experiment 1: Assessment of 'auto-microcon' results

Intent
Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 through the 'auto-microcon' workflow.

Data Analysis

The samples applicable to this experiment had Quantification values in the range 0.001ng/μL to 0.0088ng/μL, and a total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value. A percentage of samples that fell into these categories was determined.

The 'auto-microcon' data could be expressed as a function of Quantification value.

Of the DNA profile interpretation outcomes of 'success', the data was broken down further to determine the percentage of samples that were reworked prior to the DNA profile outcome of 'success'.

The percentage of samples that had an 'auto-microcon' process and led to an NCIDD upload was obtained. This data could be filtered further into the outcome from the NCIDD load, at the time of data collection.

6.2.5.2. Experiment 2: Assessment of all DNA profile results from extracts that have had a concentration step.

Intent
Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 and underwent a post-extraction concentration step using Microcon® centrifugal filter devices.

Data Analysis

The samples that were applicable to this experiment had Quantification values above 0.001ng/μL, and underwent the Microcon® process. This included the 'auto-microcon' samples, and those that had a Microcon® rework performed (termed 'manual'). This combination of data was termed 'combined data'.

A total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value.

The percentage of samples that fell into these categories ('manual' and 'combined') was determined. 'Manual' referred to the samples beyond the 'auto-microcon' range that were reworked with the Microcon® process, and 'combined' referred to all samples ('auto-microcon' and 'manual').

There was a point where the number of 'success' samples was approximately the same as the number of 'fail' samples when the Microcon® process was performed. This appeared to be approximately Quant = 0.02ng/uL. Therefore, the data was interrogated further at a Quantification value lower than this mark to determine what percentage of samples in certain ranges led to DNA profile interpretation outcomes of 'success'.

From this data, a sub-section of samples was interrogated further to evaluate the effect on DNA Intelligence that was obtained. A range of samples with Quantification range up to 0.015ng/uL was chosen and a total number of samples was determined. This Quantification value was chosen as it was the approximate value where all samples below this value that underwent a Microcon® process, led to an approximate, round figure of 85% 'failure'.

With this Quantification value chosen, the data was interrogated further. The percentage of samples in this range that were determined to be a 'success' and were reworked further was determined.

The percentage of samples that were in this Quantification range and led to an NCIDD upload was determined. This data could be filtered further into the outcome from the NCIDD load. This data could then be used to evaluate the potential for samples to not provide meaningful DNA Intelligence to QPS if the Microcon® process was re-defined in some way.

5.3. Experiment 3: Datamine of the difference in pre- and post-Microcon® Quantification values

Intent
Evaluate the difference between the values obtained from the Quantification process in samples that have had a Microcon® concentration step applied.

As this is purely a datamining experiment, only the samples that have yielded a result of 'success' was examined.

Data Analysis

The samples applicable to this experiment had Quantification values above 0.001ng/μL where the final result was 'success'.

The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/μL and 0.015ng/μL were examined.

This range was considered by the author to be able to provide a sufficient demonstration of the trend of the data.

~~7.~~6. Results and Discussion

6.1 Assessment of 'auto-microcon' results

For samples in the 'auto-microcon' Quantification range, the total number of samples that were processed this way (excluding certain samples as per Section 5.1) was N= 1449 samples.

The percentage of samples that resulted in a determination of 'fail' was 89.4% (Fig 1). As expected, the number of 'fails' increased when the Quantification decreased and approached the Limit of Detection of Quantification ie. 0.001ng/uL (Fig 2). This was considered to be due to there being less DNA detected in the extract, and therefore less DNA to concentrate.

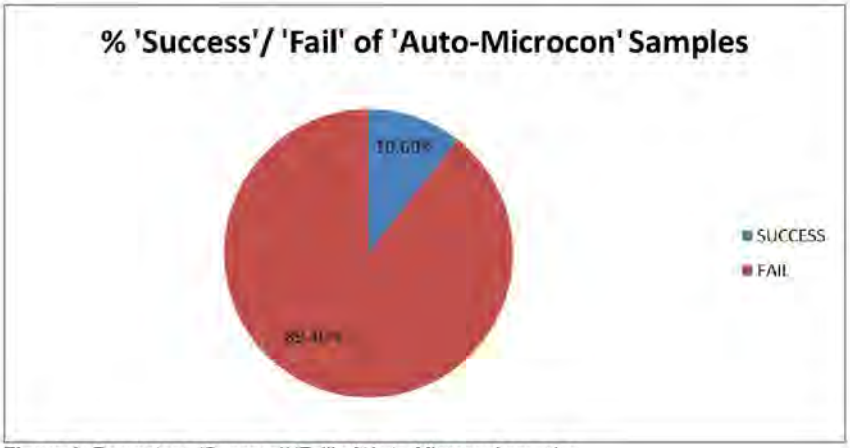

Figure 1: Percentage 'Success'/ 'Fail' of 'Auto-Microcon' samples.

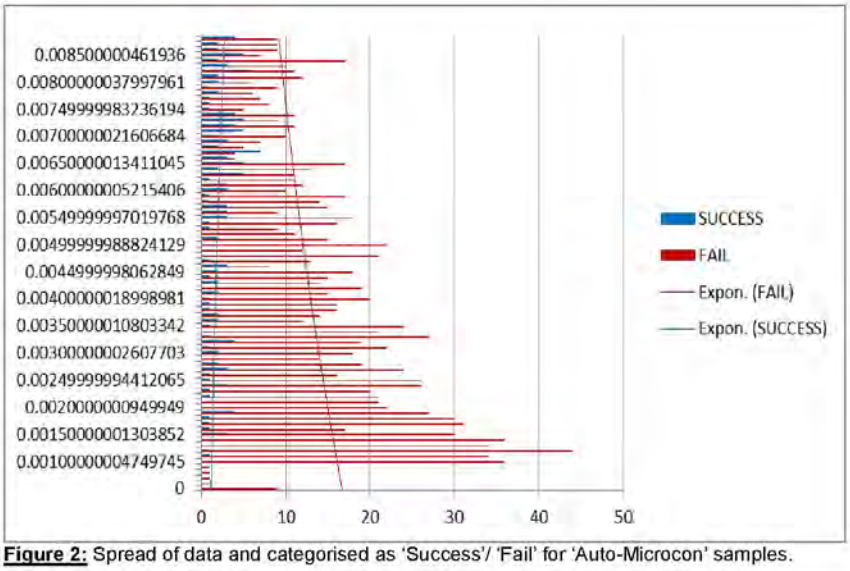

Figure 2: Spread of data and categorised as 'Success'/ 'Fail' for 'Auto-Microcon' samples.

In order to reach a DNA profile interpretation outcome of 'success', it was found that 74.7% of samples had an additional rework to the Microcon® process (Fig 3).

You are implying that "success" of automcon result is due to post mcon rework but the reworks are prob due to # of contrib. assessment No. contributors guidelines don't work for Auto-mic samples, but Rework section of report to be removed.

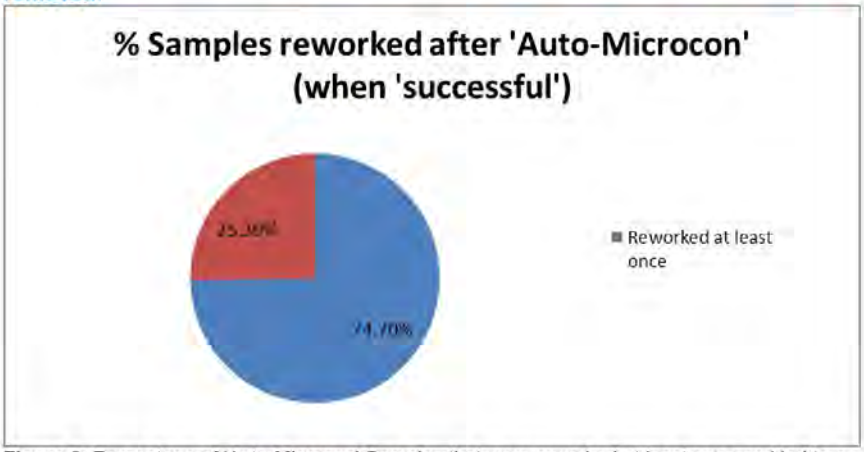

Figure 3: Percentage of 'Auto-Microcon' Samples that were reworked at least once and led to a 'successful' DNA profile outcome.

In putting the data behind Figures 2 and 3 together, if an 'auto-microcon' process was not conducted and was subsequently requested by the client for samples in this Quantification range, there would be approximately a 10% chance of obtaining a 'successful' DNA profile interpretation. Furthermore, in order to achieve that outcome, approximately 75%(this % may not be the case for vol crime under a model of "interp what you can with one amp". Highly likely that most of these reworks are to confirm No. of contrib. given the guidelines. See above.

of these 'successful' samples would have needed a further rework. This means, for these samples, there would be a turnaround time factor for the client to consider, and in a potential fee-for-service model with requesting clients, being prepared to have increased processing costs associated with these low-quant samples would be a client consideration.

If samples were not processed through the 'auto-microcon' process, what DNA Intelligence would the client miss out on? To evaluate this, the 'success' data was drilled down to the samples that had some NCIDD interaction and in particular, where they were the only samples in the case that were NCIDD-suitable for that particular profile (Fig 4). This represented 1.86% of all 'auto-microcon' samples. In looking at samples that provide *new* Intelligence, that is DNA information available for future linking, or has provided a cold-link, this equated to 1.45% of all 'auto-microcon' samples.True but only relevant for vol crime not major crime where LR's can be calculated. The definition of success here is only relevant for vol crime not major. Warm Links are captured here (LR profiles). All the data is based on Major crime samples.

This 1.45% of samples would be the pertinent value for the client to consider if the 'auto-microcon' process was not performed. In considering this, it would be important to evaluate the time and cost for processing, and the opportunity to concentrate efforts on other higher yielding samples. In saying this, with the ease of communication through the Forensic Register, these samples could process if the client has no other forensic Intelligence assisting the matter, or if the item is considered to be of critical priority.

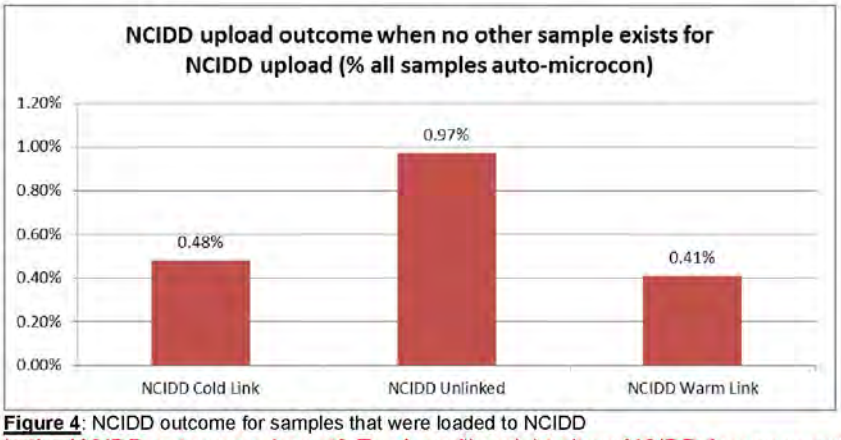

Figure 4: NCIDD outcome for samples that were loaded to NCIDD

Is the NCIDD outcome relevant? Eg. A profile might sit on NCIDD for years and not link

Ultimately, this data means that for approximately 90%(not sure how this is calculated? – this is the 89.4% value above) of samples that underwent an 'auto-microcon' process, there is arguably negligible DNA profile Intelligence for the client. If the 'auto-microcon' was not applied, there would be the following advantages, including but not limited to:

-the potential to make available at least 1449 processing positions for other samples including further available positions that would have been used for reworks,

-the lack of a need for the considerable efforts required to prepare and process Microcon® (and further rework) batches for this number of samples,

-consumable and labour savings in the end-to-end processing of these samples, and

-time and effort could be redirected in the laboratory workflow to other activities including service extensions like Y-STR profiling.

Only relevant if considering intel only samples. For major crime, we need to think about how many samples gave good LR's but no upload? Captured in warm link data.

6.2 Assessment of all DNA profile results from extracts that have had a concentration step.

All samples from 2016 that had a Microcon® process were determined. The total number of samples was N= 2201 samples, excluding certain samples as per Section 5.1.

The percentage of samples that resulted in a determination of 'fail' was 78.5% (see Fig 5). As expected, in looking at the spread of the 'combined' data, the number of 'successes' increased when the Quantification increased (Fig 6).

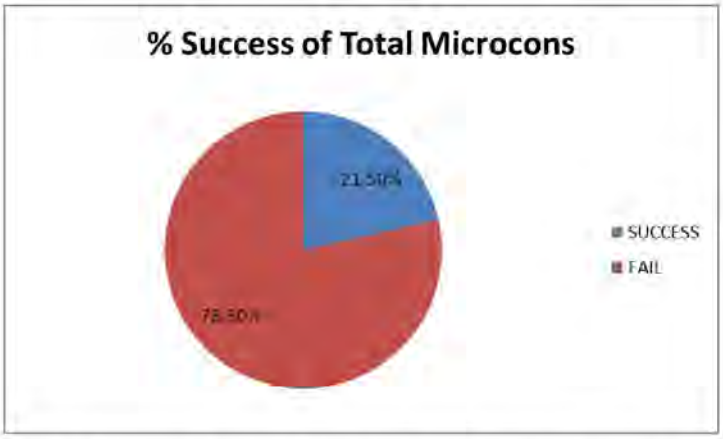

Figure 5: Percentage 'Success'/ 'Fail' of all Microcon® samples ('combined' data).

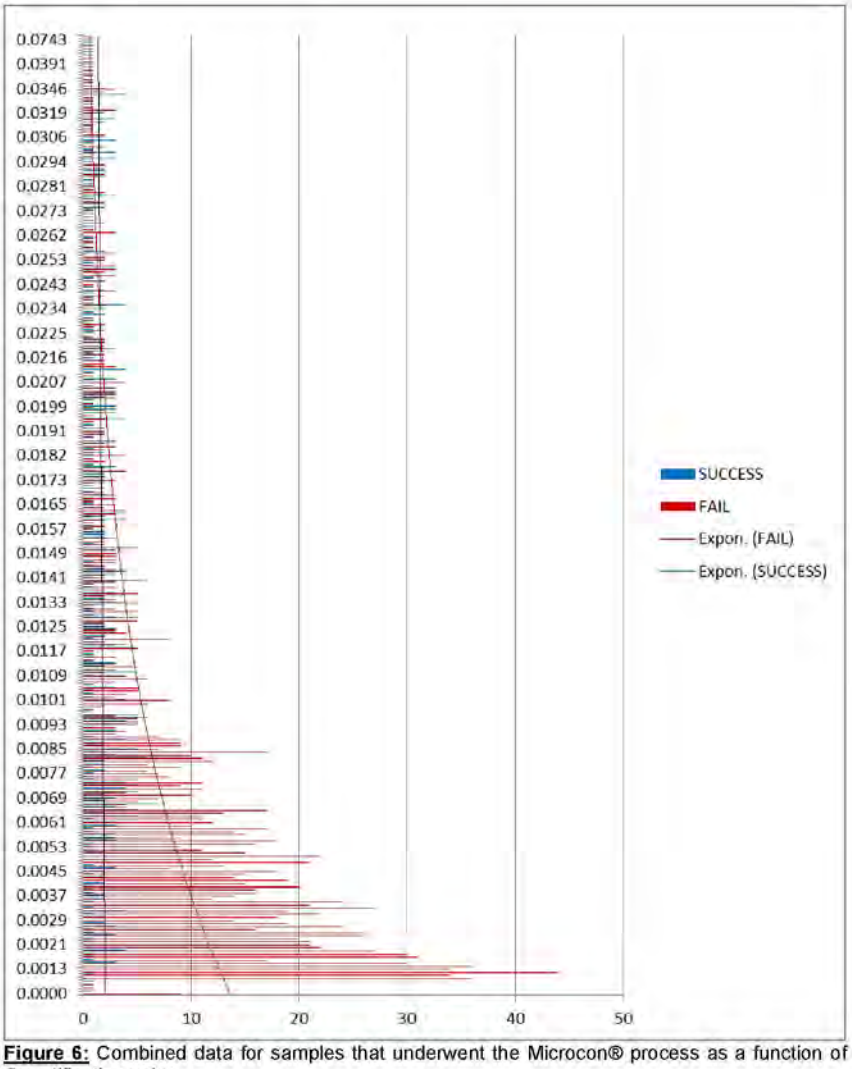

Figure 6: Combined data for samples that underwent the Microcon® process as a function of Quantification value.

As mentioned in Section 5.2, the Quantification value where there was roughly the same number of 'success' and 'fail' samples was approximately 0.02ng/uL. It must be noted that this is a rough estimate *at this* particular Quantification value, and it is based on limited samples that returned that Quantification value. It can be argued that taking a range of Quantification values to look at the overall success/fail percentages could provide the client with approximate likelihoods of obtaining meaningful DNA Intelligence.

A number of ranges were looked at to determine the percentage 'success' of samples with Quantification values in various ranges (Fig 7). The ranges were established up to the highest Quantification value of 0.02ng/uL. As expected, the percentage 'success' increased as the Quantification increased due to the higher amount of DNA in the extract available to be concentrated.

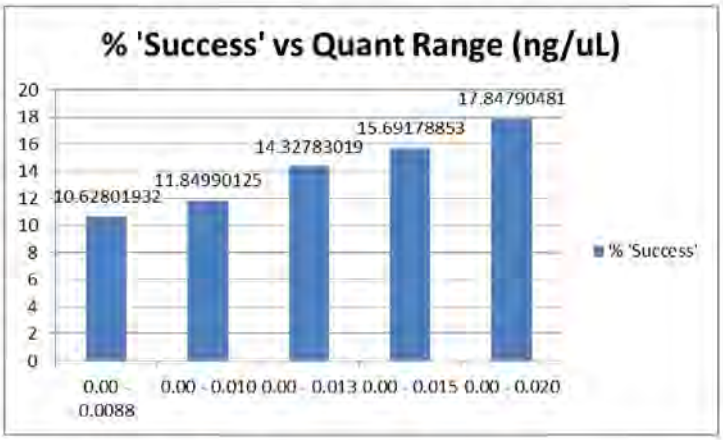

Figure 7: Percentage 'success' for samples that underwent a Microcon® process

In viewing the data in Fig 7, a limitation is that all samples that fell in the 'auto-microcon' range, had a Microcon® process performed, whereas there are samples that are in higher Quantification ranges that might not have required a Microcon® concentration rework step to yield useful DNA profiles. These samples were not evaluated.

A lower Quantification value to where the number of 'successes' roughly equalled the 'failures' was chosen to be the upper end of data ranges that were evaluated further. The value chosen was 0.015ng/uL. Table 1 and Figure 8 describe the risk to NCIDD upload for samples in these ranges if Microcon® concentration steps were not performed.

Table 1: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

	% No other samples to Upload in Quantification ranges (Q)		
	Q = 0.00ng/uL to 0.01ng/uL (total samples in range = 1519)	Q = 0.00ng/uL to 0.0133ng/uL (total samples in range = 1696)	Q = 0.00ng/uL to 0.015ng/uL (total samples in range = 1778)
NCIDD Cold link	0.92	0.88	1.01
NCIDD Unlinked	0.53	0.77	1.24
NCIDD Warm Link	0.46	0.83	0.90

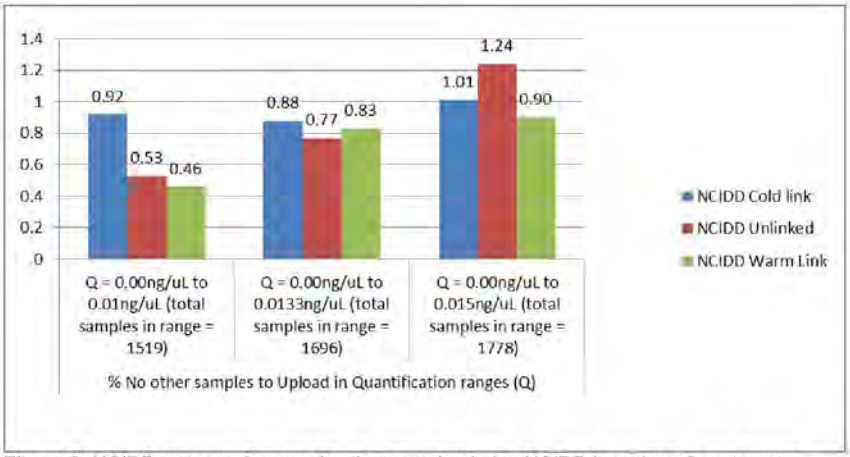

Figure 8: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

Approximately 1.45% of samples in the Quantification range up to 0.01ng/uL resulted in 'new' DNA Intelligence. This percentage is the same as that found in the 'auto-microcon' range. This percentage increased to 1.65% and 2.25% for the Quantification ranges up to 0.0133ng/uL and 0.015ng/uL respectively.
This is because most of the data was from the automcon range, the data added from 0.0088 – 0.01 would not change the outcome (the data shouldn't be combined)
For eg. 0.001-0.0088 – say there is 1000 samples in this set with 1.45% success Versus 0.0088-0.01 – say there is 10 samples in this set with 10% success. Because the first set is so huge, adding the second set will only slightly change the outcome
Being re-evaluated in v2.

The number of further reworks required to obtain 'success' outcomes decreased as the Quantification increased. This is not unexpected given higher DNA yields detected would not necessarily require as many reworks in order to yield DNA profiles.

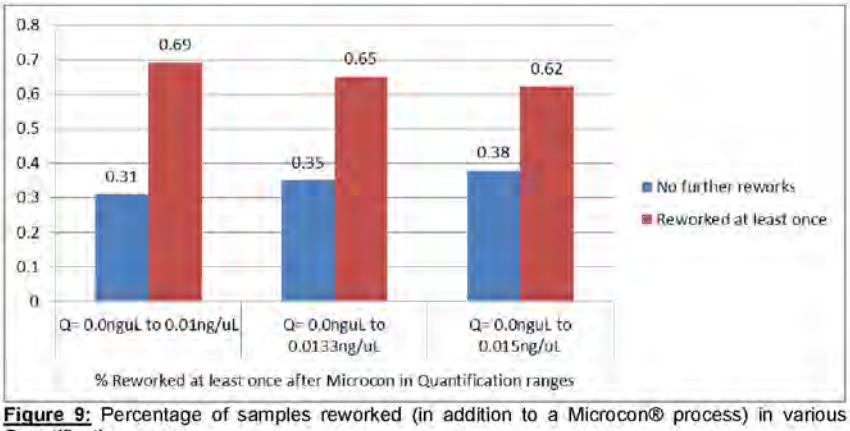

Figure 9: Percentage of samples reworked (in addition to a Microcon® process) in various Quantification ranges.

6.3 Datamine of the difference in pre- and post- Microcon® Quantification values

The samples applicable to this experiment had Quantification values above 0.001ng/μL where the final result was 'success'. The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/μL and 0.015ng/μL were examined.

As the Microcon® process concentrates the DNA extract from approximately 100uL to approximately 35uL, in theory it would be a reasonable expectation to obtain approximately two to three-fold increases in DNA Quantification after concentration. Figure 10 shows the plot of the differences found for samples that resulted in 'success'.

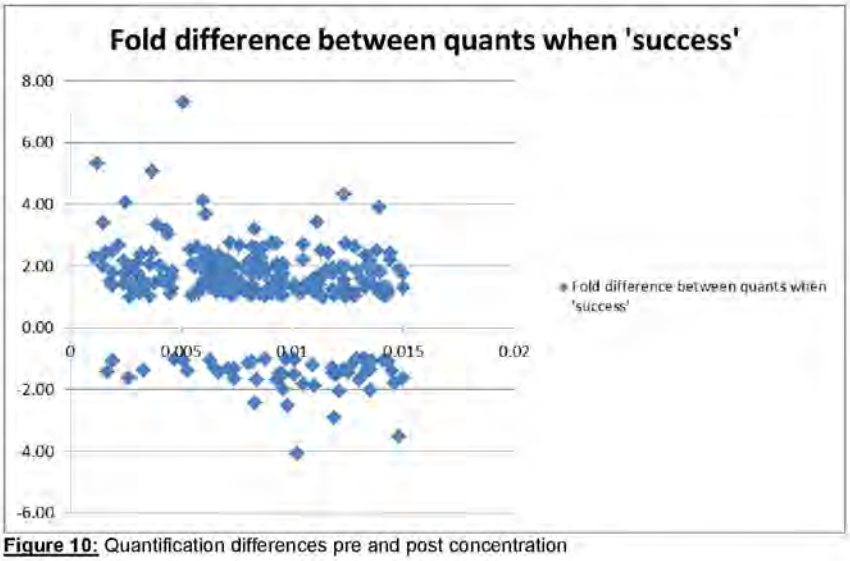

Figure 10: Quantification differences pre and post concentration

The findings are not unexpected as the scatter focusses mostly around two-fold increases in Quantification. It was also not unexpected to observe the variable results. Anecdotally, variability in success rates is found at profile management stage when assessing results of samples that have had this concentration step.

DNA can be lost in the process as seen in Fig 10 where the Quantification values decreased after concentration. Variability in results could be attributed to a number of things, including but not limited to the slight differences between operators and instrumentation, the differences in substrate type and level of degradation, and the variability in Quantification result.

8.7. Conclusion and Recommendations

The data analysis demonstrated that there was arguably minimal value in performing the 'auto-microcon' concentration step. This opinion was formed by analysing the data from 2016 where it was found that for all samples that underwent the 'auto-microcon' step, 89% did not yield meaningful results.

It was found that in considering all samples that underwent a Microcon® step at some stage in 2016, 78.5% did not yield meaningful results. As expected, when the Quantification value increased, the percentage of meaningful results increased. However, it was also demonstrated in the data analysis that the Quantification values did not always improve after Microcon®, but where they

did, the magnitude of change was roughly equivalent to the change in volume (from neat to concentrated sample).

Based on the data analysis, the following recommendations are offered:

1. Cease 'auto-microcon' processing with the following exceptions:
   a. Priority 1 samples (Critical Priority); and

   b. Coronial/DVI samples where profiles are mostly single-source and quite often incomplete profiles may be enough to provide Intelligence on possible identity.

   c. P2 samples (pending recommendation 4)

2. Cease processing all Priority 3 samples up to the Quantification value of 0.0133ng/uL (template of 200ng).
   Before choosing this value, we should assess data from 0.0088-0.0133 independently from data from 0.001-0.0088 to fully investigate the merits of choosing this value
   Have re-evaluated ranges.

3. For samples in the range described in Recommendation 2, automatically send result information via the Forensic Register to QPS at Quantification stage. This result information is recommended to be the exhibit result line of 'DNA Insufficient for Further Processing'. This recommendation is an extension to the current 'No DNA Detected' process, which looks at Priority 2 samples yielding Quantification results of less than the Limit of Detection.

4. Re-analyse Priority 2 samples in the range 0.0088ng/uL to 0.0133ng/uL after a six month period of processing to evaluate whether Recommendation 2 can be extended to Priority 2 samples – using non intel criteria to assess the results.
   Have re-evaluated ranges.

5. Communicate the change in process to QPS and ensure that QPS are aware that for samples in the ranges mentioned in Recommendations 1 and 2, that they could be requested for Microcon® concentration steps at any point in time. This request can be made via the Forensic Register after they have received the 'DNA insufficient…' result line.

   Overall, I think this idea is good. I guess my concern being that this data and analysis has been done on a certain set of samples and then trying to use this to extrapolate to future processes when we don't know what interp rules there will be for vol crime in PP21 etc.… ie comparing apples with oranges in a way.

~~7.~~8. References

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[1] QIS 19544v11 – Concentration of DNA Extracts Using Microcon Centrifugal Filter Devices

[2] PowerPlex® 21– Amplification of Extracted DNA Validation. Megan Mathieson, Thomas Nurthen, Cathie Allen. December 2012. Forensic DNA Analysis.

[3] Project #163 - Assessment of results obtained from 'automatic-microcon' samples. Josie Entwistle, Allison Lloyd, Kylie Rika, Thomas Nurthen, Cathie Allen. August 2015. Forensic DNA Analysis.



Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

January 2018

Justin Howes and Cathie Allen

Great state. Great opportunity.

Queensland Government

Project Proposal #184 Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

Published by the State of Queensland (Queensland Health), November 2017

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1. Abstract

All samples that underwent a Microcon® process were evaluated and categorised into whether there was meaningful information obtained or not. This evaluation primarily focussed on samples that underwent an 'auto-microcon' process in 2016. The results suggest there to be arguably minimal value in performing the 'auto-microcon' process due to the limited meaningful DNA Intelligence obtained from these samples. Given this, further streamlining of workflow processes could be implemented that would provide significant efficiencies such that these efforts could be better placed in processing higher DNA-yielding samples.

Given the short TAT for feedback, the Reporting 5's have combined their final feedback. Specific feedback can be found throughout the body of this document, but the combined general feedback is:

1. Can appreciate the value in streamlining processes, but concerned that data for P2 samples is being used to extrapolate for P3 results that we don't yet have interp/processing rules around.
2. Should we be extrapolating around results at all? No one ever really knows what result will be obtained from a particular sample – it has to be tested for the 'true' result to be revealed. It is a false economy to analyse result that give 'assumed known contributor' and retrospectively ascribe them nil value, as the samples are taken and submitted to see whether or not there is 'foreign' DNA present... having said this, the 'value' of each result changes according to the specific sample/case history. Not confident about removing a test that we know does have some value.
3. Note that there seems to be urgency around this proposal being implemented, which might not allow time for full consideration of all potential risks/impacts. For this reason, is it possible to just implement for P3 samples, and revisit in 3 months for viability of extension to P2 samples (see recommendations). Concerned that trying to use P2 results (with one set of interp outcomes and purpose) to forecast for P3 results (with another set of interp outcomes and purpose) is confusing, and combined with the haste, we may miss something. For example, P2 sample goes through auto-mic and gives a partial profile that doesn't match POI could provides important exclusionary intelligence for the case – have we considered the exclusionary benefits appropriately under this proposal?

2. Definitions

DNA Profile Intelligence: DNA profile information available for interpretation by Forensic DNA practitioners that is able to be provided to clients.

Fail: In this report, this is DNA profile information that was not suitable for comparing to reference DNA profiles. This word was used to filter the data into two possible outcomes (fail/success).

NCIDD: National Criminal Investigation DNA Database.

QPS: Queensland Police Service.

Success: In this report, this is DNA profile information that was obtained that was suitable for comparing to reference DNA profiles. This word was used to filter the data into two possible outcomes (fail/success).

3. Introduction

Microcon® Centrifugal Filter Devices desalt and concentrate macromolecular solutions such as DNA-containing solutions. They employ Amicon's low binding, anisotropic, hydrophilic regenerated cellulose membrane [1].

The use of Microcon® filters to concentrate extract has been a standard post-extraction process within Forensic DNA Analysis to reduce the volume of extract from approximately 100uL to ≤20μL for amplification with AmpFℓSTR® Profiler Plus®, and to ≤35μL for amplification with PowerPlex® 21 system (PP21).

Since the implementation of PP21 amplification kit within Forensic DNA Analysis for casework samples in December 2012, extracts with low Quantification values were recommended to be concentrated. Templates of <0.132ng were found to exhibit marked stochastic effects after amplification [2]. Consequently, a workflow that directed extracts automatically to a concentration step based on Quantification value was implemented ('auto-microcon' process).

Anecdotally, the suitability to provide QPS with DNA profile Intelligence from extracts that have been concentrated has been noted to be limited. Furthermore, extracts that are of low quant value that have been automatically concentrated have been observed to rarely yield DNA information for QPS.

NB. Project #163 – *Assessment of results obtained from 'automatic-microcon' samples* [3] was conducted to evaluate the results of samples that were processed with the 'auto-microcon' process. A recommendation of this project was to re-evaluate after the introduction of the Forensic Register in conjunction with the use of Quantifiler® Trio DNA Quantification Kit.

This recommendation was based on the perceived ease of retrieving data from the FR as opposed to AUSLAB, and with the thought that the FR would soon be implemented. For the purposes of this project, it is not considered essential to have the FR implemented if the data can be retrieved from AUSLAB. However, it is considered important that the data be spanning a sufficient period of

processing, and be based on the same Quantification system namely the Quantifiler® Trio DNA Quantification Kit.

The purpose of this project is to evaluate the suitability for interpretation of DNA profiles that may be obtained after the post-extraction concentration step using the Microcon® centrifugal filter devices. This evaluation includes an assessment of those samples that underwent the 'auto-microcon' process. This evaluation is based on a data mine of extracts in the year 2016 that were concentrated with Microcon® centrifugal filter devices, and assesses the 'suitability' of PP21 profile outcomes as a function of quant values obtained from using the Quantifiler® Trio DNA Quantification Kit.

This evaluation looks at two data sets as a function of the Quantification value:

1. PP21 DNA profile outcomes from extracts that were processed through the 'auto-microcon' process;

2. PP21 DNA profile outcomes from all extracts that were concentrated with the Microcon® filter devices.

~~3.~~4. Resources

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The following resources were required for this validation/project:

Forensic DNA Analysis staff and computer time to retrieve data from AUSLAB and to use Microsoft Excel.

~~4.~~5. Methods

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~~4.1.~~5.1. Data retrieval from AUSLAB (LIMS)

Data was retrieved from AUSLAB using Extended Enquiries. Data was searched for samples that had a testcode of 'XPLEX' and 'MCONC1' ordered in the year 2016 in Forensic DNA Analysis. These were High Priority (P2) samples.

The data was output with the corresponding Quantification value and the reported DNA profile interpretation (Exhibit Report Line in the Exhibit Report (EXH)) for that particular barcode. If the barcode was a sub-sample, the corresponding EXH line for the sub-sample was output.

For ease of data interrogation, the RAW data (I:\Change Management\Proposal#184 - Evaluation of the efficacy of Microcons\Data\RAW Data from AUSLAB) had a column added to describe whether the sample underwent the 'auto-microcon' process ('AUTO' = 0.001ng/μL<Quant <0.0088ng/μL) or not ('MANUAL' = Quant >0.0088ng/μL). Another column was added to describe whether there was a Quantification value returned in the data collation ('TRUE' = Quant value obtained), or not ('FALSE' = no Quant value obtained (ie. 0 ng/μL).

The data excluded samples that had not returned a DNA profile result, Quality samples (including environmental monitoring samples), have no quant value in the data export, or have quality issues noted.

5.2. Data interrogation

The data was interrogated by assessing the DNA profile outcome results reported as Exhibit Report lines as a function of the Quantification value.

The Exhibit lines were interrogated and grouped into two interpretation outcomes as follows:

1. 'Fail': DNA profile interpretation outcomes of 'Complex unsuitable for interpretation', 'No DNA profile', 'Partial unsuitable for interpretation', 'No DNA Detected';

2. 'Success': All other DNA profile outcomes including single source DNA profiles matching assumed known contributors or different reference DNA profiles, mixtures that were suitable for comparison to reference DNA profiles, DNA profiles that were suitable for loading to NCIDD.

NB. These descriptions were used to filter the data. A 'fail' does not mean there was a Quality failure in the process; a 'success' does not necessarily mean a DNA match.

~~5.~~6. Experimental Design

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~~5.1.~~6.1. Experiment 1: Assessment of 'auto-microcon' results

Intent

Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 through the 'auto-microcon' workflow.

Data Analysis
The samples applicable to this experiment had Quantification values in the range 0.001ng/µL to 0.0088ng/µL, and a total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value. A percentage of samples that fell into these categories was determined.

The 'auto-microcon' data could be expressed as a function of Quantification value.

The percentage of samples that had an 'auto-microcon' process and led to an NCIDD upload was obtained. This data could be filtered further into the outcome from the NCIDD load, at the time of data collection.

Data on the DNA profile outcomes for various suspected biological types was obtained. Furthermore, data on the profile outcomes for various substrate types was obtained.

~~7.2.~~6.2. Experiment 2: Assessment of all DNA profile results from extracts that have had a concentration step.

Intent
Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 and underwent a post-extraction concentration step using Microcon® centrifugal filter devices.

Data Analysis

The samples that were applicable to this experiment had Quantification values above 0.001ng/µL, and underwent the Microcon® process. This included the 'auto-microcon' samples, and those that had a Microcon® rework performed (termed 'manual'). This combination of data was termed 'combined data'.

A total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags

were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value.

The percentage of samples that fell into these categories ('manual' and 'combined') was determined. 'Manual' referred to the samples beyond the 'auto-microcon' range that were reworked with the Microcon® process, and 'combined' referred to all samples ('auto-microcon' and 'manual').

There was a point where the number of 'success' samples was approximately the same as the number of 'fail' samples when the Microcon® process was performed. This appeared to be approximately Quant = 0.02ng/uL. Therefore, the data was interrogated further at a Quantification value lower than this mark to determine what percentage of samples in certain ranges led to DNA profile interpretation outcomes of 'success'.

From this data, a sub-section of samples was interrogated further to evaluate the effect on DNA Intelligence that was obtained. A range of samples with Quantification range up to 0.015ng/uL was chosen and a total number of samples was determined. This Quantification value was chosen as it was the approximate value where all samples below this value that underwent a Microcon® process, led to an approximate, round figure of 85% 'failure'.

The percentage of samples that were in this Quantification range and led to an NCIDD upload was determined. This data could be filtered further into the outcome from the NCIDD load. This data could then be used to evaluate the potential for samples to not provide meaningful DNA Intelligence to QPS if the Microcon® process was re-defined in some way. By 'meaningful DNA Intelligence', this means DNA profile information that can be provided to the client that could lead to an identification of a person potentially associated to the alleged matter.

6.3. Experiment 3: Datamine of the difference in pre- and post-Microcon® Quantification values

Intent
Evaluate the difference between the values obtained from the Quantification process in samples that have had a Microcon® concentration step applied.

As this is purely a datamining experiment, only the samples that have yielded a result of 'success' was examined.

Data Analysis

The samples applicable to this experiment had Quantification values above 0.001ng/μL where the final result was 'success'.

The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/μL and 0.015ng/μL were examined.

This range was considered by the author to be able to provide a sufficient demonstration of the trend of the data.

6.7. Results and Discussion

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7.1 Assessment of 'auto-microcon' results

For samples in the 'auto-microcon' Quantification range, the total number of samples that were processed this way (excluding certain samples as per Section 5.1) was N= 1449 samples.

The percentage of samples that resulted in a determination of 'fail' was 89.4% (Fig 1). As expected, the number of 'fails' increased when the Quantification decreased and approached the Limit of Detection of Quantification ie. 0.001ng/uL (Fig 2). This was considered to be due to there being less DNA detected in the extract, and therefore less DNA to concentrate.

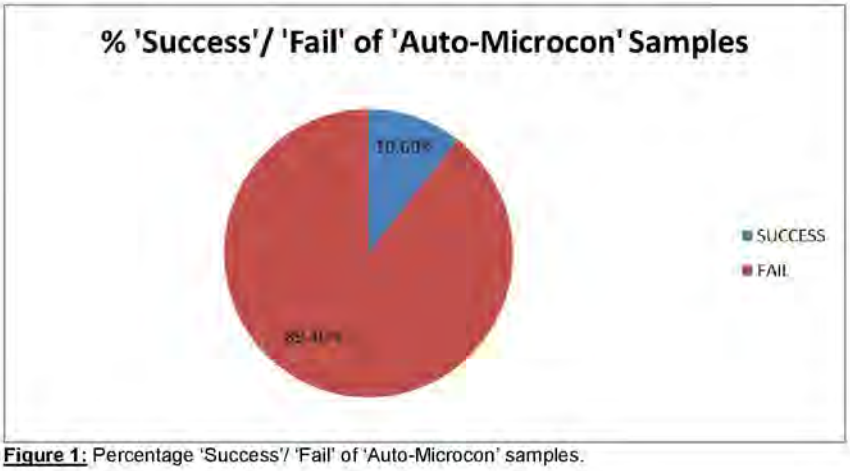

Figure 1: Percentage 'Success'/ 'Fail' of 'Auto-Microcon' samples.

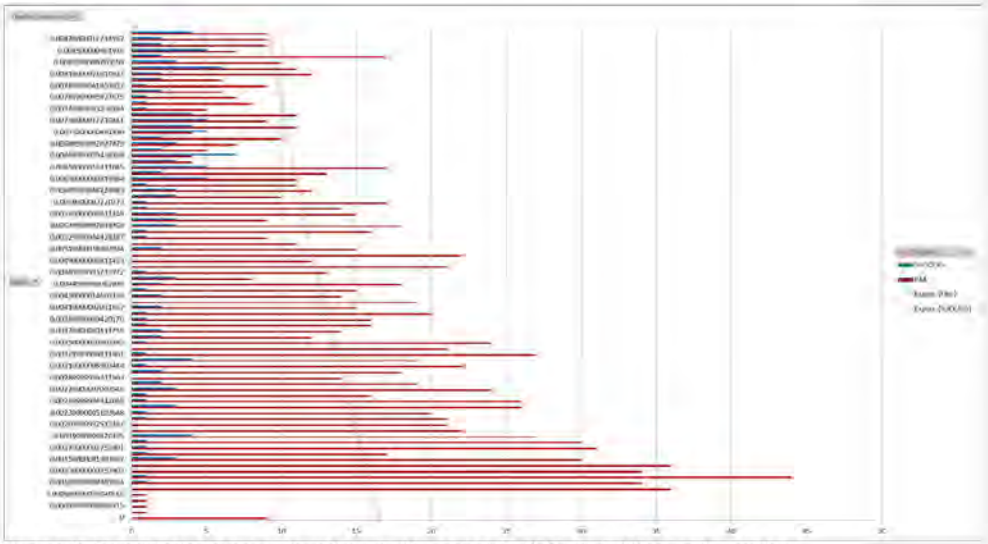

Figure 2: Spread of data and categorised as 'Success'/ 'Fail' for 'Auto-Microcon' samples.

If samples were not processed through the 'auto-microcon' process, what DNA Intelligence would the client miss out on? To evaluate this, the 'success' data was drilled down to the samples that had some NCIDD interaction and in particular, where they were the only samples in the case that were NCIDD-suitable for that particular profile (Fig 3). This represented 1.86% of all 'auto-microcon' samples. In looking at samples that provide *new* Intelligence, that is DNA information available for future linking, or has provided a cold-link, this equated to 1.45% of all 'auto-microcon' samples.

This 1.45% of samples would be the pertinent value for the client to consider if the 'auto-microcon' process was not performed. In considering this, it would be important to evaluate the time and cost for processing, and the opportunity to concentrate efforts on other higher yielding samples. In saying this, with the ease of communication through the Forensic Register, these samples could process if the client has no other Forensic Intelligence assisting the matter, or if the item is considered to be of critical priority.

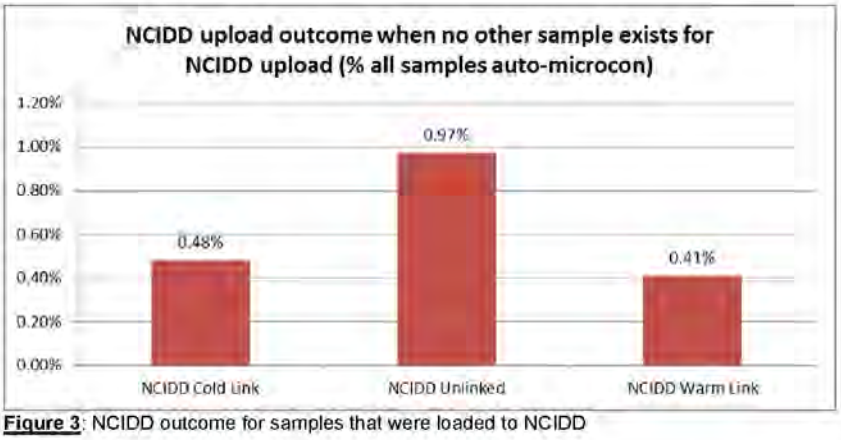

Figure 3: NCIDD outcome for samples that were loaded to NCIDD

The 'success' data was further evaluated to see if any particular substrate type or possible biological source, was more likely to lead to meaningful interpretations after an 'auto-microcon'. The data set for this evaluation was N=154 samples. These samples were broken down into three general interpretation outcomes:

- Profiles matching assumed known contributors. These were either single source DNA profiles, or mixed DNA profiles where the profile was conditioned with no information available for comparison in the remaining contribution (ie. peaks visible sub-threshold or the profile has allelic imbalance suggesting a mixture);

- Single source. These were DNA profiles that were attributed to unknowns, or matched reference DNA profiles, or were from items where ownership could not be confirmed; and,

- Mixtures where no statistical interpretation (NSIP) was performed or were suitable for comparison to reference DNA profiles for Likelihood Ratio (LR) purposes.

Figures 4 displays the DNA profile outcome as a function of the possible biological type, and Figure 5 displays the DNA profile outcome as a function of the substrate.

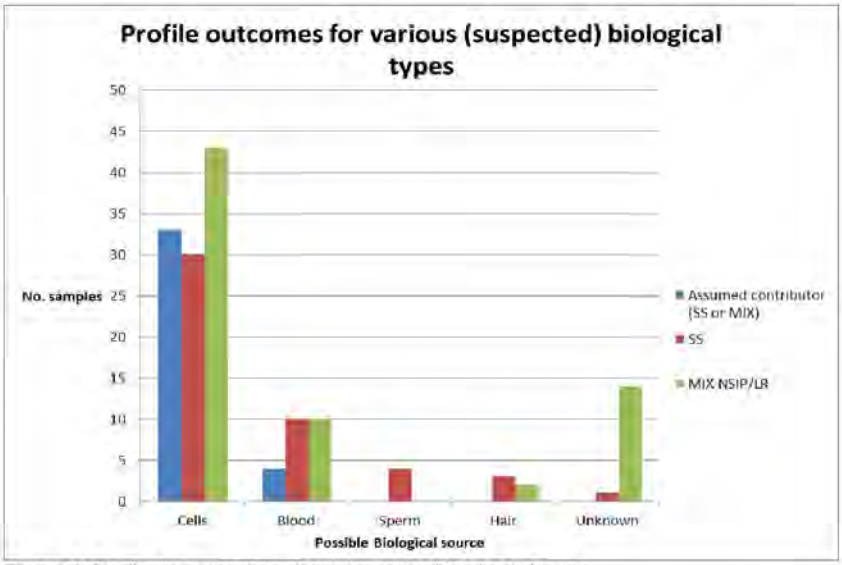

Figure 4: Profile outcomes for various (suspected) biological types

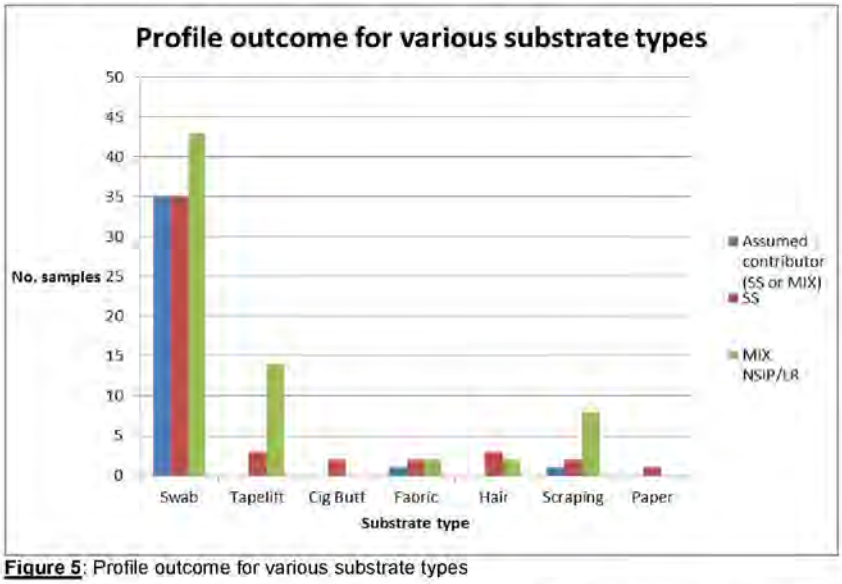

Figure 5: Profile outcome for various substrate types

Figures 4 and 5 show that there do not appear to be any obvious trends in the data. It is not unexpected to have a variety of DNA profile outcomes for different biological source types, and not unexpected for a variety of DNA profile outcomes for different substrate types. Interestingly, the number of 'assumed known contributors' is almost one-third of DNA profile outcomes for the most numerous suspected biological type (cells), and substrate type (swab). It could

be argued that this DNA profile outcome is not meaningful to the client as the results are not unexpected.

What this means is that if the client requested a Microcon® process on a particular sample that was initially in the 'auto-microcon' Quantification range, there does not appear to be a predictive element to the likely success of the microcon rework for a particular biological source type, nor substrate type.

Ultimately, for approximately 90% of samples that underwent an 'auto-microcon' process, there is arguably negligible DNA profile Intelligence for the client. If the 'auto-microcon' was not applied as a streamlining strategy, there would be the following advantages, including but not limited to:

-the potential to make available at least 1449 processing positions for other samples including further available positions that would have been used for reworks. It must be noted that it is not unusual for low-quantification samples to reworked further before determining if the profile is suitable for comparison to reference DNA profiles.

-the lack of a need for the considerable efforts required to prepare and process Microcon® (and further rework) batches for this number of samples,

-consumable and labour savings in the end-to-end processing of these samples, and

-time and effort could be redirected in the laboratory workflow to other activities including service extensions like Y-STR profiling.

7.2 Assessment of all DNA profile results from extracts that have had a concentration step.

All samples from 2016 that had a Microcon® process were determined. The total number of samples was N= 2201 samples, excluding certain samples as per Section 5.1.

The percentage of samples that resulted in a determination of 'fail' was 78.5% (see Fig 6). As expected, in looking at the spread of the 'combined' data, the number of 'successes' increased when the Quantification increased (Fig 7).

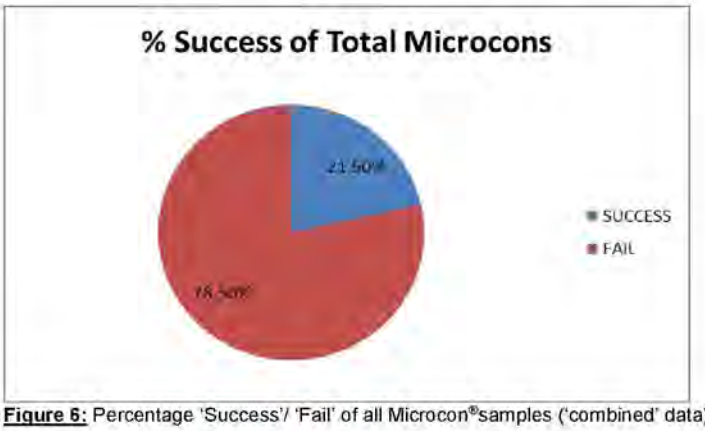

Figure 6: Percentage 'Success'/ 'Fail' of all Microcon®samples ('combined' data).

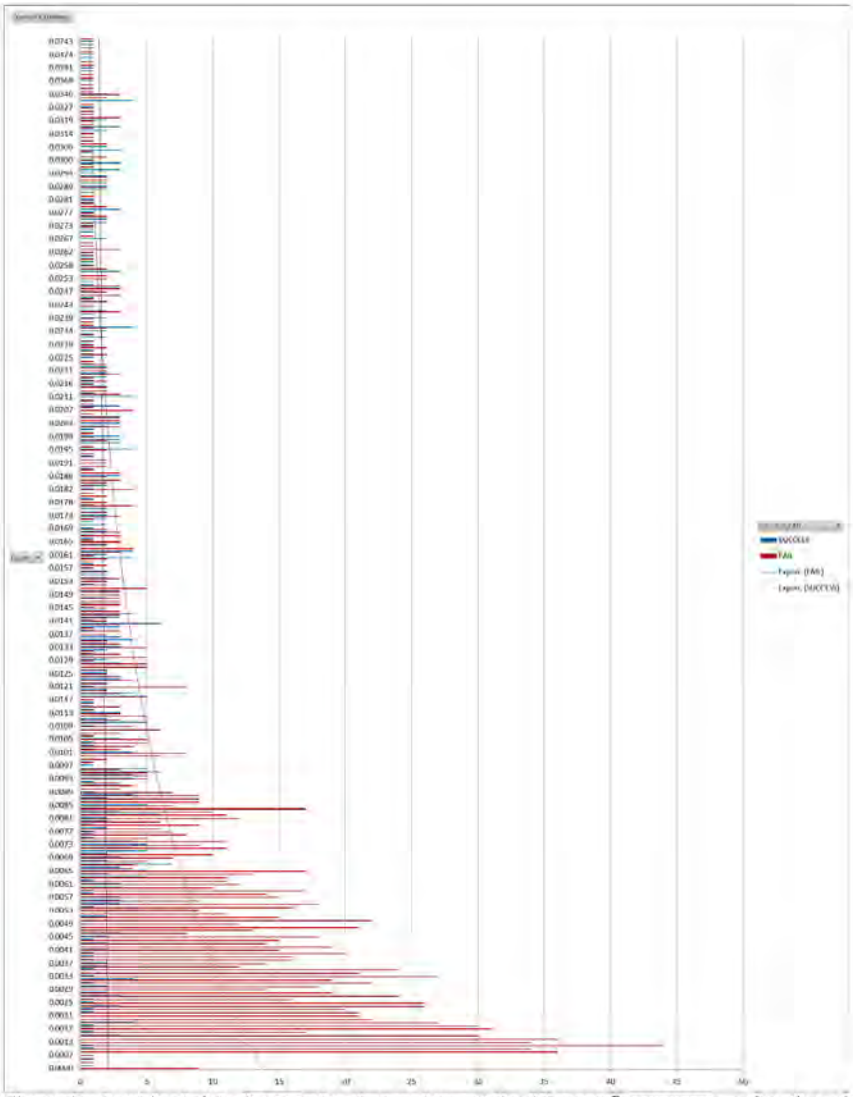

Figure 7: Combined data for samples that underwent the Microcon® process as a function of Quantification value.

As mentioned in Section 5.2, the Quantification value where there was roughly the same number of 'success' and 'fail' samples was approximately 0.02ng/uL. It must be noted that this is a rough estimate *at this* particular Quantification value, and it is based on limited samples that returned that Quantification value. It can be argued that taking a range of Quantification values to look at the overall success/fail percentages could provide the client with approximate likelihoods of obtaining meaningful DNA Intelligence.

A number of ranges were looked at to determine the percentage 'success' of samples with Quantification values in various ranges (Fig 8). The ranges were established up to the highest Quantification value of 0.02ng/uL. As expected, the percentage 'success' increased as the Quantification increased due to the higher amount of DNA in the extract available to be concentrated.

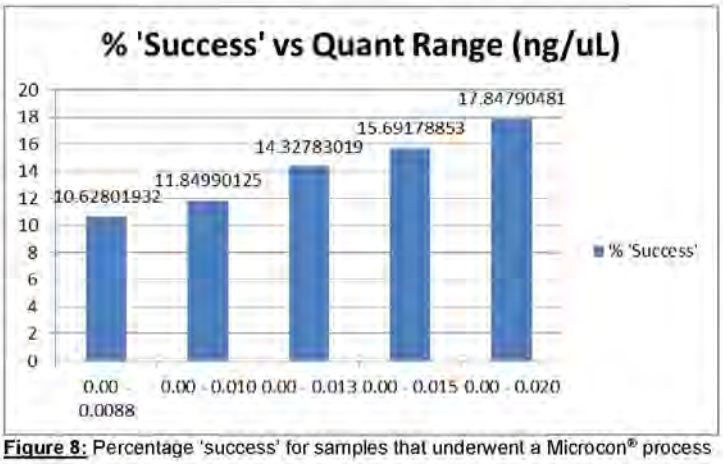

Figure 8: Percentage 'success' for samples that underwent a Microcon® process

In viewing the data in Fig 8, a limitation is that all samples that fell in the 'auto-microcon' range, had a Microcon® process performed, whereas there are samples that are in higher Quantification ranges that might not have required a Microcon® concentration rework step to yield useful DNA profiles. These samples were not evaluated.

A lower Quantification value to where the number of 'successes' roughly equalled the 'failures' was chosen to be the upper end of data ranges that were evaluated further. The value chosen was 0.015ng/uL. Table 1 and Figure 9 describe the risk to NCIDD upload for samples in these ranges if Microcon® concentration steps were not performed.

Table 1: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

	% No other samples to Upload in Quantification ranges (Q)		
	Q = 0.00ng/uL to 0.01ng/uL (total samples in range = 1519)	Q = 0.00ng/uL to 0.0133ng/uL (total samples in range = 1696)	Q = 0.00ng/uL to 0.015ng/uL (total samples in range = 1778)
NCIDD Cold link	0.92	0.88	1.01
NCIDD Unlinked	0.53	0.77	1.24
NCIDD Warm Link	0.46	0.83	0.90

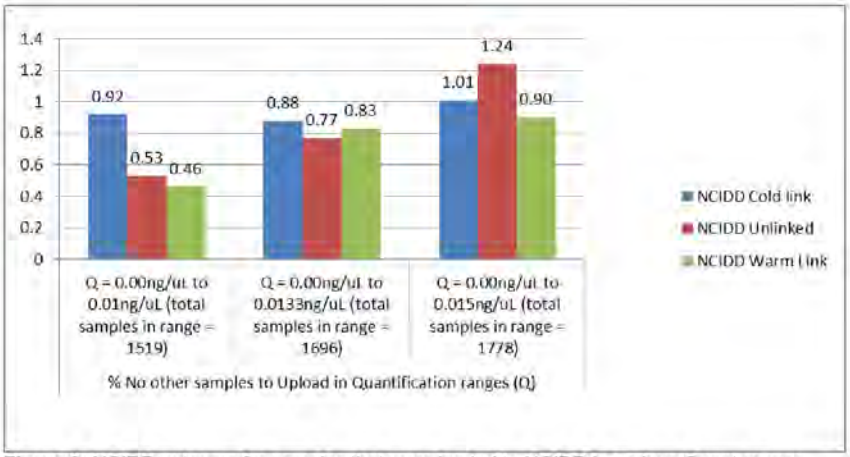

Figure 9: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

Approximately 1.45% of samples in the Quantification range up to 0.01ng/uL resulted in 'new' DNA Intelligence. This percentage is the same as that found in the 'auto-microcon' range. This percentage increased to 1.65% and 2.25% for the Quantification ranges up to 0.0133ng/uL and 0.015ng/uL respectively.

7.3 Datamine of the difference in pre- and post- Microcon® Quantification values

The samples applicable to this experiment had Quantification values above 0.001ng/μL where the final result was 'success'. The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/μL and 0.015ng/μL were examined.

As the Microcon® process concentrates the DNA extract from approximately 100uL to approximately 35uL, in theory it would be a reasonable expectation to obtain approximately two to three-fold increases in DNA Quantification after

concentration. Figure 10 shows the plot of the differences found for samples that resulted in 'success'.

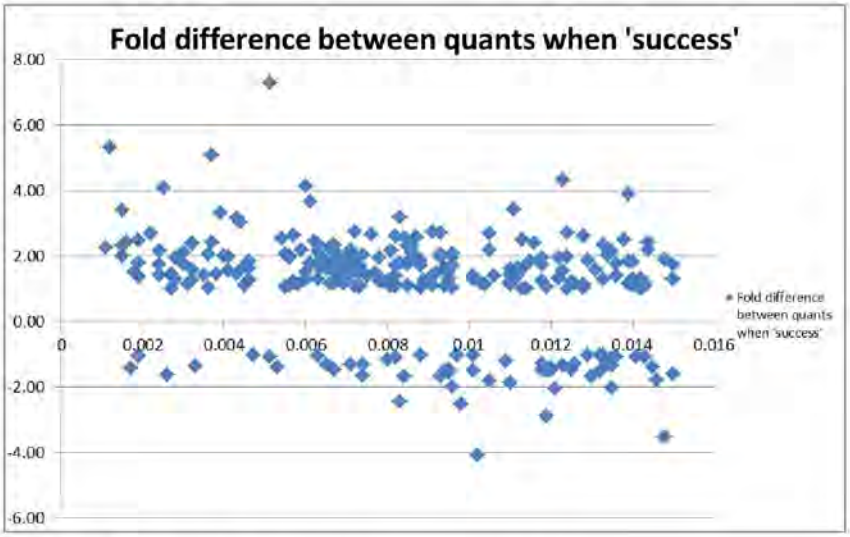

Figure 10: Quantification differences pre and post concentration

The findings are not unexpected as the scatter focusses mostly around two-fold increases in Quantification. It was also not unexpected to observe the variable results. Anecdotally, variability in success rates is found at profile management stage when assessing results of samples that have had this concentration step.

DNA can be lost in the process as seen in Fig 10 where the Quantification values decreased after concentration. Variability in results could be attributed to a number of things, including but not limited to the slight differences between operators and instrumentation, the differences in substrate type and level of degradation, and the variability in Quantification result.

~~9.~~8. Conclusion and Recommendations

The data analysis demonstrated that there was arguably minimal value in performing the 'auto-microcon' concentration step. This opinion was formed by analysing the data from 2016 where it was found that for all samples that underwent the 'auto-microcon' step, 89% did not yield results suitable for meaningful interpretation (or 'success' in this report).

It was found that in considering *all* samples that underwent a Microcon® step at some stage in 2016, 78.5% did not yield results suitable for meaningful interpretation. As expected, when the Quantification value increased, the percentage of meaningful results increased. However, it was also demonstrated in the data analysis that the Quantification values did not always improve after Microcon®, but where they did, the magnitude of change was roughly equivalent to the change in volume (from neat to concentrated sample).

Based on the data analysis, the following recommendations are offered:

~~1.~~ Cease 'auto-microcon' (Quant range: 0.001ng/uL to 0.0088ng/uL) processing for all P3 samples ~~with the following exceptions:~~

   ~~a. Priority 1 samples (Critical Priority); and~~

   ~~b. Coronial/DVI samples where profiles are mostly single-source. Quite often incomplete profiles may be enough to provide Intelligence on possible identity.~~

2. Automatically send result information via the Forensic Register to QPS at Quantification stage for samples in the Quant range: 0.001ng/uL to 0.0088ng/uL. This result information is recommended to be the exhibit result line of 'DNA Insufficient for Further Processing'. This recommendation is an extension to the current 'No DNA Detected' process, which looks at Priority 2 samples yielding Quantification results of less than the Limit of Detection (0.001ng/uL). This new EXH line is intended to act as a flag to QPS to assess the sample within the case context and decide if rework is desired/required, per recommendatioin 4 below.

3. After a six month period of processing, re-analyse samples that have had a Microcon® process performed and were in the initial Quantification range greater than 0.0088ng/uL, to evaluate whether the range from Recommendation 1 can be extended for P3 samples, and potentially include P2 samples (this needs to be examined from P2 interp rules perspective).

4. Communicate the change in process to QPS and ensure that QPS are aware that for samples in the range mentioned in Recommendations 1,

that they could be requested for Microcon® concentration steps at any point in time. This request can be made via the Forensic Register after they have received the 'DNA insufficient…' result line.

~~7.~~9. References

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[1] QIS 19544v11 – Concentration of DNA Extracts Using Microcon Centrifugal Filter Devices

[2] PowerPlex® 21– Amplification of Extracted DNA Validation. Megan Mathieson, Thomas Nurthen, Cathie Allen. December 2012. Forensic DNA Analysis.

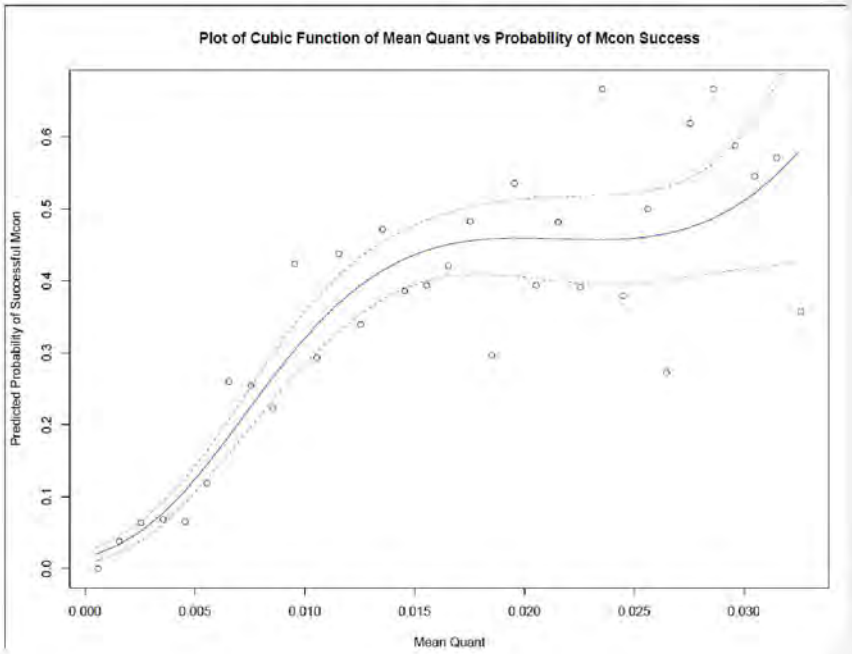
[3] Project #163 - Assessment of results obtained from 'automatic-microcon' samples. Josie Entwistle, Allison Lloyd, Kylie Rika, Thomas Nurthen, Cathie Allen. August 2015. Forensic DNA Analysis.

- To note is the use of percentages and non-normalized data to draw conclusions from the data that are not valid.
  - By not normalizing the very low quant (<0.0088ng/uL; n=1449) data which represents the bulk of the samples(n_{total}=1731), percentages derived from data combined with the above very low quant samples (eg. Figure 8 and figure 9) are artificially skewed by the large number of close-to-zero quant values. Thus, it would not be expected for there to be an insignificant increase in the percentage of successful microcons as presented in figures 8 & 9). Even if 100% of the microcons in the 0.015-0.020 range were successful (n=94), this would have little effect on the mean success rate of the n=1492 samples that have lower quants (94/1492 = 6.4%) at maximum.
  - The data needs to be normalized by obtaining the probability for the mean quant using a frequency distribution for a range of quant values.
  - My own analysis of the data shows that the data can be best modelled by a third order regression of the success/fail probability against the quant. I developed the data as a frequency distribution based on divisions of 0.001 ng/uL. The probability of success was calculated based on the outcome of all samples within a single division, thus normalizing the data. This reduced the data to 33 points. The data was analysed as a binomial distribution as is appropriate with binomial data and the 95% confidence intervals calculated.
  - These outcomes are presented in graphical and tabular form in the attached pages suggests a very different set of conclusions.
  - As can be seen from the results there is a mean success rate of approximately 30% at 0.010ng/uL up to approximately 43% at 0.015ng/uL. This is at odds with the conclusions drawn in section 7.2 of the project and with the justification for the use of 0.015ng/uL in the introduction to Experiment 2 (pg 8).
- As such, I conclude that setting the cut-off for no processing at 0.0088ng/uL is probably too high.

- Additionally, conclusion drawn from percentage values derived from non-normalized data cannot be trusted as the data is clearly skewed towards very low-level quants.

Table 1. 95% confidence intervals for the microcon success probabilities for all quant ranges. (eg. Line 6 represents the probability of success for all samples with a quant between 0.0055 and 0.0064.)

	Mean Quant for range	lower	Estimated Prob of Success	upper
1	0.001	0.061921	1.984695	2.907470
2	0.002	2.111484	3.275817	4.440151
3	0.003	3.746543	5.116828	6.487114
4	0.004	6.038001	7.574229	9.110456
5	0.005	8.936327	10.645507	12.354687
6	0.006	12.277503	14.244627	16.211752
7	0.007	15.868023	18.210662	20.553300
8	0.008	19.552401	22.337853	25.123304
9	0.009	23.205051	26.415076	29.625101
10	0.010	26.709850	30.259965	33.810081
11	0.011	29.959510	33.738579	37.517648
12	0.012	32.862823	36.769795	40.676767
13	0.013	35.350065	39.319138	43.288211
14	0.014	37.375481	41.387961	45.400441
15	0.015	38.919212	43.002380	47.085547
16	0.016	39.989907	44.204209	48.418510
17	0.017	40.625908	45.044506	49.463105
18	0.018	40.891674	45.579421	50.267168
19	0.019	40.869451	45.867744	50.866037
20	0.020	40.649724	45.969556	51.289388
21	0.021	40.323576	45.945520	51.567465
22	0.022	39.977440	45.856505	51.735570
23	0.023	39.689097	45.763385	51.837673
24	0.024	39.523421	45.726976	51.930532
25	0.025	39.526412	45.808084	52.089757
26	0.026	39.716517	46.067684	52.418852
27	0.027	40.074323	46.567177	53.060032
28	0.028	40.538169	47.368584	54.198998
29	0.029	41.021312	48.534376	56.047440
30	0.030	41.456547	50.126451	58.796354
31	0.031	41.839757	52.203470	62.567183
32	0.032	42.240691	54.815589	67.390487
33	0.033	42.793029	57.995491	73.197953


Plot of Cubic Function of Mean Quant vs Probability of Mcon Success
Predicted Probability of Successful Mcon
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.000
0.005
0.010
0.015
0.020
0.025
0.030
Mean Quant

Figures 4 and 5 show that there do not appear to be any obvious trends in the data. It is not unexpected to have a variety of DNA profile outcomes for different biological source types, and not unexpected for a variety of DNA profile outcomes for different substrate types. Interestingly, the number of 'assumed known contributors' is almost one-third of DNA profile outcomes for the most numerous suspected biological type (cells), and substrate type (swab). It could be argued that this DNA profile outcome is not meaningful to the client as the results are not unexpected.

What this means is that if the client requested a Microcon® process on a particular sample that was initially in the 'auto-microcon' Quantification range, there does not appear to be a predictive element to the likely success of the microcon rework for a particular biological source type, nor substrate type.

Ultimately, for approximately 90% of samples that underwent an 'auto-microcon' process, there is arguably negligible DNA profile Intelligence for the client. If the 'auto-microcon' was not applied as a streamlining strategy, there would be the following advantages, including but not limited to:

worth putting a % of samples rec'd?

-the potential to make available at least 1449 processing positions for other samples including further available positions that would have been used for reworks. It must be noted that it is not unusual for low-quantification samples to be reworked further before determining if the profile is suitable for comparison to reference DNA profiles.

post mic these samples are often reworked further to enable interpretation

-the lack of a need for the considerable efforts required to prepare and process Microcon® (and further rework) batches for this number of samples,

-consumable and labour savings in the end-to-end processing of these samples, and

-time and effort could be redirected in the laboratory workflow to other activities including service extensions ~~like Y-STR profiling~~.

? needed

is this what you are trying to say?

i.e. causes even more work

-benefit.

Reported profiles have better reproducibility?

as mic samples have low repro?

increases/decreases of Q value post mic

concentration. Figure 10 shows the plot of the ~~differences found~~ for samples that resulted in 'success'.

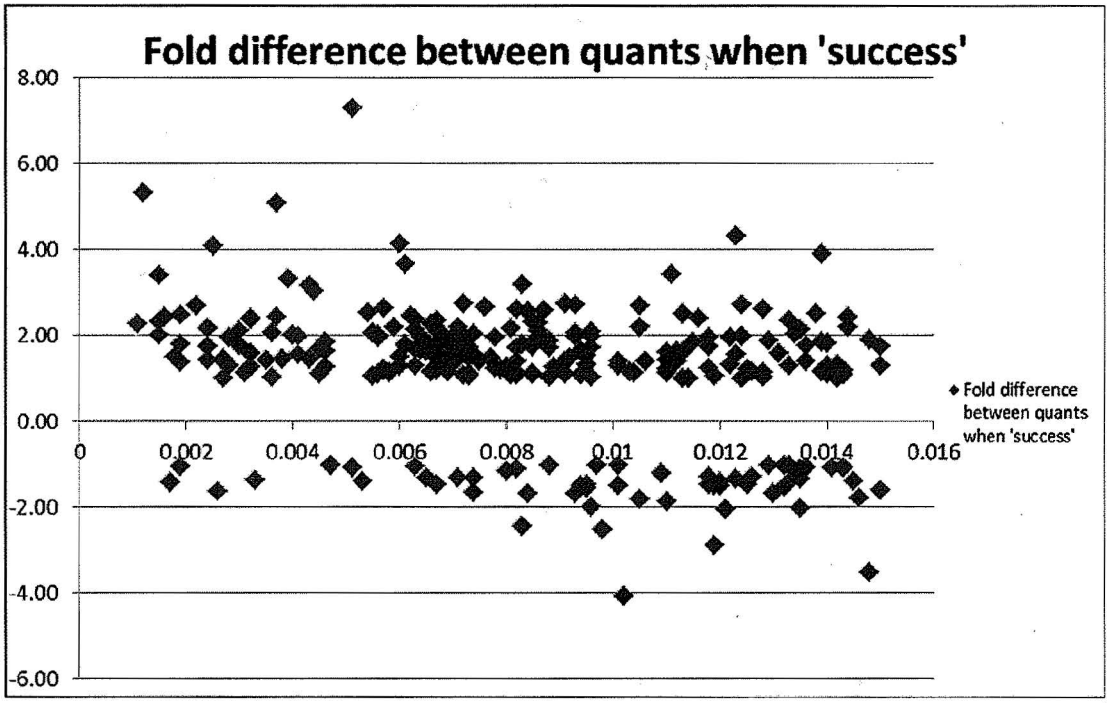


Figure 10: Quantification differences pre and post concentration

The findings are not unexpected as the scatter focusses mostly around two-fold increases in Quantification. It was also not unexpected to observe the variable results. Anecdotally, variability in success rates is found at profile management stage when assessing results of samples that have had this concentration step.

DNA can be lost in the process as seen in Fig 10 where the Quantification values decreased after concentration. Variability in results could be attributed to a number of things, including but not limited to the slight differences between operators and instrumentation, the differences in substrate type and level of degradation, and the variability in Quantification result.

8. Conclusion and Recommendations

The data analysis demonstrated that there was arguably minimal value in performing the 'auto-microcon' concentration step. This opinion was formed by analysing the data from 2016 where it was found that for all samples that underwent the 'auto-microcon' step, 89% did not yield results suitable for meaningful interpretation (or 'success' in this report).

It was found that in considering *all* samples that underwent a Microcon® step at some stage in 2016, 78.5% did not yield results suitable for meaningful interpretation. As expected, when the Quantification value increased, the percentage of meaningful results increased. However, it was also demonstrated in the data analysis that the Quantification values did not always improve after Microcon®, but where they did, the magnitude of change was roughly equivalent to the change in volume (from neat to concentrated sample).

Based on the data analysis, the following recommendations are offered:

1. Cease 'auto-microcon' (Quant range: 0.001ng/uL to 0.0088ng/uL) processing for all samples with the following exceptions:
    a. Priority 1 samples (Critical Priority); and
    b. Coronial/DVI samples where profiles are mostly single-source. Quite often incomplete profiles may be enough to provide Intelligence on possible identity.

2. Automatically send result information via the Forensic Register to QPS at Quantification stage for samples in the Quant range: 0.001ng/uL to 0.0088ng/uL. This result information is recommended to be the exhibit result line of 'DNA Insufficient for Further Processing'. This recommendation is an extension to the current 'No DNA Detected' process, which looks at Priority 2 samples yielding Quantification results of less than the Limit of Detection (0.001ng/uL).

3. After a six month period of processing, re-analyse samples that have had a Microcon® process performed and were in the initial Quantification range greater than 0.0088ng/uL, to evaluate whether the range from Recommendation 1 can be extended.

4. Communicate the change in process to QPS and ensure that QPS are aware that for samples in the range mentioned in Recommendations 1, that they could be requested for Microcon® concentration steps at any point in time. This request can be made via the Forensic Register after they have received the 'DNA insufficient...' result line.

Feedback due 20/12/2017			
Staff member	Feedback date	Feedback	Response
LBR	1/12/2017	Hi Justin Looks good to me. Just a few minor formatting comments: Figure 2 – maybe reduce to 4 decimal places?, also add X and Y axis labels Figure 6 – add X and Y axis labels Figure 7 – reduce decimals in labels Figure 10 – re-format legend so that graph has more room Thoughout – sometimes the ° is superscript and sometimes not (sorry that's very picky) Thanks Luke	Fig 2 - the pivot table uses the raw data from the Quant file. Unable to change here. Fig 6 and Fig 2 - changes the image type in the doc so now have the labels. Fig 10 fixed. Fixed superscript.
KDS	1/12/2017	Justin Feedback as follows: Abstract: A little disjointed to read – can the sentences/ideas be linked. Section 4.2 (and throughout)– I don't really like the use of the work "Fail" it indicates we did something wrong, or that there is a quality issue - which is not the case. We have processed them correctly, but the outcome from the biological submission is not informative. Can we use another term "Nil result" or "Nil Intell" or similar? Section 7: Could we/should we suggest case managers review cases on finalisation? If they think there is not much useful information in the case, and where they believe that the available profiles maybe useful (using their discretion) that they may consider manual Microcon reworks? While success rates are low, there are still potential successes. Kirsten	Abstract being re-written.
ARM	5/12/2017	Hi Kirsty, Just a few things: Abstract Suggest reword "Given this, further workflow streamlining processes could be implemented that would provide significant processing efficiencies, and cost and time savings such that these efforts could be better placed in processing higher DNA-yielding samples" to "Given this, further streamlining of workflow processes could be implemented that would provide significant efficiencies such that these efforts could be better placed in processing higher DNA-yielding samples" or "Given this, further workflow process streamlining could be implemented that would provide significant processing efficiencies in order for resources to be better utilised processing higher DNA-yielding samples" 5.2 "A total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection." I'm trying to work out why there are so many samples without quant as the whole point of m'con to 35 was so that they were quanted after microcon and they should have a pre-microcon quant as well – is there are a problem with the data export? Figure 1 ☹ Figure 2 ☹ Recommendations Recommendation 2 – I'd support up to 0.02ng/uL (template of 300ng) as this is the "cross-over" point and I'd also support implementing for both P2 and P3 samples, as recommendation 3 and 5 still give the QPS an option to ask for more work on the sample, it's easy for them to do & it's an extension of the triaging process Cheers	Abstract being re-written, and suggested wording used. Note support for higher Q value, but will go with auto-mic range for implementation and check post-implementation.

Feedback due: 23/12/2017			
Staff member	Feedback date	Feedback	Response
KAL	7/12/2017	Hi Justin I've had a look through the report (just in case it isn't signed off by the time Kirsten goes on holiday).. And with the recommendations – we will need to change the quant results upload programming in the FR to fit in line with the new values. I'm not sure how much work that would be for Troy etc. We would also then need to test the functionality works... This would include: - P1 and Coronial samples only to go to auto-microcon - P2 samples at the auto-micorcon value range to go to "DNA Insufficient" (we would have to make sure this works for samples, currently it only works for QPS enwm samples) - P3 samples – would we keep the undetermined ones as "No DNA", then those up to 0.0133ng/uL make "DNA Insufficient"? - I think that's all... Just some things to keep in mind. Thanks Kerry-Anne	
PMB	19/12/2017	Hi Justin, I've reviewed and happy with the theory and recommendations. I asked Lisa to have a look in the FR training site to see how the process for P3 samples would work once they move to PP21. I will forward you the email summarising this. Once a decision is reached on the range for quant values, we will need to submit enhancements to VSTS and create/write manual procedures for P3 samples both through Analytical and reporting. These manual processes will be in place until the enhancements are in FR. Thanks, Paula	
KDR	3/01/2018	via track changes on doc in parent folder.	
AJR	5/01/2018	via track changes on doc in parent folder.	

Feedback due 9/01/2018

Staff	Date	Feedback	Response
LBR	9/01/2018	Hi Justin Looks great, I assume the recommendations apply to P3 samples amped in PP21? I'm ready to sign. Thanks Luke	Hey, yes all samples. Do you think I should just expand this a bit? jah
		Ok excellent. Might be worth specifying. I would either add a Scope section at the start (and say that recommendations apply to all P2 and P3 samples processed with PP21, or just specify in the Conclusion and Recommendations section – perhaps at start of recommendation 2? i.e. "For all Priority 2 and 3 samples processed with PP21, automatically…."	Hey, added to R1: 1. Cease 'auto-microcon' (Quant range: 0.001ng/uL to 0.0088ng/uL) processing for all samples of Priority 2 and 3 requested to be amplified with PowerPlex 21, with the following exceptions: jah
KAL	9/01/2018	Hi Justin Looks good – apart from the typo in my name that you already know about. Thanks Kerry-Anne	Adjusted
PMB	9/01/2018	Doesn't apply to P3 with PP21. Best to be option paper as QPS should make the decision on this.	Agree
KDR and AJR	9/01/2018	via track changes on doc in parent folder.	
SMJ	9/01/2018	via notes on doc in parent folder.	
ARM	10/01/2018	Hi, I am happy with the report (pie chart excluded …) – however, I would actually be in favour of rolling out DNA insufficient to 0.02 ng/uL and consider an extension of the DNA triaging process Cheers Al	

CA-103

Cathie Allen

From: Frieberg.DaleJ[OSC] <[redacted]>
Sent: Monday, 22 January 2018 2:26 PM
To: Cathie Allen
Cc: Taylor.EwenN[OSC]; O'Malley.TroyS[OSC]; Paul Csoban; Support Officer FSG
Subject: RE: Volume Crime Samples

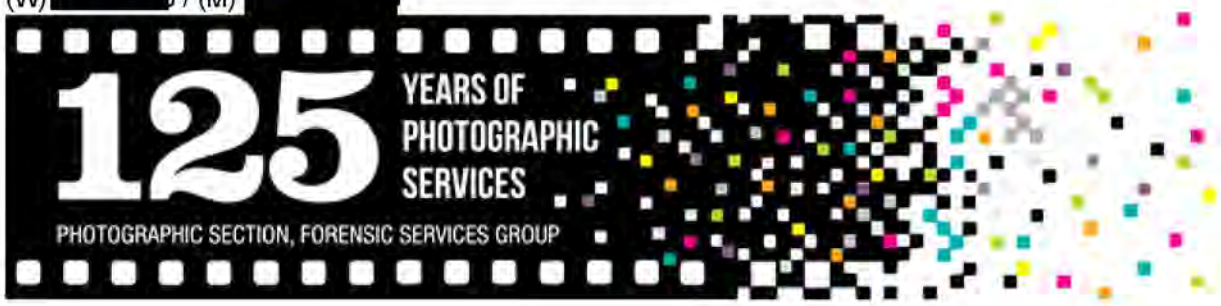
Hi Cathie,

Thank you for your email. I will have my exec sec organise a time suitable to all to meet.

Jenna, can you please touch base with Cathie and organise a time in the next couple of weeks.

D

Dale Frieberg
Superintendent
Operations Commander
Forensic Services Group
Operations Support Command
Queensland Police Service
(E)[redacted]
(W)[redacted] / (M)[redacted]



From: Cathie Allen [mailto:[redacted]
Sent: Monday, 22 January 2018 1:53 PM
To: Frieberg.DaleJ[OSC] <[redacted]>
Cc: Taylor.EwenN[OSC] <[redacted]>; O'Malley.TroyS[OSC] <[redacted]>; Paul Csoban <[redacted]>
Subject: Volume Crime Samples

Hi Dale

Last year, we met with you and Insp Scott McLaren regarding processing of Volume Crime samples, given the discontinuation of Profiler Plus kits from Applied Biosystems. From today onwards, Volume Crime samples will be processed using PowerPlex 21, as per direction by the QPS.

My team has come up with an Options paper regarding further improvements that could be made to Volume Crime workflow and I'll forward that to you later today for your review. Paul and I would like to meet with you to discuss this paper and another item – are you able to advise when you would be available to discuss these with us?

Cheers
Cathie

Cathie Allen
Managing Scientist – Police Services Stream

Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

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a | [redacted]
w | www.health.qld.gov.au e | [redacted]

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CA-104

Cathie Allen

From: Frieberg.DaleJ[OSC] <[redacted]>
Sent: Tuesday, 30 January 2018 9:36 PM
To: Cathie Allen; O'Malley.TroyS[OSC]; Taylor.EwenN[OSC]
Cc: Paul Csoban
Subject: RE: Options Paper for consideration

Hi Cathie,

Will do. Look forward to seeing you then.

D

Dale Frieberg
Superintendent
Operations Commander
Forensic Services Group
Operations Support Command
Queensland Police Service
(E)[redacted]
(W)[redacted] (M)[redacted]



From: Cathie Allen [mailto:[redacted]]
Sent: Tuesday, 30 January 2018 4:56 PM
To: Frieberg.DaleJ[OSC] <[redacted]>; O'Malley.TroyS[OSC] <[redacted]>; Taylor.EwenN[OSC] <[redacted]>
Cc: Paul Csoban <[redacted]>
Subject: Options Paper for consideration

Hi Dale

Please find attached an Options paper regarding concentration of major crime samples that we have prepared for your consideration. I'd like to discuss this on Friday with you.

Cheers
Cathie



Cathie Allen
Managing Scientist – Police Services Stream

Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

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a | [redacted]
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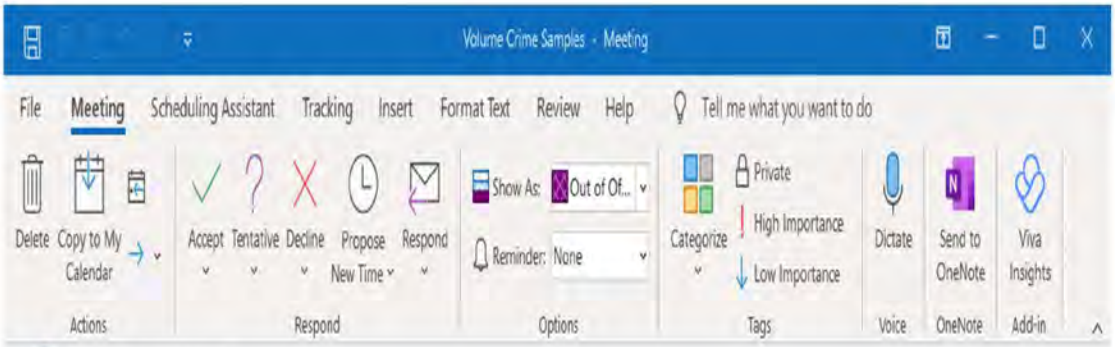
CA-105



Accepted on 25/01/2018 3:17 PM.

Volume Crime Samples

Organizer: [redacted] on behalf of Frieberg.Dale/[OSC] [redacted] Sent: Thu 25/01/2018 1:09 PM

Time: Friday, 2 February 2018 2:00 PM-3:00 PM

Location: Supt's Conference Room, level 4, PHQ

Response: ✓ Accepted Change Response

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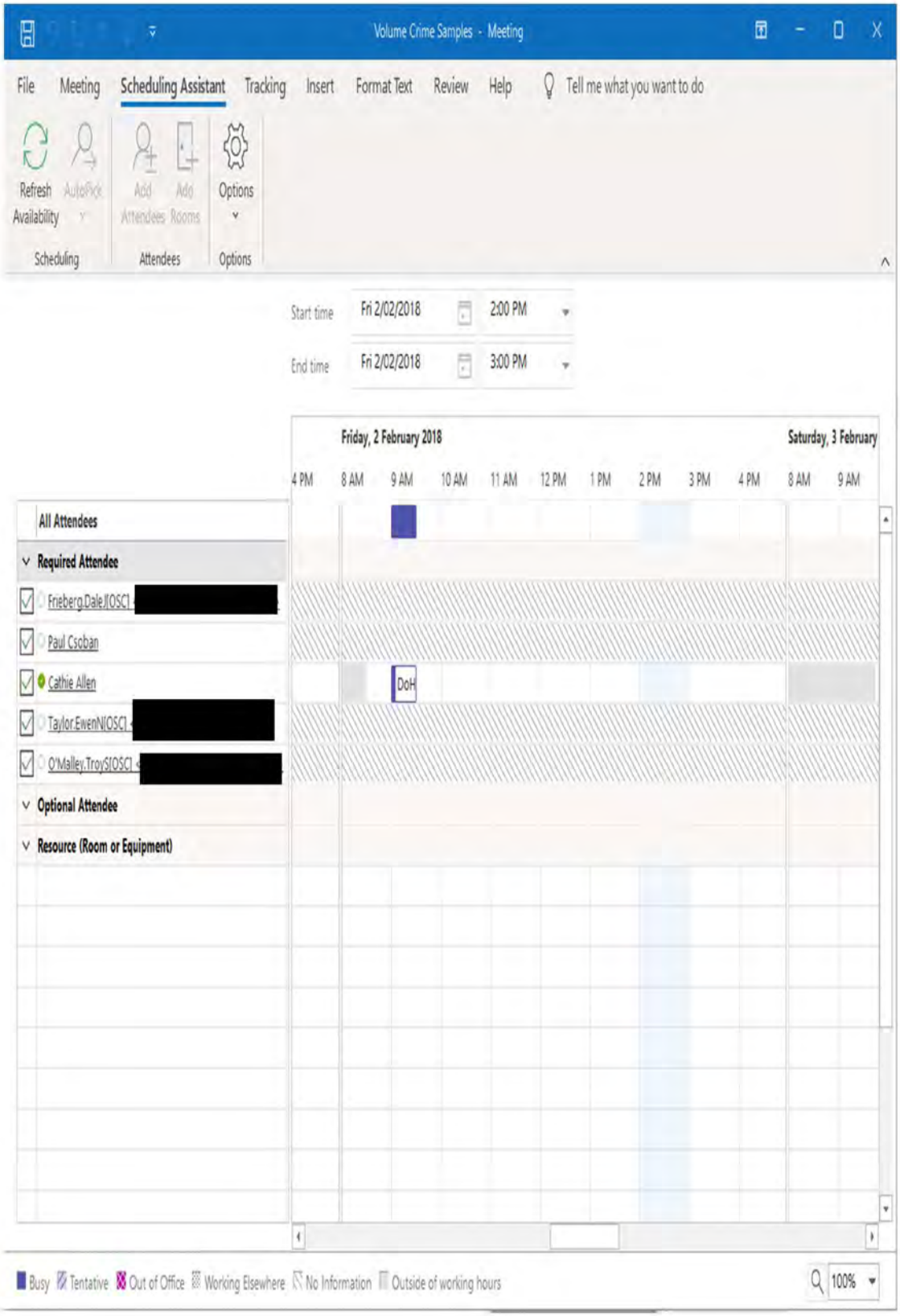
Volume Crime Samples - Meeting
File
Meeting
Scheduling Assistant
Tracking
Insert
Format Text
Review
Help
Tell me what you want to do
Refresh Availability
AutoPick
Add Attendees
Add Rooms
Options
Scheduling
Attendees
Options
Start time
Fri 2/02/2018
2:00 PM
End time
Fri 2/02/2018
3:00 PM
Friday, 2 February 2018
Saturday, 3 February
4 PM
8 AM
9 AM
10 AM
11 AM
12 PM
1 PM
2 PM
3 PM
4 PM
8 AM
9 AM
All Attendees
Required Attendee
Frieberg,Dale,IOSC1
Paul Csoban
Cathie Allen
DoH
Taylor,EwenN[OSC1
O'Malley,TroyS[OSC1
Optional Attendee
Resource (Room or Equipment)
Busy
Tentative
Out of Office
Working Elsewhere
No Information
Outside of working hours
100%

CA-106

Cathie Allen

From: Frieberg.DaleJ[OSC] <[redacted]>
Sent: Friday, 2 February 2018 3:38 PM
To: Cathie Allen; O'Malley.TroyS[OSC]; Taylor.EwenN[OSC]
Cc: Paul Csoban
Subject: RE: Options Paper for consideration

Hi Cathie and Paul,

Thank you for your time this afternoon and for discussion around this options paper. Thank you also to both Troy and Ewen with your assistance and expertise/advice around the paper.

As discussed, I am in agreement that:

- There is clear data that it is not an efficient use of time and resources to continue with the 'auto-microcon' process for Priority 2 (*Major Crime*) samples.
- Option 2. "Cease the 'auto-microcon' process for Priority 2 casework...." Would appear to be a more productive & efficient choice.
- Scientists time and resources would be better spent working samples with a higher DNA yield and more potential.
- It would be beneficial to amend the Forensic Register to provide an automated Q-Prime update advising the Investigators of the option to request further 'Auto-microcon' processing for those samples for unsolved crime, which may prove worthwhile.
- DNA staff can request this additional processing if/when a request is received from the investigators.

I trust this is of assistance.

Kind regards,

Dale.

Dale Frieberg
Superintendent
Operations Commander
Forensic Services Group
Operations Support Command
Queensland Police Service
(E) [redacted]
(W) [redacted] / (M) [redacted]



From: Cathie Allen [mailto:[redacted]
Sent: Tuesday, 30 January 2018 4:56 PM
To: Frieberg.DaleJ[OSC] <[redacted]>; O'Malley.TroyS[OSC] <[redacted]>; Taylor.EwenN[OSC] <[redacted]>
Cc: Paul Csoban <[redacted]>
Subject: Options Paper for consideration

Hi Dale

Please find attached an Options paper regarding concentration of major crime samples that we have prepared for your consideration. I'd like to discuss this on Friday with you.

Cheers
Cathie

Cathie Allen
Managing Scientist – Police Services Stream

Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

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CA-107

Paula Brisotto

From: Cathie Allen
Sent: Monday, 5 February 2018 11:30 AM
To: Allan McNevin; Amanda Reeves; Justin Howes; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone; Wendy Harmer; Thomas Nurthen
Subject: Microcon Options Paper
Attachments: Review of efficacy of Microcons_options for QPS.doc

Hi Everyone

On Friday, Paul Csoban and I met with the Superintendent of Forensic Services Group, Dale Frieberg and other QPS officers that the Supt requested to attend. We discussed the Options Paper attached, which I had provided to the Supt earlier in the week. The Supt has indicated verbally and by email that the QPS' preferred option is Option 2 – no automatic concentration of Priority 1 or Priority 2 samples.

If you have any questions regarding this, please don't hesitate to send me an email or come and have a chat with me.

Cheers
Cathie

Cathie Allen
Managing Scientist – Police Services Stream

Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

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CA-108

Cathie Allen

From: Cathie Allen
Sent: Thursday, 15 November 2018 10:54 AM
To: A/Insp Gerard Simpfendorfer ([redacted]; Supt Bruce McNab ([redacted])
Cc: Craig Russell; Insp David Neville ([redacted])
Subject: FW: Removal of the microcon step from P1 worflow.
Attachments: Review of efficacy of Microcons_options for QPS.DOC

Importance: High

Correction to one figure listed below – my apologies

Hi Gerard and Bruce

I can confirm that the Microcon process has been applied to the below four sample as requested by the QPS on the dates listed below:

[redacted]
- Snr Sgt Simpfendorfer requested Microcon 29/10/2018
- Snr Sgt Simpfendorfer requested Microcon 06/11/2018
- Snr Sgt Simpfendorfer requested Microcon 06/11/2018
- Snr Sgt Simpfendorfer requested Microcon 06/11/2018

During a meeting on 1st of Feb 2018, Paul Csoban (previous Executive Director for FSS) and I met with Supt Dale Frieberg to discuss the Options Paper that had previously been provided to the QPS for decision. During this meeting, the Superintendent agreed that Option 2 was the preferred option, which was later confirmed via email (as per below). During the discussion, the second part of Option 2 (section a) was discussed, which related to Priority 1 samples and the Superintendent indicated that Priority 1 samples should be processed the same as Major crime (P2) and Volume crime samples (P3), which is not to be automatically progressed through the Microcon process. After the approval from the QPS in Feb 2018, all samples have not automatically progressed through the Microcon process. The QPS or a Forensic DNA Analysis staff member can request a Microcon process for a sample at any time.

Automatic progression of samples through the Microcon process means that all available DNA extract will be consumed, so no further testing can be conducted on these samples after this step. This means that if a sample could yield a profile by specific Y chromosome testing for example, there would be no extract available for that testing to be conducted. It also means that samples that are eligible to be pooled together, as they are from the same item or area, are not able to be as there is no DNA extract left to undertake pooling. Scientists or Forensic officers reviewing results in the context of a case are able to request a Microcon process for a sample or samples.

As the decision on the automatic Microcon process was made last financial year, the budget for this financial year has been adjusted for that consumable, so this will increase the cost.

If the QPS wishes for P1 samples to automatically be processed through the Microcon process, which leaves no available extract for other testing, this process can be re-introduced. Please confirm if the QPS requires the re-introduction of this step.

The Options Paper reviewed 1449 (~~278~~) Major crime samples that had been progressed through the Microcon process over a one year period, as this was considered to be sufficient sample numbers to demonstrate a clear trend.

The laboratory is unable to search the FR to undertake any statistical analysis regarding 'useable' profile numbers – this was highlighted to FSS during development that large or medium scale interrogation of the FR could only be undertaken by the QPS, as they would need to construct the search and ensure the timing of the search was

undertaken so as not to add extra burden to the FR during peak operational times. If the QPS were able to generate this data, the laboratory would undertake this analysis and provide feedback. The Microcon process was no longer automatically undertaken for P1 or P2 samples from the 12th of Feb 2018.

Whilst the Microcon process has not been automatically applied to Major crime samples (P2) since mid Feb, scientists have reviewed those results and requested a Microcon process if in the context of the case it could have been of potential benefit. If the QPS undertook a search of all 'DNA insufficient' results on P1 and P2 samples since the 12th of Feb, the laboratory could undertake an analysis of the cases to determine if additional testing through the Microcon process is required. This would require resources and would reduce the number of results that are reviewed by the lab until this analysis was completed.

I await your advice regarding this. If you have any further questions, please let me know how I can assist.

Cheers
Cathie

Cathie Allen
Managing Scientist

Police Services Stream, Forensic & Scientific Services
Health Support Queensland, Queensland Health

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a [redacted]
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From: Neville.DavidH[OSC] [mailto[redacted]]
Sent: Wednesday, 14 November 2018 2:47 PM
To: Cathie Allen
Cc: Craig Russell; McNab.BruceJ[OSC]; Simpfendorfer.GerardM[OSC]
Subject: Removal of the microcon step from P1 worflow.
Importance: High

Dear Cathie
During the course of the investigation into Operation Clarify over 15 samples were submitted as Priority 1. On initial testing, four samples were reported as having insufficient DNA present for further testing. Upon receipt of that result my staff requested additional testing and each of those samples yielded a result as follows:

[redacted] - SINGLE SOURCE 20 LOCI DNA PROFILE LR > 100 BILLION (Deceased match); and POSSIBLE SUB-THRESHOLD INFORMATION
[redacted] - SINGLE SOURCE DNA PROFILE - ASSUMED KNOWN CONTRIBUTOR – (Deceased match)
[redacted] - SS DNA PROFILE 9 LOCI AND ABOVE LR > 100 BILLION (Deceased match)
[redacted] - COMPLEX MIXED PROFILE UNSUITABLE FOR INTERP OR COMPARISON

Could you confirm if the profiles for the four samples listed above were obtained after micro-concentration was performed, please. Could you also confirm if the microcon step has been removed from the workflow as a matter of routine for P1 samples. My understanding as per the below was that this was only to occur for P2. If this process

has been removed from the P1 workflow, could it please be reintroduced as it will stop delays in obtaining results that are considered urgent, please.

From: Frieberg.DaleJ[OSC]
Sent: Friday, 2 February 2018 3:38 PM
To: Cathie Allen <[redacted]>; O'Malley.TroyS[OSC] <[redacted]>
Cc: Paul Csoban <[redacted]>
Subject: RE: Options Paper for consideration

Hi Cathie and Paul,

Thank you for your time this afternoon and for discussion around this options paper. Thank you also t

As discussed, I am in agreement that:

- There is clear data that it is not an efficient use of time and resources to continue with the 'a
- Option 2. "Cease the 'auto-microcon' process for Priority 2 casework...." Would appear to be
- Scientists time and resources would be better spent working samples with a higher DNA yield
- It would be beneficial to amend the Forensic Register to provide an automated Q-Prime upda
- DNA staff can request this additional processing if/when a request is received from the invest

I trust this is of assistance.

Kind regards,

Dale.

Dale Frieberg
Superintendent
Operations Commander
Forensic Services Group
Operations Support Command
Queensland Police Service
(E) [redacted]

The removal of the microcon step in the process was agreed to on 2 February 2018 by Supt Frieberg based on the advice included in the attached paper. This paper estimates that there would be less than a 2% reduction in the number of useable results if the step was eliminated.

Based on the fact that 3 out of 4 samples for this case yielded a result when testing was continued, anecdotally it would seem that we may be missing out on more than 2% of results.

Since eliminating this step, has your laboratory undertaken any statistical analysis to determine if there has been a drop in the proportion of samples that give a useable profile, please.

There are other serious matters including homicides where testing has stopped once advice was received that there is insufficient DNA for further testing. Based on the results for this case (75% success rate for the ones received back so far), would you recommend that these cases be re-examined please.

Could you please direct your response to Gerard and Bruce.



David Neville
Inspector
DNA Management Unit | Forensic Services Group
Operations Support Command
QUEENSLAND POLICE SERVICE

Phone [redacted]
Email [redacted]
Address [redacted]

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CA-109

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A CLINICAL AND STATEWIDE SERVICE

Procedure for Case Management

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1 PURPOSE AND SCOPE

To describe the components of a case record and the storage of these records.

To describe the steps involved in compiling and completing a case record.

To ensure all analysis records and results are traceable.

2 DEFINITIONS

Case Record – consists of all information relating to a particular case. This includes all case histories, receipts, communication with clients, examination notes, analytical data, results and reports.

Sampling Scientist – Scientist who has examined exhibits for a case in accordance with the Examination of Items (17142) and/or Examination for & of Spermatozoa (17189)

Case Managing Scientist – Scientist/s who have been involved in the assessment of results and compilation of the case file in preparation for statement writing in accordance with this SOP.

Reporting Scientist – Scientist who is responsible for writing a statement for court regarding the results of a case and for presenting evidence on the results in a court of law.

3 CASE FILE

3.1 When is a case file required?

- A case file is created for every case with the exception of inactive cases - that are no longer required (as determined by QPS FIRMU/FSLU). (A case file is created for volume cases at the commencement of the sampling process).
- Each case file has a unique case number (Occurrence no., or CRISP no. or SSF no.). The Occurrence number is generated by Police. (CRISP no.'s were generated by QPS prior to occurrence numbers)
- SSF or COR number (usually coronial cases) is generated within AUSLAB.
- Any subsequent items received relating to this case are linked to the original Case #.
- Case information is recorded in AUSLAB (see 17116 Procedure for Receipt of Items and 16004 AUSLAB Users Manual – Forensic Biology).

Note: If a case contains items or documentation citing more than one case number, then enquiries must be made to the QPS DNA Unit to establish whether the cases are linked and therefore can be reported together. Records of these checks must be included in the UR notes.

3.2 Minimum requirements of a case file

- Case File Particulars form (17038)
- Case information or case history including submission and analysis request form (from police)
- Copies of receipts for items received

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3.3 How to create a Case File

Required:

1 x Case File Particulars page
Receipt page
[redacted] (case information) – if available
Receipt Barcodes

- Check on AUSLAB that a case file does not already exist for this CASE Number (Use the storage function 2, 7 to see if 2 entries exist – Note: do not confuse exhibits that may be stored with case files – case files will only be stored to compactus, filing cabinet or intray locations). If a file already exists a new one does not need to be prepared and the other file should be located and joined to the exhibit
- Place one of the barcodes for the first receipt (if multiple receipts) that is attached to the file in the centre of the box in the top right hand corner of the Case File folder. This first receipt barcode should also be the barcode that the CS screen is under in AUSLAB.
- Place another of the same barcode on the "Case File Particulars" page in the top left hand side of the page where it states Case File Barcode. If there are no barcodes attached, write the barcode which has been photocopied on the Forensic Receipt Page or print a new barcode from AUSLAB. Place one copy of each additional receipt barcodes in the additional barcodes boxes.
- On the 'Case File Particulars' page write the Case Number (or CRISP, Occurrence or QPS number) where it says 'Case #' at the top of the page. This page is finished with now and can be placed inside the folder.
- On the Case File folder write the Case Number (or CRISP, Occurrence or QPS number) at the top of the folder where it says 'Case Number'
- Where it states 'Examining Scientist' write the name of the scientist examining the case. Note: for these fields initials can be used, and multiple people can be added.
- Where it states 'Case Managing Scientist' write the name of the scientist responsible for the case management. Note: for these fields initials can be used, and multiple people can be added; this does not need to be filled out when the case file is created, it can be filled out at the time of case management.
- Where it states 'Reporting Scientist' write the name of the scientist reporting the statement, if a statement has been issued. Note: for these fields initials can be used, and multiple people can be added; this does not need to be filled out at the time the case file is created, it can be filled out at the time the statement is issued.
- Where it states Location, write the Client or the police Station that is handling the case. This is found on the Forensic Receipt page about half way down, titled "Delivery Officers Station". Just enter the Suburb (no need to put the words Police Station)
- Write Complainant's name in the top line where it state "NAMES" Write the Surname in capitals first and then a comma followed by the given names in lower case with "(COMP)" following the name. If the complainant is a company, the company name can be written on the case file, but the complainant in these cases is 'Regina'.
- Write the suspects in the following lines in the same format (one per line) with '(SUS)" following the name.
- Turn the folder to the side and fill out on the inside along the edge as indicated the CASE Number, which is the Case number (or the QPS Number).

- CASE TYPE – you will find the type of offence towards the top of page under offence Title (on Submission of Articles for Forensic Examination form). We use the CASE TYPE rather that the Crime Class Code that is generally written on the Police Form, 'Submission of articles for Forensic Examination ' e.g. Assault (S), or U/Entry etc is all you need to write. This information may also be found in AUSLAB on the CS screen.
- NAMES – Divide the line in half with a diagonal line. On the left side write the Surname of the Complainant, and on the other side of the diagonal line write the Surname of the Suspects (one on top of the other if necessary)
- Place the Case File Particulars page, QP127 (case information) and receipt page inside the case file and track in AUSLAB to the case scientist or appropriate storage location.

3.4 Additional elements of a Case File

Upon completion a case file may also contain:

- Examination notes (on approved forms obtained from QIS)
- Diagrams or photographs
- Calculations (statistical calculations must be included within the case file – refer to 17168 Procedure for DNA Profile Statistics)
- Profile Results table
- Copies of results (electropherograms or Genotyper printouts)
- Copy of statement or report
- Interpretations of results
- Records of any internal or external communication relating to the case eg. UR notes or emails.

3.5 Case file contents

Upon completion of case file, or prior to being sent for an administrative review:

- All pages must be paginated including the reverse side of pages (ie for double sided copies)
- The total no. of pages must be recorded on the front of the case file
- Post-it notes or loose pages are not permitted (Post-it tabs may be used as tabs or dividers)
- Each page must include the case number (may be in the form of a stamp or handwritten)
- Each page must include the initials of the person compiling the final case documentation (note: page numbering and initialling may be done by a scientist, or by operational or administrative officers)
- Where helpful the Case File Particulars page index should also be used

3.6 Handwritten results and corrections within the Case File

- Any calculations, changes or comments are to be initialled and dated by the person performing the action
- Any changes to electropherograms must be initialled and dated

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- Handwritten results must be initialled and dated and should include a statement "Results reviewed by both readers" or equivalent. Reviewers should also co-sign these results to verify that these results have been checked.
- No pencil (unless used in diagrams or pictorial representations)

3.7 Case file storage and movement

- **No exhibits are to be stored in the case file**. (This includes external proficiency samples – external proficiency samples are to be discarded after follow-up and feedback at staff meeting) Original police property tags or reference sample envelopes are also NOT to be stored in the case file. Photocopies are acceptable.
- **Case file movement** between analysts is to be recorded in AUSLAB storage system. If the case analyst responsible for a case is changed, this must be recorded in AUSLAB.
- **Chain of custody records** of the evidence items should also be recorded in AUSLAB storage system. Each time the exhibit is removed to examine or placed back into the freezer or compactus it must be stored to those locations in AUSLAB.

4 CASE MANAGEMENT OVERVIEW

- The purpose of case management is to prepare the case file and the associated AUSLAB records for a statement to be written by a reporting scientist if a statement is required, or for final review. To achieve this the case managing scientist may be required to:
  - Assess DNA results to determine whether result is sufficient or whether reworking will improve results – *see section 5*
  - Assess reworked and initial results to determine which is the best profile
  - Enter final EXR/EXH results into AUSLAB – *see section 6*
  - Compile case file in an order agreed upon within teams and finalise AUSLAB pages – *see section 7*
- Statements and reports are to be prepared according to 17119 (Procedure for the Release of Results)
- All results should be communicated as outlined in 23968 (Result Communications Procedure)
- It is a laboratory policy that each Reporting Scientist is responsible for looking at and interpreting all results before reporting.

5 WORKFLOW

- Blue, red and yellow cases are allocated to a case managing scientist and/or reporting scientist for case managing of the entire case. Cases may be allocated as a result of notification by FSLU by email or by insertion on the CSRC list. The CSRC list is monitored by senior scientists.
- Green and volume cases are managed via worklists – multiple scientists may do various aspects of the case management of these cases. See flowcharts in Appendices 11 & 12.

6 ASSESSMENT OF RESULTS

- When results are available an assessment of the extent of the reworks required or whether sufficient information is already available can be made. Not all results have to be available to begin assessing whether reworks are required. All results are required to perform final case management.
- Upon receipt of a case file, case manager should check that all presumptive EXR/EXHs have been validated and case file is complete and correct (as required for presumptive EXR/EXH validation)

6.1 Checking AUSLAB for results

- To check to see whether results are available for a particular sample, go to the 9plex page and press Shift-F7 to get to results history screen. If a DNA profile is present in the 9plex column, the initial 9plex has been completed. If there are test codes present in subsequent columns, the sample may have been sent for reworks by the analytical section or case manager and processing is not yet complete.
- Operational staff may be requested to print out EPGs for case files.
- It may be helpful at this stage to print out a cumulative table to obtain a summary of the samples and genotyper batch codes for results – *see section 6.2* for how to prepare cumulative tables

6.2 Assessing results for Reworks

- If a sample has failed to yield a full profile, an assessment should be made as to whether reworking is likely to improve the result and whether it is necessary to improve the result from any particular sample or if a result from the sample is not needed due to other profiles within the case.
- If it is decided a sample does not need to be reworked or if it has been reworked to the fullest extent, it becomes the final reported profile.
- **Volume crime cases**: It is laboratory policy to only rework samples from volume crime samples until 12 alleles or greater are obtained, and to only rework by re-amplification or regenescan (no nucleospins or microcons to be ordered on volume crime samples). However, if the crime scene profile has enough information to match to an evidence sample within the case, that sample may be reworked by any means to obtain the best possible profile.
- **Allelic Imbalance**. If allelic imbalance occurs in a profile, the alleles can be reported if the case scientist is confident that both alleles at the locus are real (the case scientist can also use the presence of under threshold alleles during the assessment). The case scientist should examine the profile carefully for evidence of a mixture; if there is no evidence of a mixture both alleles can be reported. This should be verified by another scientist prior to acceptance. The case managing scientist who wants to accept the alleles as true should record this on the EPG and the reviewing scientist should countersign to approve.
- If it is determined that a better profile would be beneficial to the case, the following should be considered when determining the best reworking strategy:

  a. **The type of sample** (eg blood or cells): It is expected that a blood stain should provide a good profile where as it might not be expected that a cell swab would provide the same amount of information.

b. **The quant value**: Quant values should be considered in conjunction with the sample type and examination notes.

i. Zero Quant (0ng/uL) displays in AUSLAB as "undetermined" - The type of sample will determine the rework. May be reworked anyway if it is the only sample or critical sample for a case.

ii High Quant Value (eg. 2.0 ng/uL) - A partial or NSD profile from a sample with a high quant value may indicate inhibition. A Nucleospin clean-up may be required.

iii Low Quant Value (eg. 0.008ng/uL) - Low Quant values may be expected to obtain a partial profile. Microcons of samples below these levels are worthwhile. A low quant value for a blood sample may indicate inhibition – in that case a nucleospin is required before attempting to microcon the sample. However, it should be noted that while quant values can be used as an indicator for the presence of inhibitory compounds in an extracted sample, lack of inhibition in a quant amplification does not necessarily mean there will be no inhibition in an STR amplification. This is because the different primers, target DNA and amplification conditions are used in each reaction and this could result in inhibition to one reaction and not the other. Also 2uL of extracted sample is added to a quant amplification, whereas in an STR amplification the sample may be diluted before being added (which would decrease the concentration of any inhibitory substances in the amplification reaction), or up to 20uL added to the reaction (which would increase the concentration of inhibitory substances in the amplification reaction).

For samples worked through AUSLAB-LIMS there will be additional quant information available in the 9PLEX page for the sample:

i. PSVOL: this is the calculated volume (in uL) of DNA extract to be added to the STR amplification to achieve a total DNA amount of 1.2ng of DNA template (based on quant value).

ii. CTB: this is the CT (cycle threshold) of the DNA extract. The CT is the theoretical PCR cycle where fluorescence of a quant reaction increases over a pre-set value (ie. threshold). This theoretical value is calculated by the software that interprets the output of the reaction. The CT is compared against the standard curve of fluorescence of known-concentration samples in order to calculate the quant value. A sample that provides a lower CT value (eg. 25.34) contains more initial template DNA than a sample that gives a higher CT value (eg. 27.22). Each cycle in a PCR amplification corresponds to a two-fold increase in product, therefore a difference in 1 equates to a two-fold difference in initial template amount. The CTB is expected to be between 15-40.

iii. IPCCT: this is the CT (cycle threshold) of the Internal Positive Control. The IPCCT is expected to be between 20-30 for samples containing no inhibition. If the IPCCT is >40, it is reported as 'undetermined'.

If >20 IPCCT <30, >15 CTB < 40	= OK	(pass)
If IPCCT >30, CTB >40	= FAIL	(FULL INHIB, goes to Nucleospin).
If >20 IPCCT <30, CTB >40	= OK	(little DNA)

If IPCCT >30, >15 CTB <40	= OK	(PARTIAL INHIB, Consider Nucleospin if poor results obtained)

c. **Volume sample was initially amped at.** If a sample has not been amped at max (20uL) and has not provided a full profile, a re-amp of a specific volume or at max (20uL) may be requested. A re-amp at max may also be requested when a sample has already been amped at max if some peaks are just below reportable threshold. Normal variation of peak heights between runs may obtain a result with more reportable information. (This may be used if there is very little sample remaining). Amping at multiple volumes may be required if the result is urgent. To determine the volume of sample required in the amp see below. If a sample has been amped at max, and no inhibition is evident, it might be appropriate to consider microconing.

d. **The number of alleles** obtained in a DNA profile: 12 alleles plus amelogenin are required for reporting a match on NCIDD. Samples below this stringency, but above 6 alleles may be loaded to NCIDD and searched against the database, however these samples are not routinely searched and reported. (Refer to 22619 Uploading Profiles to NCIDD, Creating and Reviewing Links)

e. **Examination Notes**: If a sample is described as dirty or sooty or if the sample was on a heavily dyed item, eg. dark denim, then a nucleospin may be required to remove any inhibitors. Samples known to contain sperm have also been observed to return an NSD profile after initial extraction with no indication of inhibition. It has been noted that nucleospin clean ups often results in improved or full profiles for these samples.

f. [redacted] **Offence Details (if available)**: If the sample is important to the case then reworks may be required. The information from the [redacted] Item packaging or from Case Conferences may assist in determining the evidential value of a particular item. If the sample does not provide any further information then there may not be any benefit to reworking.

g. **Results already obtained**. If multiple samples have been submitted for an item and 1 or more full (or sufficient) profiles have already been obtained there may be no need to continue reworking other samples from that same item. A partial matching profile is often sufficient if other better profiles already exist for the same item. This has to be considered carefully and in the context of the case. If it is suspected that there is a possibility that there may be another profile present or other contributor then reworks should be carefully considered.

6.3 Explanations of Common Reworking Methods

5.3.1 Microcon – A microcon is used to reduce the volume of a sample to increase the DNA concentration (and therefore the amount of DNA put into an amplification reaction). This is achieved by centrifuging sample through a size exclusion membrane that allows smaller molecules, such as salt and water, but not DNA, through.

Samples may be requested to be microconed to half, full or 30 uL. Microconing to half reduces the volume of the sample by approximately half; microconing to full reduces the sample volume as much as possible, usually to ~10-15uL; microconing to 30 uL reduces the volume to ~30uL.

If 24uL or greater is present in the sample after microconing, a quant will be performed on the sample. If less than 24uL is present, the sample will not be quanted and the entire

remaining volume of sample (or 20uL, if >20uL is present) will be used in the amplification reaction.

The final volume obtained from a microcon may be obtained in AUSLAB on the results history screen in the column with the microcon test code. However, if the final volume is not displayed, the case scientist can go to I:\Results\MRes and find the .txt file for the microcon batch ID the sample was run on.

Due to some variation in volumes after reworking it may sometimes be possible to rework a sample that has already been microcon concentrated. Generally a volume less than 20uL is remaining. However if the volume left is approximately 50uL or greater a further microcon may be requested.

For further information see 19544 Concentration of DNA Extract using Microcon Centrifugal Filter Devices.

Microconing might be a good reworking strategy if a sample has a low quant value, and has no indication of inhibition.(If there are indications of inhibition, should nucleospin the sample first and then microcon)

5.3.2 Nucleospin – A nucleospin clean-up is used to bind the DNA to a silica membrane which is then washed in an attempt to wash inhibitors away and purify a sample. As the final volume for a sample that has been cleaned up via nucleospin is approx. 100uL (less after quant and amp are performed) there is sufficient to Microcon the sample. It is also possible to re Nucleospin a sample if this is required.

For further information see 20967 Nucleospin Extraction of DNA

Nucleospining might be a good reworking strategy if a sample shows signs of inhibition or if examination notes suggest sample is from a dirty sample or from sperm.

5.3.3 Use a different Amp volume – Insufficient DNA in an amplification reaction could result in a partial profile. The use of too much DNA could also result in a partial profile or NSD as excess DNA in an amplification reaction can cause preferential amplification of the smaller molecular weight loci, or inhibit the reaction altogether. Case managers can request samples be re-amplified at different volumes if either of these is suspected. The maximum volume of sample that can be added to an amplification reaction is **20 uL**.

Initial amp volumes for all samples is calculated in relation to the quant value with the goal of adding 1.2ng of DNA into the amplification reaction.

$$\frac{\text{Amount of DNA(ng)}}{\text{Sample conc.(ng/µL)}} = \text{Volume of Sample Required for the Amp(µL)}$$

Example: $\frac{1.2\text{ng}}{0.1\text{ng/µL}} = 12\text{µL}$

(NOTE: Prior to CW1484 the amp volume was calculated using 2ng/uL)

Note on dilutions: samples can be requested to be diluted up to 1 in 20 as part of an amplification reaction – *see section 5.4.1* below. Higher dilutions require an extra barcode to be requested so that a manual dilution is made -*see section 5.3.6* below.

The aim of dilutions using SV2 and TV2 is to obtain a concentration of DNA of 1.2ng/uL, so that 1uL from this solution can be used in the amplification reaction (thus adding 1.2ng of DNA). Use equation below to determine values of SV2 if a dilution is required. TV2 is always 20 – SV2 (so that SV2 and TV2 add up to 20).

$$C_1V_1 = C_2V_2$$

C_1 is the concentration of the DNA extract as determine by the Quant reaction – obtained from the results history page

V_1 is the volume of the extract to be added to the dilution (*this is the value that is to be calculated* – SV2)

C_2 is the desired concentration of the dilution – usually 1.2 ng/uL as mentioned above, but the case manager may decide they would like to create a dilution with a different concentration depending on the results of the initial amplification.

V_2 is the final (total) volume of the dilution – this is *always* 20 uL

Therefore the equation may be re-written as:

$$V_1 = C_2V_2 / C_1$$

OR

$$SV2 = (1.2 \times 20) / Quant$$

Re-amping might be a good strategy if sample has loci with AI, is partial and has not been amped at max or if it is suspected there is XS DNA causing inhibition.

5.3.4 Genescaning - Re-Genescans involves re-running a specific amplification reaction product through the 3130 capillary electrophoresis instrument.

Regenescanning might be a good strategy if there are spikes, blobs or bad baseline interfering with the interpretation of the profile, or if sample has been consumed and there are peaks just below threshold that might become reportable is amp product if regenescanned.

5.3.5 Pooling of samples – Case manager can request multiple samples submitted from an exhibit be pooled. This is usually done in combination with microconing to concentrate the DNA. Take note of the maximum volumes that can be added to microcon and nucleospin columns if planning to use this method. See Appendices 7 and 8 in this document for the instructions for pooling pre-LIMS samples and 17142 Examination of Items for pooling post-LIMS samples.

Pooling of samples might be a good strategy if multiple samples have been submitted from the same area and have yielded partial or NSD profiles.

5.3.6 Dilutions – Samples can be diluted up to 1 in 20 through a re-amplification request. However, if the sample is still showing signs of excess at this dilution, it may be necessary to dilute the sample further. Scientists in the analytical section will order dilutions on samples that are identified at quant stage to require additional dilution. However, it may only become clear after a profile is obtained that a sample will need to be diluted. In this case the case manager can request a sample be diluted and then re-quanted and amplified.

Dilutions of samples may be needed if a sample is showing signs of XS or PA even when diluted 1 in 20 before an amplification.

5.3.7 Resampling – If an item sampled obtained a NSD profile after all rework options have been exhausted resampling of the item should be considered. If this is not possible other items were not initially examined should be considered.

5.3.8 Spin-baskets – A spin-basket contains the original sample that was submitted to the analytical section and extracted. If the case managing scientist determines that this sample may still contain information that cannot be obtained by any other means, they may request that the sample be re-extracted. (see Appendix 10)

5.3.9 Other Combination Reworks - If sufficient volumes remain other combinations of reworks may be possible. However this is a rare occurrence. An example may be a piece of denim submitted as NUCC (nucleospin cells) and a low quant value is obtained with a partial profile. Microcon concentration may be required to obtain further information.

6.4 Requesting Reworks

6.4.1 Reworks on Post-LIMS samples

- All reworks for current LIMS samples are carried out through the <SF7> Results History screen of the sample.
- *See sections 5.2 and 5.3* for an explanation of assessing when a rework is required and the different types of reworks available.
- The rework process is driven by specific tests codes for each rework available for a sample. Refer to 24486 Explanations of Additional Test Codes for an explanation of the reworks available in LIMS and the test codes to be used.

To request a rework:

- Enter onto the 9PLEX page of the sample
- Press <SF7> to enter into the results history screen
- Press <SF8> for 'rework sample'
- Enter in the reason for the rework, eg. partial profile
- Enter in the rework test code, eg. AMP1CW or press <F1> for the look up table
- Prompt appears 'Are you sure y/n ?' – press 'Y'
- Results History screen now displays a new column with the rework test code
- The rework for the sample will now be processed through the Analytical Section.

- If the rework is for a **re-amp,** the case manager needs to specify the volume
  - Highlight a volume field (SV1 etc.) and press <F2>
  - Prompt appears 'Are you sure y/n' – press 'Y'
  - Enter volume required and press enter
  - This step needs to be repeated for **all** volumes
  - SV1 and TV1 are used for a normal amp, eg. if the sample is to be amp'd at 3uL, then SV1 = 3, and TV1 = 17 (ie. 17uL of buffer). **SVl and TV1 must add up to 20uL**.
  - SV2 and TV2 are used when a dilution is required for an amp (ie. if an amp volume less than 1 ul is necessary, eg 1/10 ul). For a normal amp these fields need to be entered as '0'. To enter the volumes required for a dilution see 24012 Miscellaneous Analytical section Tasks.

- If the rework is for a **Regenescan**, the case manager needs to specify which amplification batch and sample position they would like regenescanned. This information is obtained from the Audit Trail (if the sample has been previously amplified multiple times, be careful to choose the correct batch). The Amplifcation Batch ID and position number of the sample for regenescan should be entered into **Specimen Notes** for the sample after the Regenescan code has been requested on the Results History screen. The information entered needs to be checked by a second case managing scientist and a second specimen note entered indicating the information is correct.

- When requesting a **microcon** rework, you must enter in **processing comments**, eg. half microcon, etc. The processing comments for microcon and nucleospin reworks display as a prompt when you enter in the rework code on the SF7 Results History page.

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- The processing comments field for microcon and nucleospin reworks are also available on the second 9PLEX page of the sample after you have requested the rework (ie. press page down from the first 9PLEX page).
- To request a **microcon straight after a nucleospin**, request a nucleospin test code only and then enter in the nucleospin processing comments the details, eg. microcon after nucleospin.

Extra barcodes required for processing of a sample

- The rework process is driven by specific tests codes for each rework available for a sample. There is a limit to the number of test codes available for reworks. eg. For case work samples, there are 3 x re-amp test codes; 2 x nucleospin test codes; 2 x microcon test codes and 1 x regenescan test code.
- If a sample requires extra reworks but the available test codes have been used, an extra barcode needs to be created for the sample. See *Appendix 6* for flowchart on how to register an extra barcode for a sample for additional reworks.
- Another process that requires the use of an extra barcode is when several samples are pooled together. See *17142 Examination of Items* for how to request pooling. Note: for pooling after initial amplification, 9PLEX codes should have already been ordered on samples to be pooled, therefore it is not necessary to enter 'pool samples' into 9PLEX processing comments.
- Samples that require dilution will also require an additional barcode to be requested for dilution. See *Appendix 9* for the instruction for requesting a dilution of a sample.
- Refer to *section 6.6* for compiling and finalising results for samples with an extra barcode for reworks, diluted DNA and the pooling of samples.

Refer to 24486 Explanations of Additional Test Codes for the rework test codes used in AUSLAB-LIMS.

6.4.2 Reworks on Pre-LIMS samples

- If a sample has been completed in DNAMaster/DAD by Analytical (ie. If a final profile has been entered into DNAMaster/DAD for that sample; now stored on DAD) then any subsequent reworks required on that sample must be carried out through AUSLAB-LIMS.
- The first rework of a Pre-LIMS sample in AUSLAB-LIMS will be different from the normal rework process in AUSLAB-LIMS. However, any subsequent reworks after the initial rework will be carried out in the normal process (See *section 5.4.1* above).
- For the initial rework through AUSLAB-LIMS, from the registration screen (shift-F10), sample type should be changed to 'TRANSFER'; sample description should be changed to contain the DNA# at the beginning; a 9plex test code should be ordered, using the processing comments to identify the type of rework required; and the DNA# should be entered into the connected barcode field once the registration has been saved. Note: Transfer must be entered before adding the 9PLEX test code
- See *Appendix 7* for how to request the pooling of samples with results in DAD in AUSLAB-LIMS and *section 6.6 and 6.7* for how to finalise and report the results.
- If a sample to be reworked in AUSLAB-LIMS has never been registered in AUSLAB before (eg. an old F# sample) see *Appendix 5* for how to request a rework.

6.5 Cofiler

- The case manager can request a sample be amplified with the Cofiler kit which amplifies an additional 4 loci.
- This should be requested from the Registration screen <Shift-F10> from the 9PLEX screen, with the test code 'COFIL'.
- The cofiler screen, once ordered will have its own results history screen which can be accessed using <Shift-F7> from the cofiler screen.
- After a COFIL test code has been requested, the case scientist should go to the results history screen for cofiler, and manually add the amplification volumes (SV1, SV2, TV1 and TV2). It is best to request a cofiler amplification after a sample has successfully provided a 9PLEX profile, then the same volumes that provided a 9PLEX profile can be used in the COFILER amplification.
- Cofiler profiles need to be saved as preferred on the Results History page using the same procedures used for 9plex results history pages (see *section 6.1* below); Cofiler tables need to be exported separately, using the same procedure as used to export results tables for 9plex results, detailed in *section 6.2*.

6.6 Sub-sampling by Analytical

- Between 29 October 2007 when the first DNA IQ casework batch was created, and 19 March 2008 when routine Off Deck Lysis procedures began, the extraction process required that some samples be sub-sampled in analytical prior to extraction.
- Samples extracted between these dates may contain a Specimen Note indicating the sample was too large and was sub-sampled by analytical scientists.
- For these samples, the case manager can request that the remainder of the sample be processed, if satisfactory results were not obtained from the extraction of the portion sub-sampled by analytical scientists.
- This is performed by copying the registration of the original sample and registering a new barcode with the sample type "TRANS". The original sample barcode should form part of the Sample Info field and "re-extract" should be entered into the 9PLEX processing comments. (*see flowchart in Appendix 10*)

6.7 Cease Work

- For any sample that requires work to be ceased on it a CWORK test code should be request from the SF7 results history screen (like any other re-work test code). Also the priority of the sample should be changed to 5 on the registration screen (shift-F10)
- This will allocate the sample to the cease work batch allocation list, then we will create batches of samples and actually cease the work on them. If samples have already been amplified they will be continued through to final results, but if the sample is at a stage prior to being amplified, it will be stopped.
- If work is to be re-started on a sample then leave the CWORK test code and order a re-work test code as appropriate. If the sample had not been extracted, then order a second barcode the same way that re-extracts are ordered.

7 FINALISING RESULTS

Once a result has been chosen as the final result for a sample, the result should be saved in AUSLAB as the best profile, and a final result line should be entered in the relevant EXR/EXH page for transfer across the forensic interface.

7.1 Saving preferred profile in AUSLAB

- The results of a sample are displayed in the Results History screen – accessed from the 9PLEX page of a sample. The Results History screen is specific for each type of test panel (eg. 9PLEX, COFIL).
- This screen lists all of the results that have been obtained through routine work and rework. One column is used per rework test code.
- The column contains the test code of the rework, the quant result, the profile result and the genotyper ID.

<u>To finalise a sample with a preferred profile</u>

- From the 9PLEX page press <SF7>, this takes you into the results history screen
- To select the preferred profile, move the cursor (by using the arrow keys) onto the column of the preferred profile, and press <F7> - an asterisk will be displayed on the top of this column
- Press <SF6> to save the preferred profile. This copies the preferred profile onto the 9PLEX page.
- To change the preferred profile, simply enter back into the results history page and repeat the above steps, for the new preferred profile. (Note: the asterisk sometimes by default display on the first column in the Results History screen).



Diagram 1: Results History screen

- **NOTE:** Changes are able to be made to the saved preferred profile, eg. if the scientist thinks that a peak is excess stutter instead of a true peak. However, any changes should be made on the Results History screen and the preferred profile re-saved and need to be made <u>before</u> the 9PLEX page is reviewed. Additionally, the scientist making the changes needs to insert an audit entry stating why they made the change. To insert an audit entry, enter onto the 9PLEX page, press <SF8> for the audit trail, and then press <F5> to insert an audit entry. These changes also need to be reflected on the EPG print out for the sample. (The original genotyper file is not to be altered)

- To complete a 9PLEX page in AUSLAB-LIMS. The 'DNA Profile Result' field and the 'Completed Date' field automatically populate when a profile is saved as the preferred profile to the 9PLEX page. If the 9PLEX page needs the profile section to stay blank (eg. Diluted DNA) then these fields need to be manually entered with 'Completed' and the date.

7.2 Printing cumulative tables

- Cumulative, or results, tables may be prepared in the initial stages of case management to assist with printing EPGs – cumulative results table list all samples from a case in one excel table, including which Genotyper plates they have been run on.
- Cumulative tables must also be prepared at the conclusion of case management to represent final results.
- Cumulative tables are excel files. The table formatting can be changed to suit the preferences of a particular team or reporting scientist. **Results should not be edited in the cumulative table** – all changes to results should be made through AUSLAB with appropriate audit entry or through the DADI by a Corrections User

7.2.1 Post-LIMS (AUSLAB) Cumulative Tables

The Cumulative Results table displays selected results for all samples registered under a particular UR number. If you are on the 9PLEX page for a case the Cumulative Results table will display all profile information for each sample.

To create a Cumulative table for results:

- Enter onto a 9PLEX page of a sample for a particular case
- Press <F9> from the 9PLEX page, this will display the Cumulative Results for the case
- Press <Control F11>
- Prompt appears "OK to save table to disk ? (y/n)" - press 'Y'
- Prompt appears "Enter filename: "
- Type in the file name and destination that you want the file to save to, eg. H:\[redacted].txt **Note**: it is essential to include the **'.txt'** extension at the end of the file name.
- Open the macro 'QIS 19952R1 Cumulative Results v0.2.xls' located in I:\Macros.
- Press the button 'Import New Results' and enter your initials
- Navigate to find the saved Cumulative Results file and double-click on it.
- The macro will then import the Cumulative Results into a table format
- The output file that was saved to the H drive can then be deleted.

NOTE: The Cumulative Results function will **only** display samples for one particular UR number. All evidence samples, even if associated to the case, and including COR samples and other CASE associated cases, will not pull into the one Cumulative Results table. A Cumulative Results table has to be exported for each different UR number. To combine the different UR numbers in a table see below.

NOTE: The Cumulative Results table will only display profiles for samples where the preferred profile has been saved to the front 9PLEX page. Although a sample may have profile results available in the <SF7> Results History page, the profile won't be pulled into the Cumulative Results table until a preferred profile is saved. (see *section 8.1* for saving preferred profiles)

Not Current



Diagram 2: Cumulative Results table in AUSLAB

To combine different UR numbers in a table:

- Export separate Cumulative Results tables for each different UR number that needs to be displayed together in a final table by the previously mentioned method.
- Import the first file into the macro 'QIS 19952R1 Cumulative Results v0.2.xls'
- Then press the 'Append Data' button and enter your initials
- Navigate to find the next saved Cumulative Results file and double-click on it.
- Continue to append each file

Note: The name associated with evidence samples will not by default be displayed in the table. They can be manually added to the Sample Info field on the registration screen by the case managing scientist, or changed on the excel spreadsheet.

7.2.2 Pre-LIMS (DNAmaster/DAD) Results Tables

- Pre- LIMS, all results were loaded into an excel spreadsheet known as DNAmaster. In 2008 these results were transferred to the DNA Analysis Database (DAD).
- Results can be retrieved from DAD using the Interface (DADI). Refer to Use of DNA Analysis Database Interface (25583)

7.3 Requesting a profile be uploaded to NCIDD

- Case managers are responsible for choosing a representative profile for each unique profile seen within a case for upload to NCIDD.
- Profiles must have at least 12 alleles for NCIDD matching.
- Profiles that match known deceased person and profiles that match complainants in sexual assault cases are not to be uploaded to NCIDD. See 22619 Uploading Profiles to NCIDD, Creating and Reviewing Links for QHFSS policy on which case work samples can be uploaded to NCIDD
- Once a case manager has chosen samples that should be uploaded, they need to print out an upload form and attach to it a copy of the profile to be uploaded.

- If the profile matches to a reference profile within the case, the case manager should fill out the warm link section of the form.
- If the profile to be uploaded is part of a mixture, the case manager must circle on the upload form which part of the mixed profile is to be uploaded (eg. major profile) and a validated mixture page should also be attached to the form.

Note: Profiles of less than 12 alleles may be loaded to NCIDD in special circumstances. Please consult with the Senior Scientist in Volume Crime before requesting profiles of less than 12 alleles be uploaded as any matches will be reported through an intelligence report (and not through EXR/EXH or statement).

7.3.1 Printing an NCIDD upload form from AUSLAB

- The form to upload a sample to NCIDD is a print report on the 9PLEX page. Therefore, to obtain the upload form for a sample, press <SF11> on the 9PLEX page, then <F7> and direct to a printer.

7.3.2 Printing an NCIDD upload form from DADI

- To obtain an upload form for a sample with results on DNAmaster/DADI, open DADI and search for the sample and click on the Print Upload Form button. Refer to Use of DNA Analysis Database Interface (25583)
- **Note**: a barcode will need to be printed from AUSLAB and attached to the form in the appropriate location for these samples.

7.4 Requesting a mixture page in AUSLAB

- If a mixture is present in a profile, and it is possible to separate the mixture out into major/minor contributors or if the mixture can be conditioned against a known profile, a mixture page should be used.
- Any interpretations of mixed profiles are performed using the appropriate request code in AUSLAB which provides a mixture interpretation page for that sample.
- Mixtures should only be interpreted by competent persons. See 17168 Procedure for DNA Profile Statistics

Not Current

To request a mixture interpretation page:

- Enter onto the 9PLEX page of the sample
- Press <SF10> to enter into the sample registration screen
- Enter in the test code required, ie. MIXT for major/minor, MIXC for conditioning
- Save registration <F7>,<F4>,<F4> to return to the main 9PLEX page and page down until the mixture page appears
- Profile details and mixture determinations can now be entered manually (by first pressing <F2>, or <SF2> for bulk edit).
- The completed date must also be filled out manually by the case manager at the time of the interpretation of the mixture.

To print the mixture interpretation page press <SF11> on the mixture interpretation page, then <F7> and direct to a printer. This page should be included in the casefile, and has to be attached to the upload form if the sample is to be loaded to NCIDD.

7.5 Final EXR/EXHs

Final EXR/EXHs should be entered in accordance with 17119 Procedure of Release of Results and in consultation with 23008 Explanations of EXR Results

Example (of how a final EXR will be entered – EXH pages appear slightly different):

Lab No.	Rev'd	Result/Status	Linked No.	Warm Link Name
[redacted]		9 loci DNA profile	[redacted]	[redacted]

Where:

"[redacted]" is the barcode of the sample;

"9 loci DNA profile" is the result

"[redacted]" is the barcode of the reference sample that the profile from the sample matches. (Note: to be included in this field the reference sample must be an evidence sample that has been taken by QPS in relation to this specific case).

"[redacted]" is the name associated with the reference sample of barcode [redacted]

Note: If a profile obtained from a casework sample does not match any reference profiles within a case (or if the case has no reference profiles), 'UK M1' (for a male profile); or 'UK F1' (for a female profile); or 'UK1' (if gender is undetermined) is entered into the Linked No. field (nothing is entered into the Warm Link Name field.

7.6 Finalising Results for Extra Barcodes

Where an extra barcode has been used for the purposes of pooling or for additional reworking when the number of rework codes has been exhausted, there are some additional steps that need to be taken in AUSLAB to make sure there is a clear link between the two barcodes and to explain why the final result for a sample may be reported under a different barcode to the barcode a presumptive result was reported under.

7.6.1 Finalising 9plex pages with extra barcodes

- Every 9plex page should have a profile saved as preferred (unless sample was transferred to a new barcode before it produced a 9plex result, eg. samples pooled after extraction, samples diluted by analytical after quant).
- Connected barcode field should contain all barcodes that have been used in the processing of the sample and/or all barcodes a sample has been pooled with.
- Accepted barcode field should contain barcode under which final preferred result was obtained, even if it is the same barcode as on the 9PLEX page.

7.6.2 Finalising EXR/EXH pages for samples with extra barcodes

- If the final preferred result is under the same barcode as the original barcode used to report the presumptive results, the final result can be reported via EXR/EXH under the same barcode. (It is not necessary to inform QPS via EXR/EXHs that the sample has undergone additional processing under a different barcode, if that processing did not yield an improved result)
- If the final preferred result is different to the original barcode used to report presumptive results (but refers to the same sample), the EXR/EXH line: 'Sample processed and final results under' should be used in the manner described below. The final result is then reported under the barcode that it was processed under.

Example 1:

A TMB positive swab with barcode [redacted] was sampled and submitted to analytical. The sample was diluted in analytical due to an excessive quant value. This diluted sample assigned the barcode [redacted] and continued through the amplification process. The profile for [redacted] was assessed to be male, full and unique within the case (with no reference profiles).

Lab No.	Rev'd	Result/Status	Linked No.	Warm Link Name
[redacted]		Presumptive blood test pos. Submitted-results pending		
		Sample processed and final results under	[redacted]	
		9 loci DNA profile. Uploaded to NCIDD	UK M1	

Example 2:

Wet and dry swabs of the handle of a knife were taken and submitted separately to the analytical section. Exhibit barcode (knife) – [redacted] Wet swab – [redacted] Dry swab – [redacted] The presumptive EXR/EXH was entered under barcode for the wet swab (no EXR/EXH was entered for the dry swab, as it is a redundant result for the knife). Both the wet and dry swab yielded partial profiles with only NR peaks, and it was decided to pool the samples. Samples were pooled under barcode [redacted] and processed further. A partial profile (13 alleles) matching that of the suspect (John Smith), barcode: [redacted]

Lab No.	Rev'd	Result/Status	Linked No.	Warm Link Name
[redacted]		No presump. test reqd. Submitted-Results pending		
		Sample pooled and final results under	[redacted]	
		Partial DNA profile		[redacted]

7.7 Finalising Results in AUSLAB for Pre-LIMS samples

This is for samples that were initially processed under the DNAmaster system, but have since undergone additional processing under LIMS.

- Samples processed pre-LIMS were assigned an additional identifier by the analytical section – a DNA#. This number was used to identify samples during processing in analytical.
- Samples extracted through DNAMaster and further worked in AUSLAB-LIMS will have results stored in both DNAMaster/DAD (sample ID – DNA#) and AUSLAB (sample ID – barcode).
- When this has occurred this should be highlighted by filling out the Connected Barcode field on the 9PLEX page for with sample with the DNA#.
- Note: Any samples processed pre-LIMS will have a 9PLEXX page for all DNAmaster/pre-LIMS processing. The 9PLEXX page does not have a display section for the profile of the sample.
- If the final preferred profile is in DNAmaster/DAD, the Accepted Barcode field should be filled out with the DNA #
- If the final preferred profile is in AUSLAB, the Accepted Barcode field should be filled out with the sample barcode.
- **EXR/EXH page will be filled out with the appropriate AUSLAB barcode (following the system as detailed in the above sections), regardless of which system the sample was being processed under when it produced the best profile.**

8 CASE FILE COMPILATION

- Prior to submitting a case file for final review/statement the following is required:

a. CASE FILE

i. Ensure that all items/exhibits have been prioritised appropriately.

ii. Ensure that appropriate reworks of samples have been performed. Refer to section 9.

iii. Establish (if required) whether further testing needs to be performed

iv. Ensure that all samples are finalised and a preferred profile saved on the 9PLEX page.

v. All Genotyper printouts must be included in the case file. Each should have a brief description of the sample (ie cig butt – i/s d/s door). The best profile for each sample is selected and stamped with 'Reported Profile'. Note on any profiles containing AI whether the alleles can be confirmed. If the alleles cannot be confirmed the case scientist must make an assessment of the profile to determine if it is a true allele. If it is considered a true allele then both alleles should be reported. If it is not considered as a true allele then the smaller peak should be reported as an NR. This should be written on the printout of the Genotyper and initialled and dated. The final profile entered in DAD or in AUSLAB should also reflect this. Notes to confirm alleles at loci with AI and decisions to accept unconfirmed alleles should be signed by the person making the note and by the reviewer.

vi. Ensure that the 'Reported Profile' is correctly uploaded to DAD or is the saved preferred profile in AUSLAB.

vii. Ensure that the FTAR receipt is printed out for each evidence sample. To print the FTAR receipt page: enter onto the FTAR page, then press <SF11>, then <F7> and direct to a printer. All evidence samples can be viewed on the Shift F9 page in AUSLAB. Ensure that all evidence samples associated with the case are present in the final table.

viii. Ensure that appropriate profiles have been selected and uploaded to NCIDD. To determine which samples can be loaded to NCIDD refer to 22619. The NCIDD category for person samples is located on the FTAR page in AUSLAB (Eg. Profiles that match to the complainant or are limited purpose can not be loaded to NCIDD.) Samples are usually chosen for their evidentiary value. For each case choose only 1 example of each profile to load to the database. Eg For a B&E if the same profile was obtained from a shoe and a fridge both inside a house the fridge profile would be chosen as it is harder to explain why the profile is obtained from an object that is either permanent or not easily moved. Attach a barcoded copy of the profile to the upload form (AUSLAB form or 17050 Database uploading and searching). Ensure that the relevant EXR/EXH has been validated before submitting the Upload form to Results Management.

ix. Enter appropriate EXR/EXHs (Refer to 17119 Procedure for Release of Results).

x. If required (ie if statement) ensure that profiles requiring a genotype frequency (partial, full & major/minor) have had BRB stats appropriately performed and that the interpretation of units of measurement (e.g. billions) is correct

xi. Ensure that any mixed profiles have been correctly interpreted using the Major/Minor Contributor & Conditioning worksheets or the mixture interpretation pages in AUSLAB. A photocopy of the worksheet or a print-out of the page from AUSLAB has to be attached to the 17050 form or AUSLAB print out if the sample is being added to NCIDD.

xii. If required ensure that any complex mixtures are interpreted correctly with appropriate 'Popstats' hypotheses and/or calculations.

b. CASE FILE COMPILATION

i. The following is a guideline for the physical compilation of a case file.

ii. Page Numbering

- The Case File Particulars page is always Page 1 (except upon reactivation, the additional Case File Particulars page will be numbered page 1 and the original Case File Particulars page will be kept and renumbered the next consecutive number in the case file).
- Then Case Files are numbered from the back of the case file to the front.

iii. The items listed are in order from the back of the case file. *This is a guide for Volume Crime cases.*

- Receipt details and QP127's
- Photocopies of Packaging
- Examination Notes
- EPG (Genotyper Printouts) of all runs of crime scene sample. The best profile for each sample is stamped with a "Reported Profile" stamp. The description of the item to which each EPG relates should be written at the top of each printout. They should be in the same order as the Final Results Table with the "Reported Profile" at the top of each group of profiles for each sample.
- Any BRBStats or POPSTATS printout, Contributors to a Mixture records or Conditioning Records should be included alongside the relevant EPG.
- EPG (Genotyper Printouts) of every evidence sample. The best profile of each sample is stamped with a "Reported Profile" stamp. The name of the person must be written at the top of each printout.
- An FTAR page (from AUSLAB) should be produced for each evidence sample and be placed in the file alongside the EPG.
- Final Results Table. Any handwritten results or entries in tables must be signed and dated.
- Statement
- Any communications (UR Notes) regarding the case
- Case File Particulars Page (at the very front).
- If a case is reactivated any additional information is added on top of the original Case File Particulars Page (such as EPGs of an evidence sample, new Results table) and a new Case File Particulars page must be added (QPS No, case barcode etc should be filled out)

iv. The suggested order for items, listed in order from the front of the case file. *This is a guide for Major Crime cases.* (note: this system is particularly useful for large or complex case files)

- Copy of final statement
- Most recent printout of UR notes
- QP127s, receipts and receipt summary exam notes

- Outer packaging form and corresponding photo/photocopies (photocopy or photograph of QHFSS packaging not necessary if described adequately in notes)
- Result table (sorted on Client Reference No.)
- Stats (if same stat otherwise others after EPG for that sample)
- Reference samples – AUSLAB printout then EPG
- Exam notes:
    - Photocopies of exhibit packaging
    - Hand written notes
    - Diagrams
    - Photos
    - EPGs
    - Mixture interpretation sheets if applicable
    - Stats if applicable
- Result table is sorted on client reference column (excluding the reference samples). This enables all the submissions including re-works to be grouped together.
- Each item and its corresponding paperwork is to be ordered into the file in a logical order (either in line with the result grabber or in line with order of appearance of items in statement)
- To aid in a reader focussed statement, statement is written by grouping items by whom/where they are attributed to.

c. CASE FILE WITH STATEMENT (Refer to 17119 Procedure for Release of Results)

i. Statements contain all items received at QHFSS (even those not examined)

ii. Statement must align with the EXR/EXHs previously reported or to be reported

iii. All evidence samples have been included

iv. Complainant ("Regina" where no complainant is specified or complainant is a company) and Defendant categories are correct and appear on the statement correctly

v. The correct assisting information (pre-blurbs) has been used for the testing and examination completed.

vi. Statistics correct and printout included in case file

vii. 1 copy of the statement is included in the file (photocopy is not made until review is complete). No DRAFT statements are to be included. All peer review comments should be recorded in AUSLAB.

d. CASE FILE (Administrative Tasks)

i. Page number each page (including the reverse of the page if both sides have been used).

ii Initial & CASE No. each page

iii Include the total number of pages in the table on the front of the case file and initial and date as indicated.

Not Current

iv The Case File contents section should be filled out on the Case File Particulars page (17038) for larger cases where it may assist in the location of particular areas of the case file.

e. AUSLAB

i **EXR/EXH page** (Refer to 17119 Procedure for Release of Results)

ii **FB Methods page –** Note every procedure used in the examination, analysis and case management of the particular case with a 'Y'.

iii **9PLEX page** – Each samples needs a preferred profile saved to the 9PLEX page. The 'completed date' and the 'DNA profile result' will automatically populate when the preferred profile for a sample is saved.

iv **FBEXAM –** ensure is validated. (N/A may be used if the field is empty but requires an entry e.g Examination Trolley)

v **CS** – If statement a statement request has not been received, change the status to "Sent to Peer" and validate. If statement is required, leave as "Started" and pass case to reporting scientist. If it is thought that a statement may be required, a UR note can be entered requesting FSLU make enquiries with QPS.

vi **Return Destruction and Report Release Details** – Validate these.

vii Add a Tech Review Page if required (FBTR) (Refer to 17113 Technical Review to determine when a Technical Review is Required).

viii Add an FBCALC Page if POPSTATS or BRBStats have been used complete and validate.

f. REACTIVATED CASES

i Same as routine cases however an additional Admin and Tech Review (if required) must be requested on a new barcode (as the AUSLAB records would have already been completed when the case was originally finalised).

ii When a case file is reactivated the case status must be changed to "Reactivated" and the case completed date should be deleted from the CS page.

iii A UR note should be made detailing the reason for the re-activation. eg. Reactivated for further examination of exhibits, or Reactivated for statement purposes only. This is helpful to property point when deciding whether or not exhibits can be returned to QPS.

iv A new case file particulars page is required to easily distinguish between the part of the file that has been reviewed and the newly added pages.

v The reviewer may be specified on the Admin and Tech review pages.

vi Upon reactivation, an assessment of profiles uploaded to NCIDD should be undertaken. In July 07, it was decided (in conjunction with QPS) that all crime scene profiles (except Known Deceased) could be uploaded. To do this retrospectively was considered too laborious and not undertaken, but we would like to capture these profiles on cases that are reactivated.

9 COMPLETING A CASE

1 Case files can be written off in AUSLAB as "Report Issued", "Analysed – Report Not Required" or "No Testing Required". This is only completed after the appropriate peer

reviews have been performed. "Analysed Report not Required" and "Report Issued" should be used by DNA Analysis Scientists.

- Report Issued – used where a report has been released – eg. statement
- Analysed Report not required – used when the file has been completed and a statement is not required.
- No testing required – used when notification is received that the results are no longer required. (Refer to 16004 AUSLAB Users Manual for finalising cases with no testing required).

Notification of cases where no testing is required comes primarily through the FSLU (Forensic Sciences Liaison Unit). Details will be stored in UR notes or in an email printout from an Investigating Officer. Inactive files are to be written off as "No Testing Required" and may be reactivated if necessary. These files do not require an administrative review. Cases with any testing commenced (including examination) require an Administrative Review. Refer to 17123 Administrative Review.

2 An official report is an official document, which is signed and dated, and the organisation has accountability via the authorised analyst signing the report. Refer to 17119 Procedure for Release of Results for authorised formats.

10 STORAGE OF FILES

1 Active case files are stored with the case analyst or in the designated storage location for the work area.

2 Case files on hold (ie, not allocated to a case analyst) are stored sequentially in a filing cabinet in an agreed place.

3 Upon completion, case files should be stored sequentially in the compactus. It is important to have access to files in the event of client enquiries. Upon completion scientists should transfer cases to FBCFF1 (AUSLAB Case File Finish location), administrative staff will then store case files to the compactus.

4 If files are subsequently removed from the compactus, or from one point to another the AUSLAB storage system must be used.

5 Files should be returned to the compactus as soon as possible.

6 Case files and records are kept indefinitely.

11 EVIDENCE MANAGEMENT

1 All attempts are made to ensure that items received for examination are properly packaged, labelled and accompanied by the appropriate documentation, (refer to 17116). Any abnormalities or departures from the specified conditions are to be recorded and feedback provided to the QPS Forensic Standards Unit by ordering a Forensic Biology Feedback test code (FERRO).

2 **Note:** Examples of situations that should be recorded:

- Forensic Register issues – incorrect QPS number
- Packaging – items received wet, glass not in correct packaging
- Labelling – Exhibit labelled incorrectly or not at all
- Storage – Incorrect storage conditions

3 Refer to 17167 Forensic Biology – Procedure for the Retention and Storage of Items for details on storage of items. All items stored in the freezers and exhibit room are to be recorded and easily identified. All items should be packaged properly, sealed and

signed and labelled clearly. Movement of items should be tracked in the AUSLAB storage system.

12 CASE FILE MANAGEMENT OFF SITE

COURT

- When case files are required for court appearances they should be tracked in AUSLAB to the reporting scientist's intray and then the borrowed function should be used.
- A comment shall be recorded when prompted (and retained in the audit trail) documenting why the case file is to be removed.
- If the case file is requested by court officials offer a photocopy of the file. As the case file is the original copy and this must be retained by QHFSS DNA Analysis.

OTHER

- If a case file is to be removed for any other purpose than for court the same procedure should be followed.
- However the person removing the file is solely responsible for maintaining chain of custody and confidentiality at all times.
- There are some rare circumstances where an original case file may be required off-site and not be in the custody of a DNA Analysis staff member (eg Freedom of Information Requests). Where this is the case the Team Leader must be notified in advance. The entire case file must be photocopied and kept within DNA Analysis. UR notes should be completed explaining the circumstances, where the file is going, provide a contact name if possible and where possible the anticipated return date. When the original case file is returned the copy should be destroyed.

13 COURT APPEARANCES

1 Notices to attend and give evidence should be recorded in AUSLAB.

2 Any court appearances should be recorded in AUSLAB. A CCD code should be requested and the page filled out appropriately.

14 REFERENCES

Keith Inman and Norah Rudin. Good Forensic Practice - Obligations of the Analyst; Chapter 10. Principles and Practice of Criminalistics. CRC Press 2001.

15 ASSOCIATED DOCUMENTS

1 See QIS for access to controlled forms used in casework and the analytical section.

2 16004 AUSLAB Users Manual Forensic Biology

3 17113 Technical Review

4 17116 Receipt of Items

5 17119 Procedure for the Release of Results

6 17122 Receipt of Reference Samples

7 17123 Administrative Review

8 17137 Interpretation and Acceptance of Results using Profiler and COfiler

9	17142	Examination of Items
10	17167	Procedure for the Retention and Storage of Items
11	17168	Procedure for DNA Profile Statistics
12	19544	Concentration of DNA Extract using Microcon Centrifugal Filter Devices
13	20967	NucleoSpin Extraction of DNA
14	22619	Uploading Profiles to NCIDD, Creating and Reviewing Links
15	23008	Explanations of EXR Results
16	23959	Storage
17	23968	Result Communications Procedure
18	24469	Batch functionality in AUSLAB
19	25583	Refer to Use of DNA Analysis Database Interface

16 AMENDMENT HISTORY

Revision	Date	Author	Amendments
1	11 Nov 1998	V Ientile	
2	28 Mar 2001	V Ientile	
3	11 Jun 2001	V Ientile	
4	18 Jul 2001	V Ientile	
5	08 Jan 2002	V Ientile	9(3) – Completed case codes for FACTS
6	21 Nov 2002	V Ientile	Changes to section 9, completing a case
7	19 Nov 2003	V Ientile L Freney	Refer to AUSLAB. Remove FACTS in many places
8	07 Jun 2005	M Gardam	Included requirements for paperwork in case file ie No loose pages
9	03 Aug 2006	M Gardam	List of reference articles added
10	25 Sep 2006	M Gardam	Off site case file management, compilation of case file, case management.
11	13 Feb 2007	L Weston	Update with processes for AUSLAB-LIMS
11	April 2008	QIS2 Migration Project	Headers and Footers changed to new CaSS format. Amended Business references from QHSS to FSS, QHPSS to CaSS and QHPS to Pathology Queensland
12	10 April 2008	J Connell	Transferred section on preparing case file for presumptive EXR/EXH validation to Examination of Items SOP; inserted subheadings and table of contents; changed order of information to reflect current processes; expanded on reworking information and other processes undertaken as part of case management; added information regarding dilutions and requesting processing of samples sub-sampled in analytical; summarised finalisation requirements for samples with extra barcodes; added examples for entering final EXR lines. Hyperlinked associated documents.

Document

17 APPENDICIES:

1. The Case Management Screen in AUSLAB.
2. Methods Used in Casework in AUSLAB
3. Completing a Case with Work Done in AUSLAB.
4. Requesting reworks for Pre-LIMS samples (registered in AUSLAB)
5. Requesting reworks for Pre-LIMS samples (not registered in AUSLAB)
6. Requesting extra reworks for AUSLAB-LIMS samples in AUSLAB
7. Pooling Pre-LIMS samples (registered in AUSLAB)
8. Pooling Pre-LIMS samples (not registered in AUSLAB)
9. Requesting a dilution
10. Requesting extraction of the remainder of a sample that has been sub-sampled in analytical
11. Green and Volume Worklists – case assessment and OO tasks
12. Overview of Green and Volume Case Management Workflow

Not Current

17.1 Appendix 1: The Case Management Screen

AUSLAB test code: CS
Purpose:

The Case Management Screen is requested on the first laboratory number registered for the case. These should be only one Case Management screen for each case.

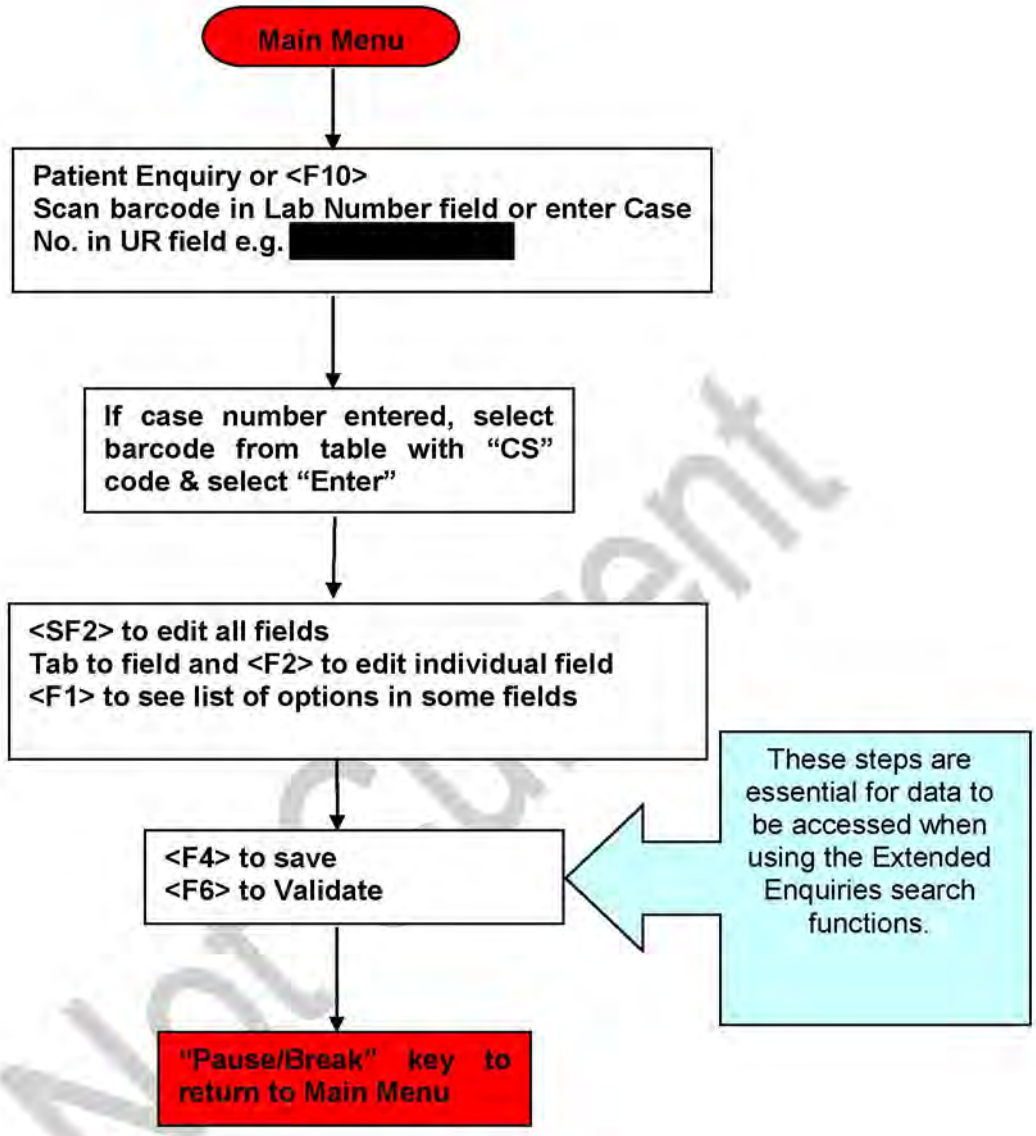
The Case Management screen provides general details on the case.

Definitions:

- **Status** – This is the case status and is used to track the workflow in the milestones page. Options for this field are:
  - RECEIVED – case has been received but not allocated.
  - ALLOCATED – case has been allocated to a case scientist
  - AWAITING ADVICE – more information has been requested. Case is on hold until further notice. This status is not tracked in the milestones.
  - STARTED – Examination has commenced
  - SENT TO PEER REVIEW – case has been completed and has been sent for Administrative and/or Technical review.
  - RETURNED FROM PEER REVIEW – case has been returned to Case Scientist for amendments during review process. Only used if changes are required, is not tracked in the milestones.
  - REPORT ISSUED – case has been completed and statement has been sent.
  - ANALYSED-REPORT NOT REQUIRED – case has been completed but no statement has been requested.
  - NO TESTING REQUIRED – case has been written off, no work was required.
  - REACTIVATED – case has been reopened for more work or statement preparation.
  - IS STATEMENT REQUIRED – Is fed back to QPS so that IO can inform FSLU if a statement is required.
  - ON HOLD SAMPLED AND STORED – Used for low priority cases for samples that have not been sent for processing.

- **People involved in the case (Surname, First, DOB, Class)** – Names, dates of birth and classes of people involved in the case, e.g. complainants, suspects, defendants, deceased, elimination. Use <F1> Help to see list of options.
- **Case Scientist** – Scientist who has been allocated the case, generally the reporter.
- **Primary Case Scientist** – Scientist who has performed the examinations.
- **Case Type** – e.g. Armed Robbery, Assault, Murder, Property, Proficiency Testing, Paternity, Sexual Assault, Coronial/DVI, Major Investigation and Miscellaneous. Use <F1> Help to list of options. This is supplied by QPS.
- **Crime Class Code** – information provided by the police, subdivisions of the case type categories.
- **Operation** – used to record police operation name if applicable.
- **Investigating Officer** – Contact officer for the case.
- **Due Date** – Date results are required, used mainly for Coronial/DVI cases or major investigations.
- **Court Date** – Date of court proceedings. May be Committal or trial. Details are recorded in UR notes.
- **Operational Priority** – Used to assist in case prioritisation. Use <F1> Help to see list of options.
- **Date Completed** – date case is completed and sent for review.
- **Exhibits** – indicates status of exhibits. Use <F1> Help to see list of options.

To Access and Edit the Case Management Screen:



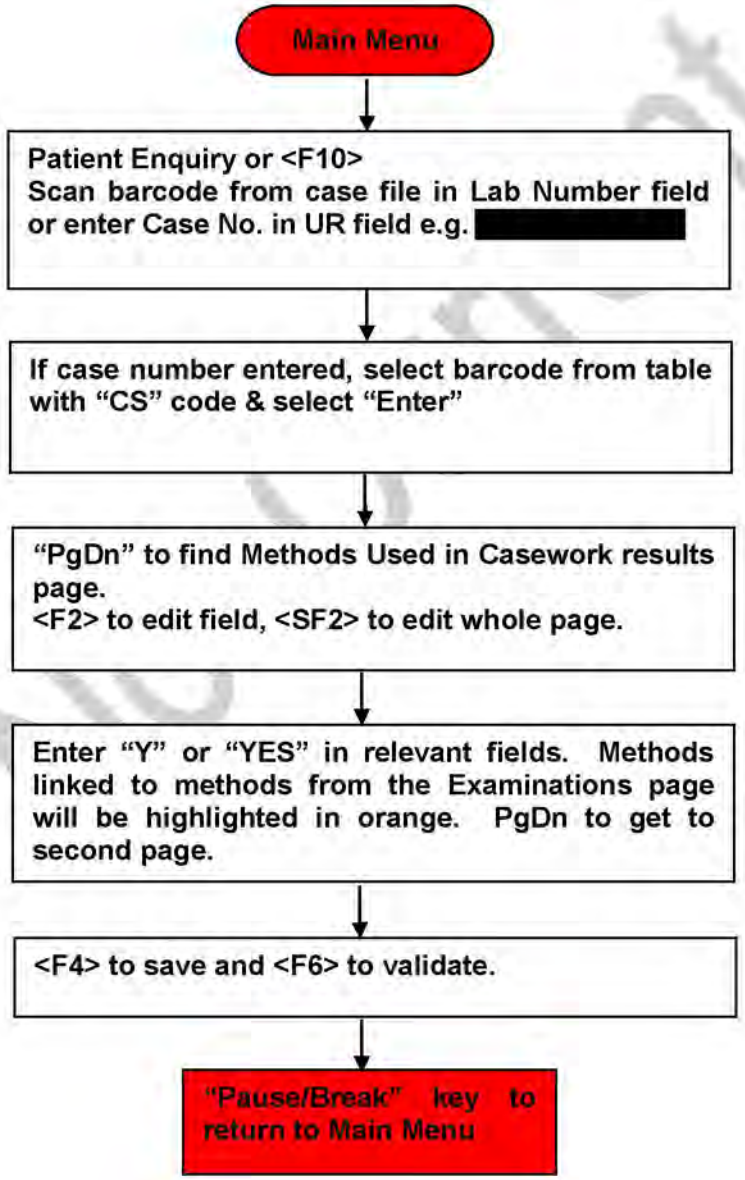
Not Current

17.2 Appendix 2: Methods Used in Casework

Purpose: The Methods Used in Casework results pages record all methods referred to in the examination of items in the case. This page records the method numbers, the latest revision of the documents can be accessed through QIS.

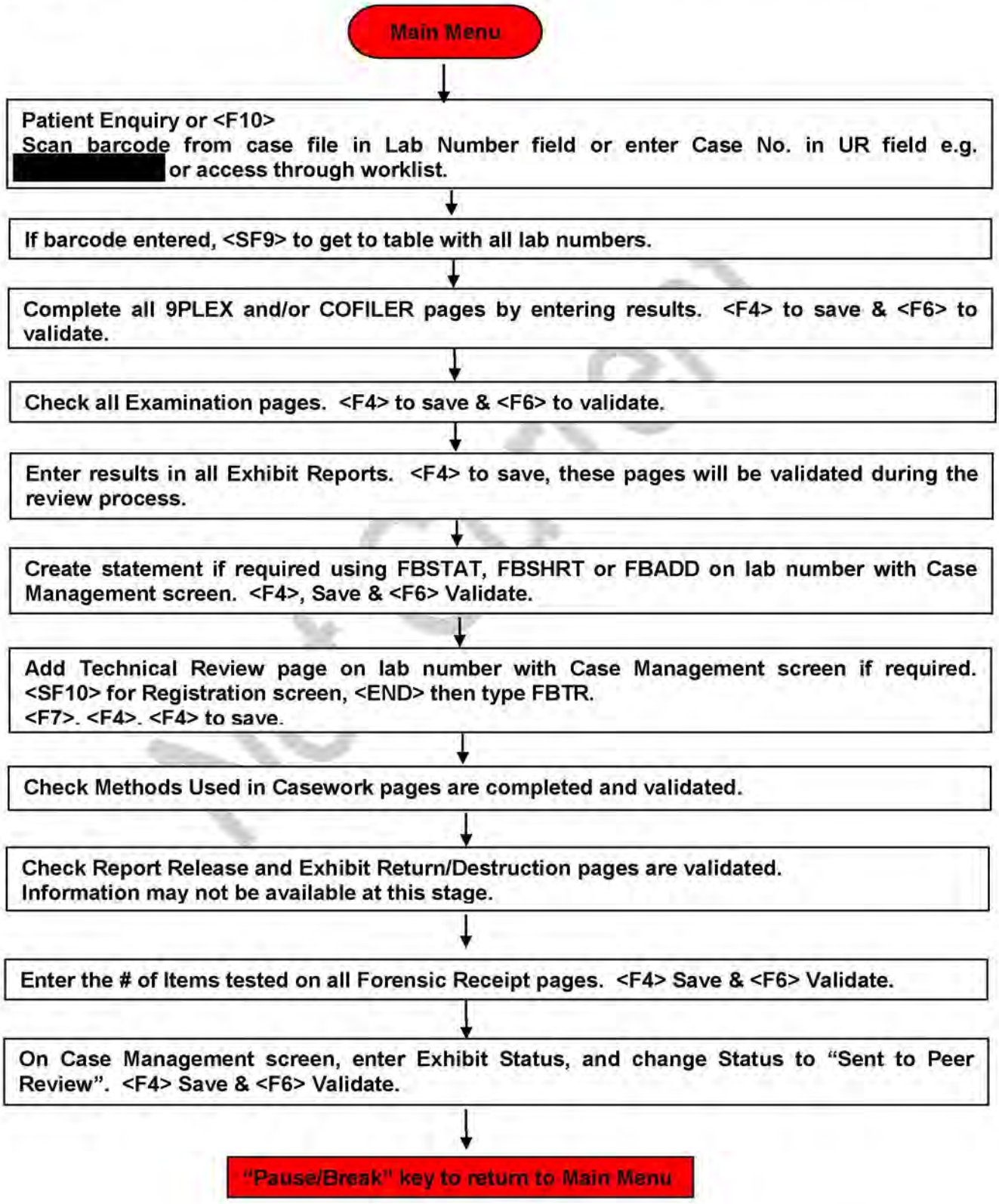
Methods used in the examination of items (such as Acid Phosphatase, Blood Screening and Microscopy) are linked to entries on the Examinations page and are highlighted in orange on the Methods Used in Casework pages when these fields are filled out on the Examinations page for items within the case.

Actions:



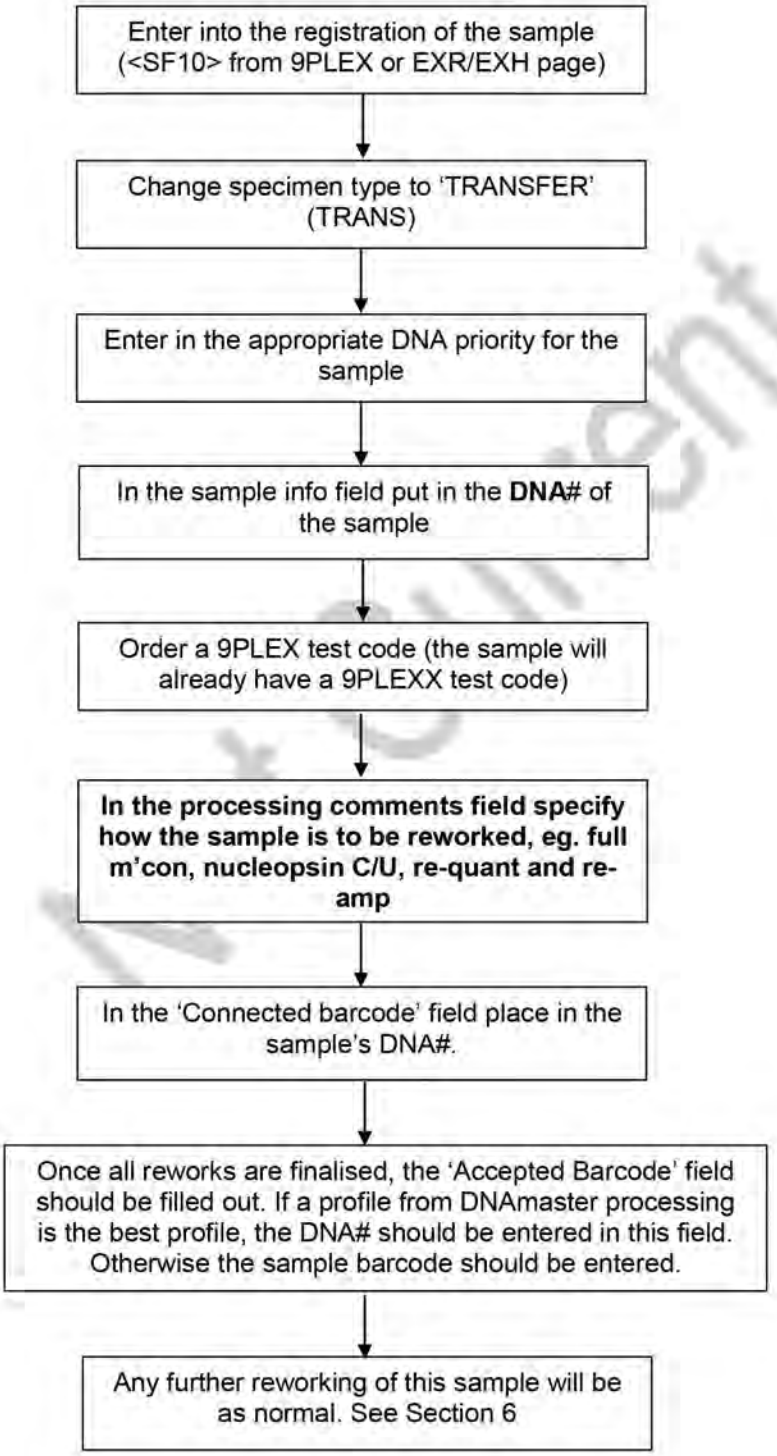
17.3 Appendix 3: Completing a Case with Work Done

This flowchart describes the steps required to complete a case in AUSLAB. This details what fields must be entered in all results pages. The individual instructions for each step provide more details.



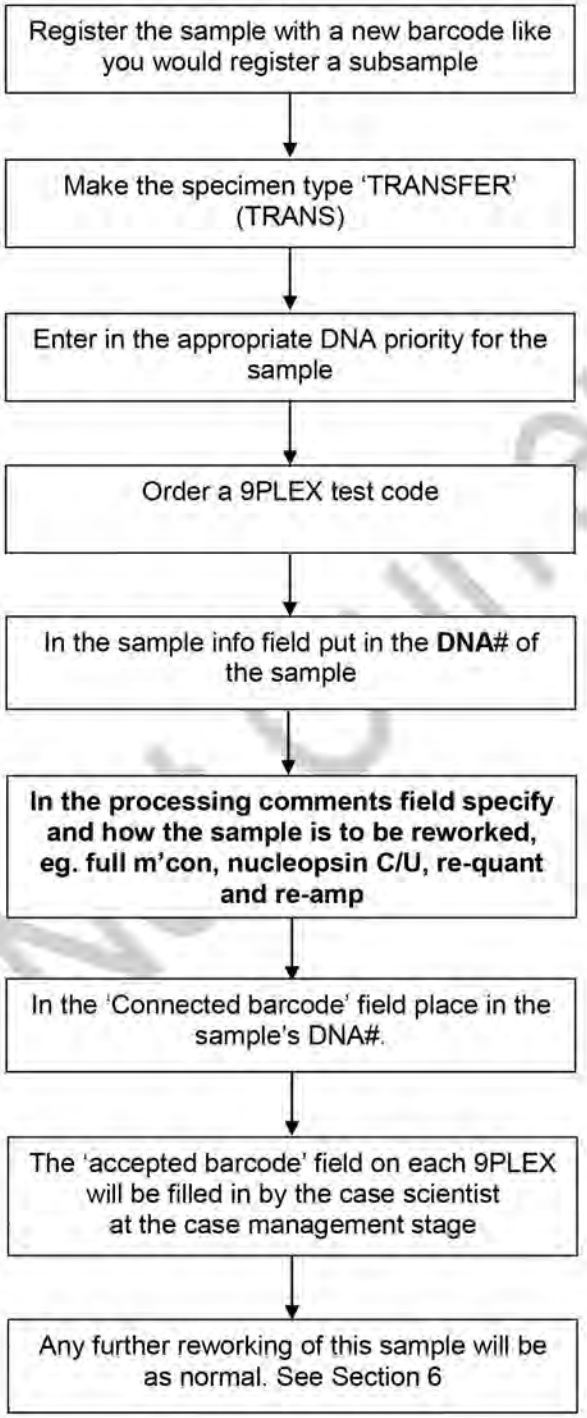
17.4 Appendix 4: Requesting reworks for Pre-LIMS samples (registered in AUSLAB)

If a sample has been completed in DNAMaster/DAD by Analytical (ie. If a final profile has been entered into DNAMaster/DAD for that sample) then any subsequent reworks required on that sample must be carried out through AUSLAB-LIMS



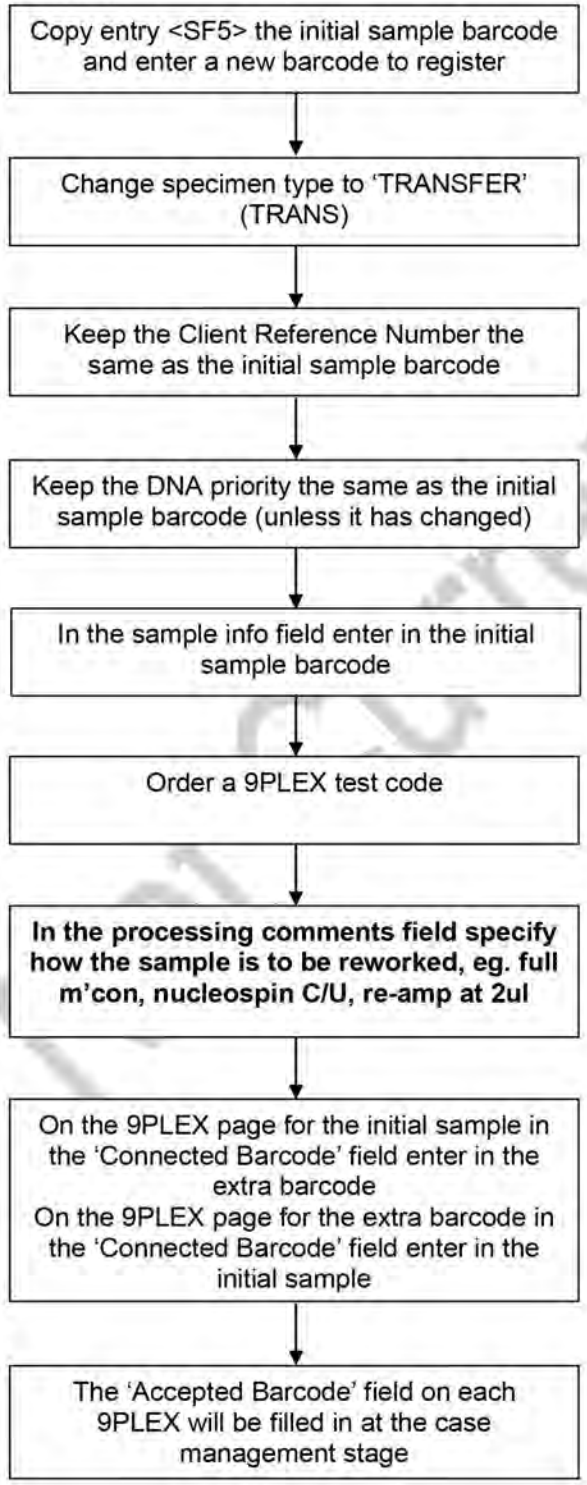
17.5 Appendix 5: Requesting reworks for Pre-LIMS samples (not registered in AUSLAB)

If a sample has been completed in DNAMaster/DAD by Analytical (ie. If a final profile has been entered into DNAMaster/DAD for that sample) then any subsequent reworks required on that sample must be carried out through AUSLAB-LIMS. Note: this is only for old cases that are not registered in AUSLAB.



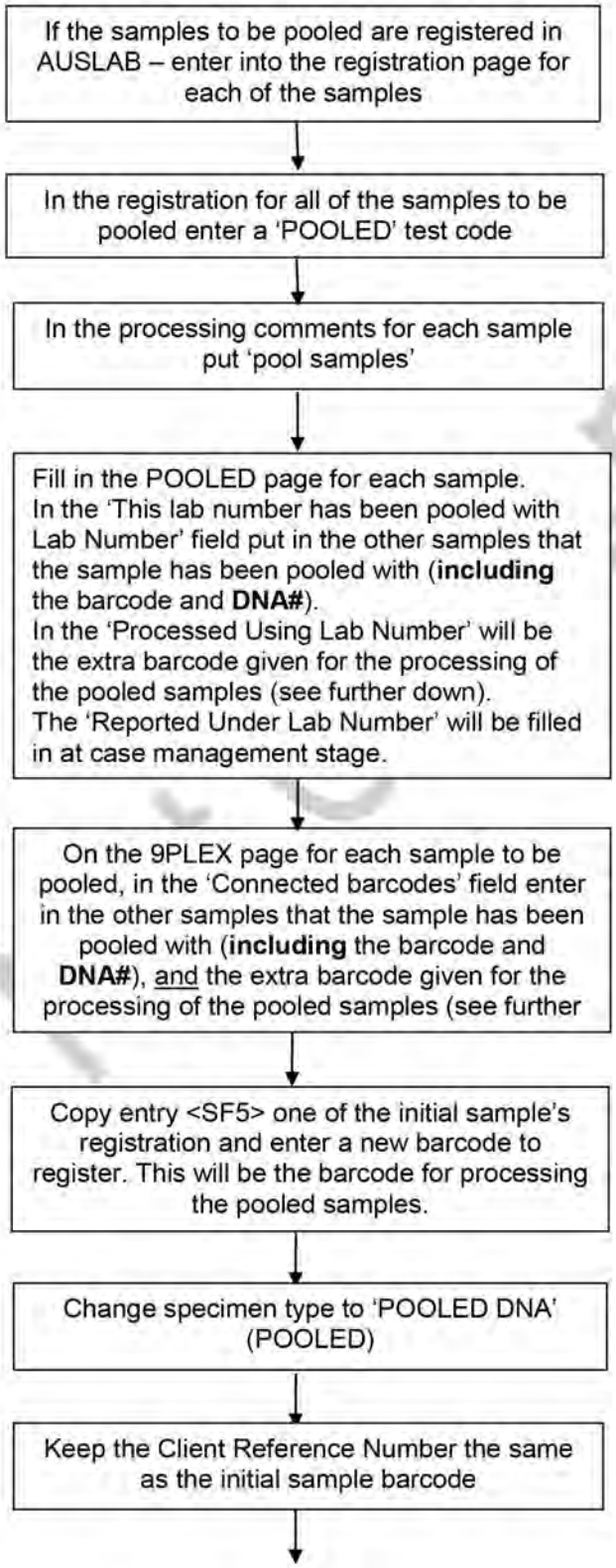
17.6 Appendix 6: Requesting extra reworks for LIMS samples in AUSLAB

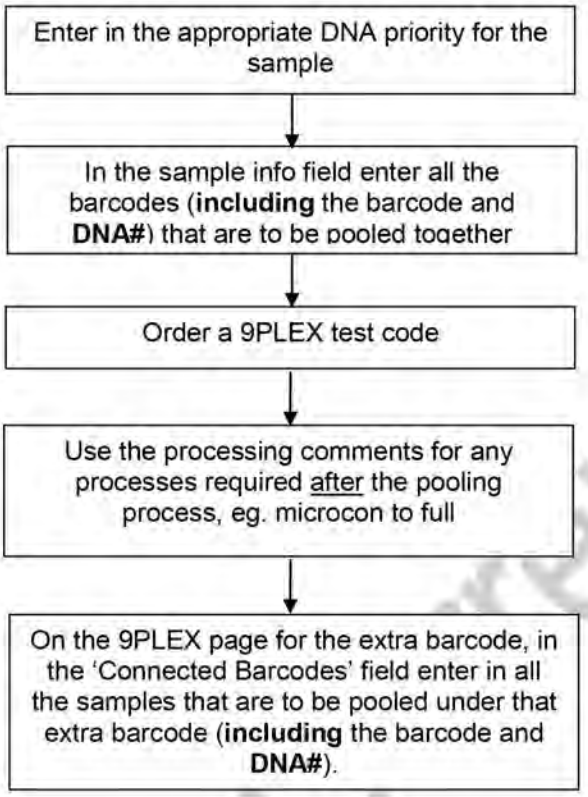
This is for samples that have always been processed in LIMs, but where the number of rework test codes has been exhausted.



17.7 Appendix 7: Pooling Pre-LIMS samples (Registered in AUSLAB)

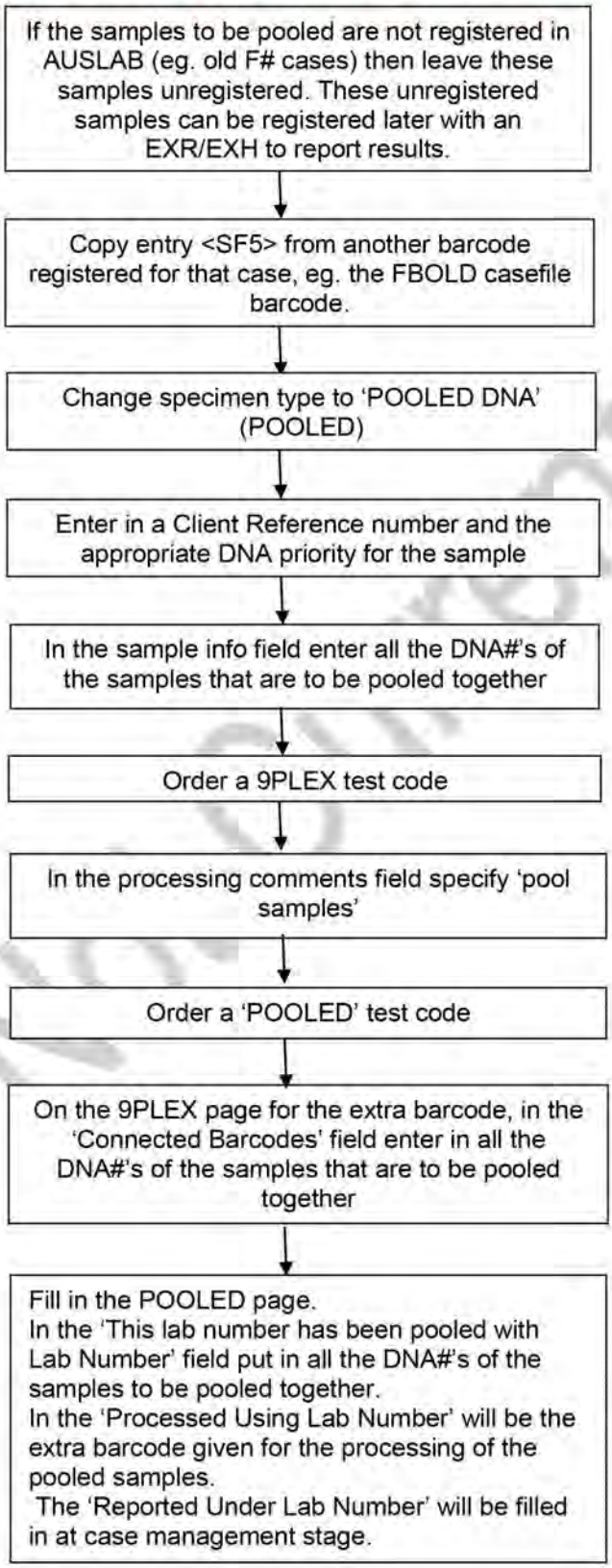
This is for pooling samples that have already undergone some processing under the DNAmaster/DAD system, but it has now been decided by the case manager to pool them.




Enter in the appropriate DNA priority for the sample
In the sample info field enter all the barcodes (**including** the barcode and **DNA#**) that are to be pooled together
Order a 9PLEX test code
Use the processing comments for any processes required after the pooling process, eg. microcon to full
On the 9PLEX page for the extra barcode, in the 'Connected Barcodes' field enter in all the samples that are to be pooled under that extra barcode (**including** the barcode and **DNA#**).

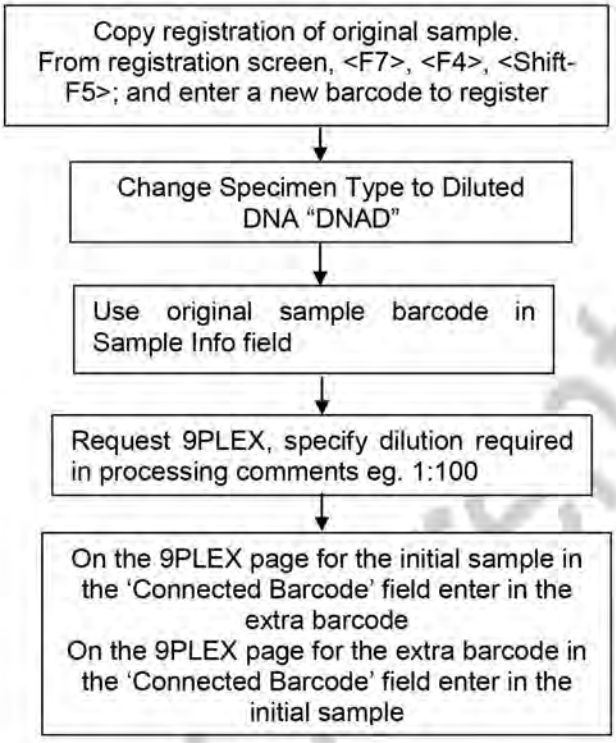
Not Current

17.8 Appendix 8: Pooling Pre-LIMS samples (not registered in AUSLAB)



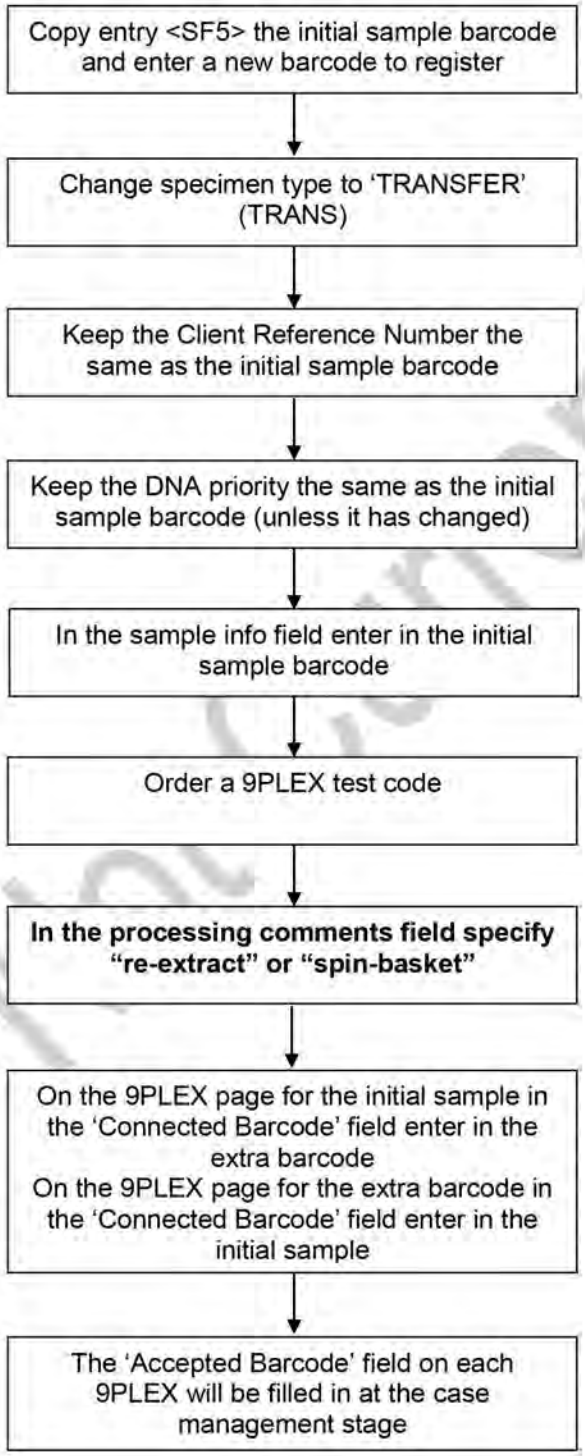
17.9 Appendix 9: Requesting a Dilution

For dilutions exceeding 1 in 20

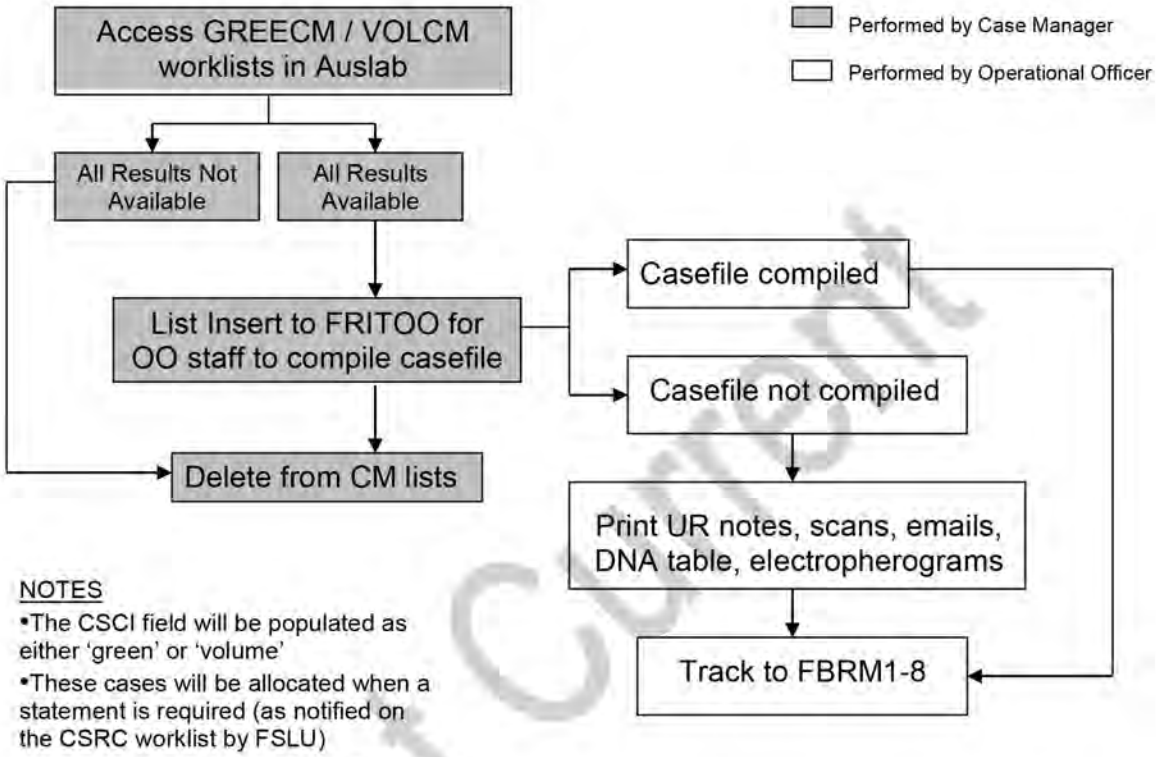


Not Current

17.10 Appendix 10: Requesting extraction of the remainder of a sample that has been sub-sampled in analytical, or for re-extraction of a spin basket



17.11 Appendix 11. Green and Volume Worklists – case assessment and OO tasks

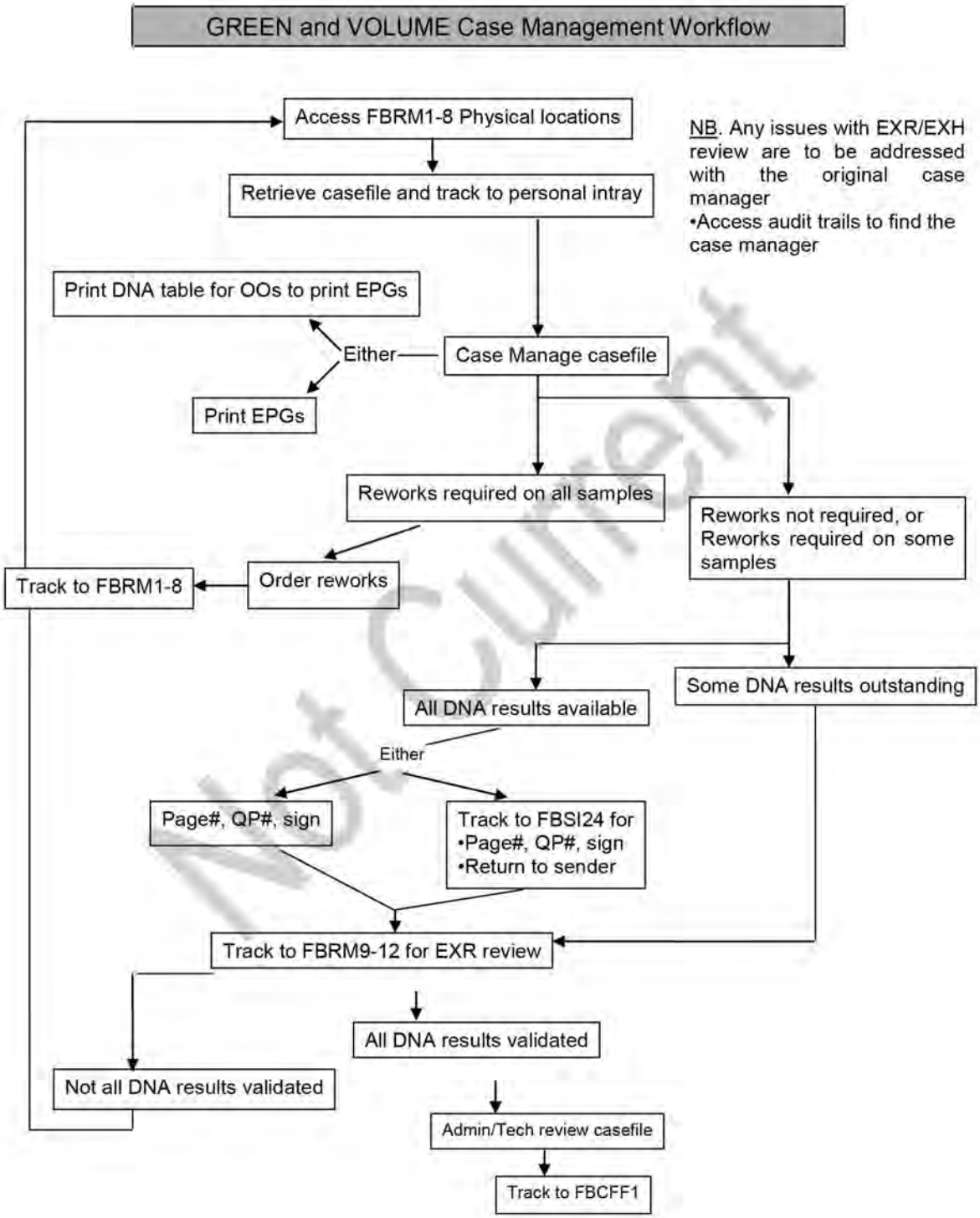


NOTES

- The CSCI field will be populated as either 'green' or 'volume'
- These cases will be allocated when a statement is required (as notified on the CSRC worklist by FSLU)

Not Current

17.12 Appendix 12. Overview of Green and Volume Case Management Workflow



Not Current

Explanations of Exhibit Report Results

1. Purpose

To provide explanations for the results available for the EXR/EXH result/status field

2. Scope

AUSLAB is the case management computer system used within the DNA Analysis section. AUSLAB utilises EXR/EXH pages to report information relating to exhibits to the Queensland Police Service. This document provides clear explanations for the results available for the EXR/EXH result/status field, which are available for DNA Analysis staff, and also QPS DNA Results Management Unit (DRMU).

3. ASSOCIATED DOCUMENTS

16004 AUSLAB Users Manual – DNA Analysis
17117 Procedure for Case Management

4. EXPLANATIONS

4.1 Blood Examination

1 **Presumptive blood test neg. Submitted for cells**
This item/sample tested negative to a presumptive test for blood (TMB). This item was submitted for general cell DNA testing.
Mnemonic = PBNSC

2 **Presumptive blood test pos. Submitted-results pending**
This item/sample tested positive to a presumptive test for blood (TMB) and was submitted for DNA testing. Results are pending.
Mnemonic = 1BPPSR

3 **Presumptive blood test neg.**
This item/sample tested negative to a presumptive test for blood (TMB).
Mnemonic = PBTN

4 **Presumptive blood test positive**
This item/sample tested positive to a presumptive test for blood (TMB).
Mnemonic = PREBT

Not Current

4.2 Seminal Fluid Examination

1 **Presump. PSA test positive, submitted - results pending**
This item/sample tested positive to a presumptive test for Prostate Specific Antigen (PSA) which is a component of seminal fluid. This item was submitted for DNA testing. Results are pending.
Mnemonic = PAPPRP

2 **Presump. AP test positive, submitted - results pending**
This item/sample tested positive to a presumptive test for seminal fluid (AP). This item was submitted for DNA testing. Results are pending.
Mnemonic = PPSRP

3 **Presump. PSA test positive, no sperm found**
This item/sample tested positive to a presumptive test for Prostate Specific Antigen (PSA) which is a component of seminal fluid. No spermatozoa were detected by microscopy. This item was submitted for DNA testing. Results are pending.
Mnemonic = PPSANS

4 **Micro positive for sperm. Submitted-results pending**
Spermatozoa were detected on this item/sample by microscopy. This item/sample was submitted for DNA testing. Results are pending.
Mnemonic = SPPDNA

5 **Micro neg for sperm**
Spermatozoa were not detected on this item/sample by microscopy.
Mnemonic = MNS

6 **Semen not detected**
Spermatozoa were not observed and/or seminal fluid was not detected on the item/sample tested. QHFSS recommends QPS to commence further examination on items relating to this case if applicable.
Mnemonic = SEMND

4.3 Saliva Examination

1 **Presump saliva positive. Submitted-results pending**
This item/sample tested positive to a presumptive test for saliva (Phadebas) and was submitted for DNA testing. Results are pending.
Mnemonic = PSPSRP

2 **Presump saliva negative. Submitted for cells**
This item/sample tested negative to a presumptive test for saliva (Phadebas). This item/sample was submitted for general cell DNA testing.
Mnemonic = PSNSC

3 **Submitted as cells, Presump saliva test pending**
This item/sample was submitted for general cell DNA testing. The item/sample will be tested with the presumptive test for saliva (Phadebas). Results are pending.
Mnemonic = SACPSP

Not Current

4 **Presump saliva test negative**
This item/sample tested negative to a presumptive test for saliva (Phadebas).
Mnemonic = PSTN

5 **Presump saliva test positive**
This item/sample tested positive to a presumptive test for saliva (Phadebas).
Mnemonic = PSTP

4.4 Hair Examination

1 **Hair located. Not suitable for analysis**
Hair/s were located on this item/sample. They were observed using microscopy and deemed unsuitable for DNA testing due to no observed cellular material, or possible animal origin.
Mnemonic = HLNSA

2 **Hair located. Submitted results pending**
Hair/s were located on this item/sample. These hairs have been submitted for DNA testing. Results are pending.
Mnemonic = HLSRP

The following comment can be used when examinations were undertaken on items but no hair was located or the item was a substance other than hair, and therefore no further examination was conducted e.g. A4 tapelifts, clothing.

3 **No hair located. No further examination conducted**
The item/sample was examined for the presence of hair and none was located. This could be due to no hair present or item is substance other than hair. No further testing for hair was conducted on this item.
Mnemonic = NHLNE

4.5 General Examination

1 **Submitted-results pending**
This item/sample was submitted for DNA testing. Results are pending.
Mnemonic = SRP

2 **Sample unsuitable for analysis**
This item/sample is unsuitable for DNA testing due to, but not limited to: excess dirt, or the presence of mould.
Mnemonic = UNSS

3 **Items Prioritised. Not examined at this time**
This item/sample has been prioritised based on case information provided by QPS. Examinations may be conducted in the future.
Mnemonic = IPNE

Not Current

4 **Items prioritised, not submitted at this time**
This item/sample has been prioritised and as such samples taken from this exhibit have not been submitted at this time.
Mnemonic = IPNST

5 **Submitted as cells**
This item/sample was submitted for general cell DNA testing.
Mnemonic = SAC

6 **Sample pooled and processed under**
This item/sample was pooled and submitted for DNA testing under the barcode sent with this exhibit report. The final results will be reported under the barcode.
Mnemonic = SPP

7 **Entire sample consumed**
The entire item/sample was consumed during examination.
Mnemonic= ESCD

The following comment should be used when the original barcode has undergone further processing under a new barcode, and the reported profile result is under this new barcode, which needs to be reported to QPS.

8 **Sample processed and final results under**
This item/sample was processed under the barcode sent with this exhibit report. The final results will be reported under that barcode.
Mnemonic = SPFRU

The following comment can be used when multiple items were received together under one exhibit barcode, of which only some of the items were selected for examination.

9 **Multiple items - not all tested**
This exhibit consisted of multiple items packaged together under one exhibit barcode, of which not all were selected for examination. If more or all of the remaining items are required to be examined, this can be completed upon request.
Mnemonic = MINAL

The following comment must follow "Multiple items – not all tested"

10 **All items now tested**
All items for this exhibit have now been examined.
Mnemonic = AINT

The following comment can be used when examinations were undertaken on items, but no biological material was detected, and therefore no samples were submitted for DNA testing.

11 **No further examinations conducted**
This item/sample was tested for the possible presence of biological material and none were detected. No further testing was conducted on this item.
Mnemonic = NFEC

Not Current

The following comment can be used when manipulation of an item examined by QPS were undertaken by QHFSS staff prior to submitting for DNA extraction, manual or automated. This EXR/EXH line should be used for general manipulation only. More specific EXH lines are listed below.

12 **Sample required manual intervention prior to extraction**
This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the extraction process.
Mnemonic = SRMI

The following comment can be used when manipulation of a swab submitted by QPS was undertaken by QHFSS staff prior to submitting for DNA extraction, manual or automated, due to the swab stick being too long.

13 **Sample required manual intervention – swab stick too long**
This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as the swab stick was too long and required shortening to enable downstream processing. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process. The ideal stick length should be no more than 24mm total length (swab stick plus swab head).
Mnemonic = MISSTL

The following comment can be used when manipulation of an item examined by QPS was undertaken by QHFSS staff prior to submitting for DNA extraction, manual or automated, due to excess substrate.

14 **Sample required manual intervention – excess substrate**
This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as excess substrate was contained within the tube. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process.
Mnemonic = MIES

The following comment can be used when manipulation of a tapelift examined by QPS was undertaken by QHFSS staff prior to submitting for DNA extraction, manual or automated, due to the tapelift being rolled incorrectly.

15 **Sample reqd manual intervention– tlift rolled incorrectly**
This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as the tapelift was rolled incorrectly, impeding downstream processing. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process.
Mnemonic = MITRI

The following comment can be used when a sample is to be placed on hold until advice is received from QPS before any examination can commence.

Not Current

16 **Sample on hold, awaiting advice**
This item/sample has been placed on hold and is awaiting additional information from QPS before processing can recommence. This information may relate to, but is not limited to; examination priority, screening requirements.
Mnemonic = SOHAA

4.6 Exception reporting to QPS for Evidence Recovery

The following EXR/EXHs should be used in place of a FERRO when items are submitted incorrectly by QPS for DNA testing.

1 **Hair located on the outside of an in-tube submission**
A hair was located either outside the tube or partially hanging in and out of the tube. It is unclear if this hair was part of the collected item or incorrectly transferred during collection. This hair/hair portion has been stored and will only be analysed if a request is provided.
Mnemonic = HOIS

2 **Multiple items incorrectly submitted under single barcode**
Multiple items, or multiple AP positive areas have been submitted under a single barcode identifier. Each item requires its own unique barcode, as the barcode is used for reporting purposes to both the forensic register and the National Criminal Investigation DNA Database. Each item will be allocated a new barcode for processing and reporting purposes.
Mnemonic = MIISB

3 **Labelling discrepancy**
There is a labelling discrepancy (Occurrence number or sample description) between the exhibit packaging and the AUSLAB/Forensic Register interface records. This sample can not be processed until the labelling discrepancy is resolved. The discrepancy will be highlighted to the QPS Sample Management Unit for clarification in the first instance, and if unable to be resolved, will be referred to the appropriate QPS officer for resolution. Please ensure all labelling details are correct before submission to the DNA Analysis Laboratory
Mnemonic = LDIS

4 **No barcode on sample**
The item/sample provided in a tube was not labelled with a barcode. A barcode is required for the processing of the item and for continuity purposes. A barcode the same as that attached to the packaging has been affixed to the item.
Mnemonic = NBOS

5 **On hold - Insufficient information provided for testing**
There was insufficient information provided with this submission to determine what type of analysis is required for this item/sample e.g., saliva, semen. This sample is to be placed on hold until further information on the testing requirements for this sample is provided.
Mnemonic = OHII

6 **Incorrect submission of cigarette butt**
This cigarette butt was received in a tube. Items provided in a tube are intended to be submitted directly for DNA processing with minimal manual intervention. This sample required further examination as it was received as a whole cigarette butt. Please

Not Current

submit whole cigarette butts in a Crime Scene Sample envelope or as a sub-sample of the filter paper.
Mnemonic = ISCB

FINAL RESULTS

Note 1: The following final results cover samples processed using the Profiler® Plus (P+) and Powerplex® 21 (PP21) amplification kits. Some EXH lines are to be used for one kit only. Other EXHs are generic and can be used for either kit. At the end of each comment, the kit or kits that can be used with be denoted in brackets.

Note 2: For all final results containing a match to a reference barcode, the QPS DRMU update the expanded comments as per the following example:

Examples:
PowerPlex® 21 and STRmix™: *SS DNA profile less than 9 loci LR > 100 billion* - This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from **[QPS inserts barcode of ref sample and other details such as name and DOB]**. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.

Profiler Plus: *9 loci DNA profile. Uploaded to NCIDD* – This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from **[QPS inserts barcode of ref sample and other details such as name and DOB].** The DNA profile obtained from barcode **[QPS inserts barcode number of the crime scene sample]** has been selected for loading to NCIDD and will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.

POWERPLEX® 21 and STRmix RESULTS

The follow comments are for use results processed using PowerPlex® 21 and interpreted with the STRmix™ Expert System.

4.7 Single Source DNA profiles (PP21)

The following comment will be used for unknown contributors only.

1 **Single Source DNA profile**
The DNA profile obtained from this item/sample indicated the presence of one contributor. Any reference samples associated to this case have been excluded as donors of this DNA. This DNA profile has therefore been designated as an unknown. A statistical interpretation has not been performed.
Mnemonic = 1SS
(PP21)

Not Current

The following comments will be used when a reference evidence sample is provided for comparison.

2 **Single Source- low support for contribution**
This item/sample provided a partial DNA profile which indicated the presence of one contributor. Only limited information has been obtained and this information matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. Statistically, this DNA profile provides low support that the associated barcode sent with this exhibit report is the donor of this DNA. Further information can be provided if required.
Mnemonic = 1SSLOW
(PP21)

3 **Single source DNA profile < 9 loci LR 100 – 1000**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS9L1
(PP21)

4 **Single source DNA profile < 9 loci LR 1000 - 10 000**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS9L2
(PP21)

5 **Single source DNA profile < 9 loci LR 10 000 - 100 000**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS9L3
(PP21)

6 **Single source DNA profile < 9 loci LR 100 000 - 1 million**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.

Not Current

Mnemonic = 1SS9L4
(PP21)

7 **SS DNA profile < 9 loci LR 1 million - 1 billion**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS9L5
(PP21)

8 **SS DNA profile < 9 loci LR 1 billion - 100 billion**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS9L6
(PP21)

9 **SS DNA profile less than 9 loci LR > 100 billion**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS9L7
(PP21)

10 **SS DNA profile 9 loci and above LR 1 million - 1 billion**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS9L8
(PP21)

11 **SS DNA profile 9 loci and above LR 1 billion- 100 billion**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 billion and 100 billion times

Not Current

more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS9L9
(PP21)

12 **SS DNA profile 9 loci and above LR > 100 billion**
This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1S9L10
(PP21)

13 **Single source 20 loci DNA profile LR > 100 billion**
This item/sample provided a DNA profile that indicated the presence of one contributor. It obtained all of the DNA information potentially available. This DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.
Mnemonic = 1SS20L
(PP21)

14 **Single Source DNA profile - assumed known contributor**
This item/sample provided a DNA profile that indicated the presence of one contributor. The associated barcode matches this DNA profile. Based on information provided to the laboratory, it has been assumed that the associated barcode is the donor of this DNA. Given this assumption, no statistical interpretation has been performed.
Mnemonic = 1SSAKN
(PP21)

The following comments will be applied when a single source DNA profile is selected for loading to the National Criminal Investigation DNA Database (NCIDD).

15 **NCIDD upload single source DNA profile**
A single source DNA profile was obtained from the item/sample. This DNA profile has been selected for loading to NCIDD, and it will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile.
Mnemonic = 1SSNCD
(PP21)

16 **NCIDD Intel upload - single source partial profile**
This item/sample gave an incomplete single source DNA profile which contained insufficient information for NCIDD matching as it was below the QHFSS stringency for reporting a match on NCIDD. The profile has been selected for loading to NCIDD for intelligence purposes. This incomplete DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be statistically evaluated

Not Current

and reported as a likelihood ratio. Depending on the amount of information in this DNA profile, the strength of the support for inclusion will vary.
Mnemonic = 1SSIND
(PP21)

17 **NCIDD Intel upload - interim single source profile**
This item/sample gave an interim result of an apparent single source DNA profile. This DNA profile has been selected for loading to NCIDD for intelligence purposes, as this sample is currently undergoing further processing. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that the final result may vary. Any reference samples subsequently received will be statistically evaluated against the final DNA profile and reported as a likelihood ratio.
Mnemonic = 1SSINI
(PP21)

The following comments will be applied when a single source DNA profile is unable to be loaded to NCIDD (if an EXH is required if the only sample in a case).

18 **Single source DNA profile < NCIDD matching stringency**
The incomplete DNA profile obtained from this item/sample indicated the presence of one contributor. Any reference samples associated to this case have been excluded as donors of this DNA. This DNA profile has therefore been designated as an unknown. The DNA profile was below the QHSS stringency for reporting a match on NCIDD, and has therefore not been loaded to NCIDD. A statistical interpretation has not been performed.
Mnemonic = 1SSLND
(PP21)

19 **Single source DNA profile- unsuitable for NCIDD searching**
The incomplete DNA profile obtained from this item/sample indicated the presence of one contributor. Any reference samples associated to this case have been excluded as donors of this DNA. This DNA profile has therefore been designated as an unknown. The DNA profile contained insufficient information for searching on NCIDD, and is therefore unable to be loaded to NCIDD. A statistical interpretation has not been performed.
Mnemonic = 1SSUND
(PP21)

Not Current

4.8 Mixed DNA profiles (PP21)

Non-conditioned EXHs

The following comments will be used for unknown contributors only.

1 **Two person mixed DNA profile**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. In the absence of a reference sample/s for comparison, a statistical interpretation has not been performed.
Mnemonic = 2MX

(PP21)

2 **Three person mixed DNA profile**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. In the absence of a reference sample/s for comparison, a statistical interpretation has not been performed.
Mnemonic = 3MX
(PP21)

The following EXH line will be used when a mixed DNA profile is obtained from a sample, and after deconvolution, the amount of DNA contributed by any or each individual falls below the level at which the DNA profile can be reliably interpreted. See 17117 *Procedure for Case Management* for details.

3 **Mix DNA contribution unsuitable for interpretation**
The mixed DNA profile result for this sample has been deconvoluted in an attempt to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a DNA contribution which was unsuitable for further statistical interpretation, and therefore is unable to be compared to any other DNA profiles obtained within this case.
Mnemonic = 2MXUI
(PP21)

The following comments will be used when a reference evidence sample/s is/are provided for comparison.

4 **2 person mix - low support for contribution**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. The DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Please contact DNA Analysis if further information is required.
Mnemonic = 2MXLOW
(PP21)

5 **2 person mix - support for contribution 100 to 1000**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 2MX1
(PP21)

6 **2 person mix - support for contribution 1000 to 10 000**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 2MX2
(PP21)

7 **2 person mix, support for contrib 10 000 - 100 000**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 2MX3
(PP21)

8 **2 person mix- support for contrib 100 000 to 1 million**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 2MX4
(PP21)

9 **2 person mix - support for contrib 1 million - 1 billion**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 2MX5
(PP21)

10 **2 person mix- support for contrib 1 billion - 100 billion**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 2MX6
(PP21)

11 **2 person mix profile - support for contrib > 100 billion**
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 2MX7
(PP21)

12 **3 person mix - low support for contribution**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. The DNA profile provides low support for the proposition that the

Not Current

associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.
Mnemonic = 3MXLOW
(PP21)

13 **3 person mix - support for contribution 100 to 1000**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
Mnemonic = 3MX1
(PP21)

14 **3 person mix - support for contribution 1000 to 10 000**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
Mnemonic = 3MX2
(PP21)

15 **3 person mix - support for contrib 10 000 - 100 000**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
Mnemonic = 3MX3
(PP21)

16 **3 person mix - support for contrib 100 000 to 1 million**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
Mnemonic = 3MX4
(PP21)

17 **3 person mix - support for contrib 1 million - 1 billion**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
Mnemonic = 3MX5
(PP21)

Not Current

18 **3 person mix- support for contrib 1 billion - 100 billion**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
Mnemonic = 3MX6
(PP21)

19 **3 person mix profile - support for contrib > 100 billion**
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.
Mnemonic = 3MX7
(PP21)

Conditioned/Remaining Mixed DNA profile EXHs

The following comments will be used when a reference evidence sample/s is/are provided for conditioning a two or three person mixed DNA profile.

20 **2 person mixed profile - conditioned on**
This item/sample provided a DNA profile that indicated the presence of two contributors. Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this mixed DNA profile. Given this assumption, no statistical interpretation has been performed.
Mnemonic = 2MXCON
(PP21)

21 **3 person mixed profile - conditioned on**
This item/sample provided a DNA profile that indicated the presence of three contributors. Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this mixed DNA profile. Given this assumption, no statistical interpretation has been performed.
Mnemonic = 3MXCON
(PP21)

22 **2 person mix remaining - low support for contrib.**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, then the DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.
Mnemonic = 2MXRL
(PP21)

Not Current

23 **2 person mix remaining - support for contrib 100 to 1000**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
Mnemonic = 2MXR1
(PP21)

24 **2 person mix remaining- support for contrib 1000 to 10000**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
Mnemonic = 2MXR2
(PP21)

25 **2 person mix rem - support for contrib 10 000 to 100 000**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
Mnemonic = 2MXR3
(PP21)

26 **2 person mix rem- support for contrib 100000 to 1 million**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
Mnemonic = 2MXR4
(PP21)

27 **2 person rem- support for contrib 1 million to 1 billion**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
Mnemonic = 2MXR5
(PP21)

Not Current

28 **2 person rem - support for contrib 1 billion -100 billion**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
Mnemonic = 2MXR6
(PP21)

29 **2 person mix rem - support for contribution > 100 billion**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.
Mnemonic = 2MXR7
(PP21)

30 **3 person mix remaining - low support for contrib.**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, then the DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.
Mnemonic = 3MXRL
(PP21)

31 **3 person mix remaining - support for contrib 100 to 1000**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 3MXR1
(PP21)

32 **3 person mix remaining- support for contrib 1000 to 10000**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 3MXR2
(PP21)

Not Current

33 **3 person mix rem - support for contrib 10 000 to 100 000**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 3MXR3
(PP21)

34 **3 person mix rem- support for contrib 100000 to 1 million**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 3MXR4
(PP21)

35 **3 person rem - support for contrib 1 million to 1 billion**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 3MXR5
(PP21)

36 **3 person rem - support for contrib 1 billion-100 billion**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 3MXR6
(PP21)

37 **3 person mix rem - support for contribution > 100 billion**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.
Mnemonic = 3MXR7
(PP21)

Not Current

NCIDD loading

The following comments will be applied when a contribution of DNA from a mixed DNA profile (2 or 3 person mixture) is deconvoluted and selected for loading to NCIDD.

38 **NCIDD upload - mixed DNA profile**
The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a fully deconvoluted DNA profile. The associated barcode/unknown designation sent with this exhibit report is consistent with this deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this deconvoluted DNA profile has been assigned a sub-sample barcode number. The deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
Mnemonic = 2MXNCD
(PP21)

39 **NCIDD upload - conditioned contribution**
The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and 'remaining' have been applied. The conditioned contribution described by the associated barcode has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile.
Mnemonic = 2MXCND
(PP21)

40 **NCIDD upload remaining contribution**
The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and 'remaining' have been applied. A remaining contribution has been separated after conditioning the mixed DNA profile. The associated barcode/unknown designation sent with this exhibit report is a possible donor of DNA to the 'remaining contribution'. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received for the identification of an unknown component will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
Mnemonic = 2MXRND
(PP21)

Not Current

41 **Mix Remaining DNA contribution unsuitable for NCIDD**
The mixed DNA profile result for this sample has been deconvoluted in an attempt to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and 'remaining' have been applied. The remaining contribution separated after conditioning the mixed DNA profile was unsuitable for searching on NCIDD, and is therefore unable to be loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this remaining contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
Mnemonic = 2MXUND
(PP21)

Powerplex® 21 INTEL EXHs

Please see section 4.15 for additional Intel EXH comments for P+ and PP21.

42 **NCIDD upload - Intel mixed DNA profile**
The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a partially deconvoluted DNA profile able to be loaded to NCIDD for intelligence purposes. The associated barcode/unknown designation sent with this exhibit report that is consistent with this deconvoluted DNA profile is therefore a possible contributor to this mixed DNA profile. For ease of reference, this deconvoluted DNA profile has been assigned a sub-sample barcode number. The deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
Mnemonic = 2MXIND
(PP21)

43 **2 person mixed profile - conditioned on – Intel**
This item/sample provided a DNA profile that indicated the presence of two contributors. For Intelligence purposes, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically evaluated against the mixture without a contribution being assumed and the result reported as a likelihood ratio.
Mnemonic = 2MXCI
(PP21)

44 **3 person mixed profile - conditioned on - Intel**
This item/sample provided a DNA profile that indicated the presence of three contributors. For Intelligence purposes, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically

Not Current

evaluated against the mixture without a contribution being assumed and the result reported as a likelihood ratio.
Mnemonic = 3MXCI
(PP21)

45 **2 person mixed profile - remaining Intel – NCIDD**
This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor for intelligence purposes only, some or all of the components of the DNA profile from the designated unknown sent with this exhibit report are represented within the remaining DNA profile. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
Mnemonic = 2MXRIN
(PP21)

46 **3 person mixed profile - remaining Intel – NCIDD**
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor for intelligence purposes only, some or all of the components of the DNA profile from the designated unknown sent with this exhibit report are represented within the remaining DNA profile. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
Mnemonic = 3MXRIN
(PP21)

The following comment will be used when an Intelligence Report is required to explain the interpretations made in order to load a contributor of DNA to NCIDD.

47 **Mixture contribution loaded to NCIDD - see Intel report**
The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. A DNA contribution was able to be deconvoluted for loading to NCIDD, and further information about this will follow in an intelligence report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile the, strength of the support for contribution will vary.
Mnemonic = 2MXNIR
(PP21)

Not Current

Non-contribution Mixture EXHs

These following comments will be applied when the Likelihood ratio calculated by STRmix™ is <1.

48 **2 person mix - supports non contribution**
This item/sample provided a DNA profile that indicated the presence of two contributors. The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.
Mnemonic = 2MXNC
(PP21)

49 **3 person mix - supports non contribution**
This item/sample provided a DNA profile that indicated the presence of three contributors. The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.
Mnemonic = 3MXNC
(PP21)

50 **2 person mix remaining - supports non contribution**
This item/sample provided a DNA profile that indicated the presence of two contributors. If it is assumed that the barcode sent with the above exhibit report (2 contributor mixed profile, conditioned on) has contributed, the statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.
Mnemonic = 2MXRNC
(PP21)

51 **3 person mix remaining - supports non contribution**
This item/sample provided a DNA profile that indicated the presence of three contributors. If it is assumed that the barcode sent with the above exhibit report (3 contributor mixed profile, conditioned on) has contributed, the statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.
Mnemonic = 3MXRNC
(PP21)

Inconclusive Mixture EXHs

These following comments will be applied when the Likelihood ratio calculated by STRmix™ equals 1.

52 **2 person mixed DNA profile - inconclusive**
This item/sample provided a DNA profile that indicated the presence of two contributors. The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other reference samples may provide a different statistical interpretation.
Mnemonic = 2MXINC
(PP21)

53 **3 person mixed DNA profile - inconclusive**
This item/sample provided a DNA profile that indicated the presence of three contributors. The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this

Not Current

exhibit report, comparison to other reference samples may provide a different statistical interpretation.
Mnemonic = 3MXINC
(PP21)

4.9 NSD or no further processing Final Results (PP21 and P+)

The following comment will be used when there are no peaks observed in the DNA profile obtained.

1 **No DNA profile**
A DNA profile was not obtained from this item/sample, due to, but not limited to: no DNA present, poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.
Mnemonic = NOPROF
(PP21 or P+)

The following comment will be used when there are no peaks above threshold in profile obtained from the sample, and an indication of possible additional DNA was observed. This should indicate to QPS that there was something observed, but does not meet the thresholds for comparing and reporting.

2 **No DNA profile – possible sub-threshold peaks**
A DNA profile was not obtained from this item/sample, however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. This could be due to, but not limited to: poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.
Mnemonic = NDPPTP
(PP21 or P+)

For Powerplex 21: The following comment is entered into the EXH when the quantitation value is less than the limit of detection (LOD) for quantitation, and there is no indication of inhibition. This sample will not proceed to amplification. QPS can request processing of the sample to restart should they require it.
For Profiler Plus, the following comment is entered into the EXH for Volume Crime Priority 3 samples only when the quantitation value is undetermined, and there is no indication of inhibition.

3 **No DNA detected**
This item/sample was submitted for DNA analysis; however no DNA was detected above the limit of detection at the quantitation stage. No further processing was conducted on this item. QPS can submit a request to QHFSS for a continuation of this processing if required.
Mnemonic = NDNAD
(PP21 or P+)

The following comment is used when the quantitation value falls below the point at which the results would be considered unreliable for interpretation. These samples will not proceed to amplification. See 17117 *Procedure for Case Management* for details.

4 **DNA insufficient for further processing**
This item/sample was submitted for DNA analysis; however the amount of DNA detected at the quantitation stage indicated the sample was insufficient for further

processing (due to the limitations of current analytical and interpretational techniques). No further processing was conducted on this item. Please contact DNA Analysis if further information is required.
Mnemonic = DIFP
(PP21)

The following comment will be used for Priority 3 Volume Crime samples processed using Profiler® Plus only. This comment encompasses instances when no DNA profile is obtained, and no DNA profile, possible sub threshold peaks are obtained. This comment indicates to QPS that for Volume Priority 3 samples, no reportable DNA profile was obtained.

5 **No reportable DNA profile**
A DNA profile above QHFSS standard reporting thresholds was not obtained from this sample/item. This may be due to, but not limited to: no DNA present, poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.
Mnemonic = NRDP
(PP21 or P+)

4.10 Suspect Check Results (PP21 and P+)

The following comment will be used when the barcode of a nominated suspect has been provided for an intelligence reference sample from the QPS DRMU, and it does NOT match or can be excluded as a contributor of DNA to the crime scene profile.

1 **Suspect check Action - No Match**
The nominated suspect can be excluded as a potential contributor to the DNA profile obtained from this item/sample.
Mnemonic = SCANM
(PP21 or P+)

The following comment will be used when the barcode of a nominated suspect has been provided for an intelligence reference sample from the QPS DRMU, and there is insufficient information in the DNA profile obtained from the crime scene sample to determine if the nominated person could be a potential contributor.

2 **Suspect check - insufficient information to compare**
There was insufficient information in the DNA profile obtained from this item/sample to determine if the nominated suspect could be a potential contributor.
Mnemonic = SCII
(PP21 or P+)

The following comments will be used with STRmix™ for comparisons of provided intelligence reference samples against mixed DNA profiles obtained from crime scene samples (where the profile is suitable for comparison).

3 **Suspect check - low support for contribution**
The DNA profile provides low support for the proposition that the nominated suspect is a possible donor of DNA to this mixed DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
Mnemonic = SCLOW
(PP21)

Not Current

4 **Suspect check - support for contribution 100 to 1000**
This DNA profile is between 100 and 1000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
Mnemonic = SCSC1
(PP21)

5 **Suspect check - support for contribution 1000 to 10 000**
This DNA profile is between 1000 and 10 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
Mnemonic = SCSC2
(PP21)

6 **Suspect check- support for contribution 10 000 to 100 000**
This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
Mnemonic = SCSC3
(PP21)

7 **Suspect check - support for contrib 100 000 - 1 million**
This DNA profile is between 100 000 and 1 million times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
Mnemonic = SCSC4
(PP21)

8 **Suspect check- support for contrib 1 million - 1 billion**
This DNA profile is between 1 million and 1 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
Mnemonic = SCSC5
(PP21)

9 **Suspect check- support for contrib 1 billion- 100 billion**
This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
Mnemonic = SCSC6
(PP21)

Not Current

10 **Suspect check - support for contribution > 100 billion**
This DNA profile is greater than 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.
Mnemonic = SCSC7
(PP21)

4.11 General Final Results (PP21 and P+)

The following comment should be used there is an indication of possible additional DNA observed below the limit of reporting (LOR). This should indicate to QPS that there was something observed along with the reportable DNA profile, but does not meet the thresholds for comparing and reporting.

11 **Possible sub-threshold information**
The presence of possible additional DNA was observed within the DNA profile obtained from this item. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. This sub-threshold information did not interfere with the interpretation of the reportable DNA components in the DNA profile obtained from this item.
Mnemonic = PSTI
(PP21)

12 **No further work required as per advice from QPS**
QPS have provided advice that no further work is required for this item/sample. Testing has been ceased and the sample stored.
Mnemonic = NWQPS
(PP21 or P+)

The following comment will be used when QPS have advised they do not require testing, but a DNA profile has been obtained. This comment will indicate to QPS that the sample has undergone DNA testing; however no interpretation was performed as per their advice.

13 **QPS advised no further work required – results available**
QPS have provided advice that no further work is required for this item/sample. Please note that this item/sample has undergone DNA testing and results are available, however these have not been interpreted at this stage. QPS can submit a request to QHFSS for an interpretation of the DNA results if required.
Mnemonic = NWQPSR
(PP21 or P+)

The following comment will be used when information has been obtained from the Queensland Police Service that testing is now required for an item.

14 **Testing restarted on advice from QPS**
QPS have provided advice that testing is now required for this item/sample. Testing has been restarted.
Mnemonic = TRQ
(PP21 or P+)

Not Current

The following comment will be used when a DNA profile previously reported as uploaded to NCIDD is removed from NCIDD due to information provided by the police, or other circumstances in which the DNA profile should not be on NCIDD, such as a change in NCIDD category, or the DNA profile is replaced by better profile from a different barcode.

15 **DNA profile removed from NCIDD**
The DNA profile obtained from this item/sample has been removed from NCIDD following advice from QPS, a change in the NCIDD category, or a profile with more information has been obtained.
Mnemonic = PRNCID
(PP21 or P+)

The following comment is to be used when a final result has already been reported (e.g. partial profile) for that sample but for whatever reason it has undergone further reworking and a new final result needs to be reported (e.g. full profile).

16 **This sample has undergone further processing**
This item/sample has undergone further processing and an improved DNA profile has been obtained.
Mnemonic = SUFP
(PP21 or P+)

The following comment can be used when a request has come from QPS for further work on a sample to be conducted. This line will be used when there is no further processing that can be undertaken e.g. no extract left after microcon, current processes have already been exhausted, or computer software programs are not compatible (e.g. 3100 to GMIDX).

17 **No further work able to be conducted on this sample**
This item/sample has been assessed and it has been determined that no further processing can be conducted on this sample, due to, but not limited to: no DNA extract left for further testing, current DNA profile improvement processes have already been exhausted.
Mnemonic = NFWA
(PP21 or P+)

Not Current

PROFILER® PLUS RESULTS

The following comments are for the majority to be used with results processed using Profiler® Plus and interpreted with the Kinship statistical software. Please note: there are some EXHs below that can be used for both PP21 and P+, as indicated by the kit in brackets after the comment.

4.12 Full Profile Final Results (P+)

The following comment should be used when a full DNA profile was obtained from the sample and this profile is to be uploaded to NCIDD.

20 **9 loci DNA profile. Uploaded to NCIDD**
This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile has been selected for loading to NCIDD and will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.

Mnemonic = FUPNPN
(P+)

The following comment should be used when a full DNA profile was obtained from the sample. This sample will not be uploaded to NCIDD.

21 **9 loci DNA profile**
This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report.
Mnemonic = FUPROF
(P+)

The following comment should be used when a full DNA profile was obtained from the sample and this profile is to be uploaded to NCIDD, and an indication of possible additional DNA was observed. This should indicate to QPS that there was something observed along with the full DNA profile, but does not meet the thresholds for comparing and reporting.

22 **9 loci DNA profile- NCIDD- possible sub-threshold peaks**
This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. These sub-threshold peaks did not interfere with the interpretation of the reportable DNA components in the 9 loci DNA profile obtained, which has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = DPNPTP
(P+)

The following comment should be used when a full DNA profile was obtained from the sample, and an indication of possible additional DNA was observed. This should indicate to QPS that there was something observed along with the full DNA profile, but does not meet the thresholds for comparing and reporting.

23 **9 loci DNA profile - possible sub-threshold peaks**
This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the 9 loci DNA profile obtained.
Mnemonic = DPPTP
(P+)

4.13 Partial Profile Final Results (PP21 and P+)

The following comment should be used when a partial DNA profile was obtained from the sample, greater than the stringency for reporting a match on NCIDD (12 alleles or greater). This sample will not be uploaded to NCIDD.

Not Current

1 **Partial DNA profile**
This item/sample gave a partial DNA profile. Where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.
Mnemonic = PDNA
(P+)

The following comment should be used when a partial DNA profile was obtained from the sample and this profile is to be uploaded to NCIDD (12 alleles or greater).

2 **Partial DNA profile. Uploaded to NCIDD**
This item/sample gave a partial DNA profile. Where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This partial DNA profile has been selected for loading to NCIDD and will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = PAPNPN
(P+)

The following comment should be used when a partial DNA profile was obtained from the sample which is less than the stringency for reporting a match on NCIDD (less than 12 alleles and greater than 5 alleles). This indicates to the QPS DRMU that a partial DNA profile was obtained that could be used for comparison, but does not have enough alleles to obtain a match and be reported as a cold link through Auslab. This sample should not be uploaded to NCIDD.

3 **Partial DNA profile. Insufficient for NCIDD matching**
This item/sample gave a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = PDNAIN
(P+)

The following comment should be used when a partial DNA profile was obtained which has very little information and is considered insufficient for informative comparison. This indicates to the QPS DRMU that a partial DNA profile was obtained that should not be used for comparison to a reference sample.

4 **Partial DNA profile unsuitable for comparison purposes**
This item/sample gave a partial DNA profile which was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information within the DNA profile. This may be due to, but not limited to: poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.
Mnemonic = PPUCP
(PP21 or P+)

The following comment should be used when a partial DNA profile (12 alleles or greater) was obtained from the sample and this profile is to be uploaded to NCIDD, and an indication of possible

Not Current

additional DNA was observed. This should indicate to QPS that there was something observed along with the full DNA profile, but does not meet the thresholds for comparing and reporting.

5 **Partial DNA profile- NCIDD- possible sub-threshold peaks**
This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained, which has been selected for loading to NCIDD. This partial DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = PDNPTP
(P+)

The following comment should be used when a partial DNA profile (12 alleles or greater) was obtained from the sample, and an indication of possible additional DNA was observed. This should indicate to QPS that there was something observed along with the full DNA profile, but does not meet the thresholds for comparing and reporting.

6 **Partial DNA profile - possible sub-threshold peaks**
This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained.
Mnemonic = PDPTP
(P+)

The following comment should be used when a partial DNA profile (less than 12 alleles and greater than 5 alleles) was obtained from the sample, and an indication of possible additional DNA was observed. This should indicate to QPS that there was something observed along with the partial DNA profile, but does not meet the thresholds for comparing and reporting. It will also inform QPS DRMU that the partial DNA profile could be used for comparison to other DNA profiles, but does not have enough alleles to obtain a match and be reported as a cold link through Auslab. This sample should not be uploaded to NCIDD.

7 **Partial profile, insuff NCIDD- pos. sub-threshold peaks**
This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained. This partial DNA profile was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).

Not Current

Mnemonic = PPINPT
(P+)

The following comment should be used when a partial DNA profile was obtained which has 3 alleles out of a possible 18 alleles and is therefore unable to be loaded and searched on NCIDD. This EXR/EXH line indicates to the QPS that a partial DNA profile with limited information was obtained that may have enough information to be compared to other DNA profiles for inclusion or exclusionary purposes.

8 **Partial DNA profile, 3 of 18 DNA components**
This item/sample gave a partial DNA profile which contained 3 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = PD3C
(P+)

The following comment should be used when a partial DNA profile was obtained which has 4 alleles out of a possible 18 alleles and is therefore unable to be loaded and searched on NCIDD. This EXR/EXH line indicates to the QPS that a partial DNA profile with limited information was obtained that may have enough information to be compared to other DNA profiles for inclusion or exclusionary purposes.

9 **Partial DNA profile, 4 of 18 DNA components**
This item/sample gave a partial DNA profile which contained 4 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = PD4C
(P+)

The following comment should be used when a partial DNA profile was obtained which has 5 alleles out of a possible 18 alleles and is therefore unable to be loaded and searched on NCIDD. This EXR/EXH line indicates to the QPS that a partial DNA profile with limited information was obtained that may have enough information to be compared to other DNA profiles for inclusion or exclusionary purposes.

10 **Partial DNA profile, 5 of 18 DNA components**
This item/sample gave a partial DNA profile which contained 5 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).

Mnemonic = PD5C
(P+)

4.14 Mixed DNA Profile Final Results

Major DNA profile (P+)

The following comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles and the major DNA profile was a full DNA profile. The major DNA profile will not be uploaded to NCIDD.

1 **Mixed DNA profile. Major component**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The full major DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report.
Mnemonic = MIPMAC
(P+)

The following comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles. This major DNA profile was a full DNA profile and will be uploaded to NCIDD.

2 **Mixed DNA profile. Major component uploaded to NCIDD**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile has been selected for loading to NCIDD. The full major DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = MIPMUN
(P+)

The following comment should be used when a partial mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles. This partial major DNA profile will not be uploaded to NCIDD, however this comment should be used when the major DNA profile is 12 alleles or greater.

3 **Mixed profile, partial major component**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile. Where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.
Mnemonic = MPPMA
(P+)

The following comment should be used when a partial mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles. This partial major DNA profile will be uploaded to NCIDD.

Not Current

4 **Mixed DNA profile, partial major component uploaded to NCIDD**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile which has been selected for loading to NCIDD. Where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = MPPMAN
(P+)

The following comment should be used when a partial mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles. This major DNA profile was a partial DNA profile less than the stringency for reporting a match on NCIDD (less than 12 alleles and greater than 5). This indicates to the QPS DRMU that the major DNA profile was a partial DNA profile that could be used for comparison, but does not have enough alleles to obtain a match and be reported as a cold link through Auslab. This sample should not be uploaded to NCIDD.

5 **Mixed profile, major component insuff for NCIDD matching**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = MPMAIN
(P+)

Not Current

Minor DNA profiles (P+)

The following comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles and the minor DNA profile was a full DNA profile. This minor DNA profile will not be uploaded to NCIDD.

6 **Mixed DNA profile. Minor Component**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The full minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report.
Mnemonic = MIPMIC
(P+)

The following comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles and the minor DNA profile obtained a full DNA profile. This minor DNA profile will be uploaded to NCIDD.

7 **Mixed profile, minor component uploaded to NCIDD**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile has been loaded to NCIDD. The full minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = MPMINC
(P+)

The following comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles and the minor DNA profile was a partial DNA profile that contained information which could be used for comparison purposes. This minor DNA profile will not be uploaded to NCIDD, however this comment should be used when the minor DNA profile is 12 alleles or greater.

8 **Mixed profile, partial minor component**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile. Where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.
Mnemonic = MPPMI
(P+)

The following comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles and the minor DNA profile obtained information that could be reported as a cold link on NCIDD (12 alleles or greater). This partial minor DNA profile will be uploaded to NCIDD.

9 **Mixed DNA profile, partial minor component uploaded to NCIDD**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which has been selected for loading to NCIDD. Where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = MPPMIN
(P+)

The following comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles. This minor DNA profile was a partial DNA profile less than the stringency for reporting a match on NCIDD (less than 12 alleles and greater than 5). This indicates to the QPS DRMU that the minor DNA profile was a partial DNA profile that could be used for comparison, but does not have enough alleles to obtain a match and be reported as a cold link through Auslab. This sample should not be uploaded to NCIDD.

Not Current

10 **Mixed profile, minor component insuff for NCIDD matching**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = MPMIIN
(P+)

The following comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles. This minor DNA profile was a partial DNA profile which has very little information and is considered insufficient for informative comparison.

11 **Mixed profile- Minor component unsuitable for comparison**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information obtained.
Mnemonic = MPMUC
(P+)

The following comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor Components. This minor component was a mixed DNA profile from two or more contributors. An evidence sample or unknown contributor (e.g. uk m1) could not be excluded as a contributor to this mixed DNA profile. There will always be a name associated with this sample in the *Linked No.* field of the EXR/EXH.

12 **Mixed DNA profile, complex minor component cannot exclude**
This item/sample gave a mixed DNA profile DNA profile which indicated the presence of DNA from more than two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile indicated the presence of DNA from more than one contributor. The DNA profile obtained from the barcode sent with this exhibit report cannot be excluded as being a possible contributor of DNA to the minor component of this mixed DNA profile.
Mnemonic = MDNA1
(P+)

The following comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor DNA profiles. This minor component was a mixed DNA profile from two or more contributors. At this stage, the minor component cannot be interpreted further as no reference sample was obtained that when compared, could be 'included' (i.e. not excluded) as having contributed to the complex minor DNA profile, or comparison with additional reference sample may be possible if forthcoming. There will be no name associated with this line in the *Linked No.* field of the EXR/EXH.

13 **Mixed profile, complex mixed minor component**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from more than two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile indicated the presence of DNA from more than one contributor. This minor DNA profile cannot be interpreted further as no

Not Current

reference sample has been received for direct comparison; or alternatively, comparison with additional reference samples may be possible if forthcoming.
Mnemonic = MPRO
(P+)

The following comment should be used when a mixed DNA profile was obtained from this sample that could be separated into Major and Minor Components. This minor component was a mixed DNA profile from two or more contributors. Due to the unknown number of contributors or the partial nature of the minor DNA profile, no meaningful interpretation or comparison could be performed. There will be no name associated with this sample in the *Linked No.* field of the EXR/EXH.

14 **Mixed profile- complex minor unsuit for interp or compar.**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile indicated the presence of DNA from more than one contributor. This minor DNA profile is too complex for meaningful interpretation or comparison purposes due to the unknown number of potential contributors and/or the limited amount of information within the minor DNA profile.
Mnemonic = MPCMU
(P+)

The following comment is for the rare occurrence where the major is female and the minor is only a Y (no STRs). DRMU will occasionally call to ask whether the minor DNA profile indicated male origin, and this EXH line will provide this information.

15 **Mixed profile, minor profile insuff – indicated male origin**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile did not contain sufficient information for comparison purposes other that to say it indicated it was of male origin.
Mnemonic = MPMPIM
(P+)

The following comment should be used when a mixed DNA profile was obtained from this sample that could be separated into major and minor DNA profiles. This minor DNA profile was a partial DNA profile which obtained 3 alleles out of a possible 18 alleles and is therefore unable to be loaded and searched on NCIDD. This EXR/EXH line indicates to the QPS that a partial minor DNA profile with limited information was obtained that may have enough information to be compared to other DNA profiles for inclusion or exclusionary purposes.

16 **Mixed profile, minor comp. 3 of 18 DNA components**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 3 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = MPMC3

Not Current

(P+)

The following comment should be used when a mixed DNA profile was obtained from this sample that could be separated into major and minor DNA profiles. This minor DNA profile was a partial DNA profile which obtained 4 alleles out of a possible 18 alleles and is therefore unable to be loaded and searched on NCIDD. This EXR/EXH line indicates to the QPS that a partial minor DNA profile with limited information was obtained that may have enough information to be compared to other DNA profiles for inclusion or exclusionary purposes.

17 **Mixed profile, minor comp. 4 of 18 DNA components**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 4 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = MPMC4
(P+)

The following comment should be used when a mixed DNA profile was obtained from this sample that could be separated into major and minor DNA profiles. This minor DNA profile was a partial DNA profile which obtained 5 alleles out of a possible 18 alleles and is therefore unable to be loaded and searched on NCIDD. This EXR/EXH line indicates to the QPS that a partial minor DNA profile with limited information was obtained that may have enough information to be compared to other DNA profiles for inclusion or exclusionary purposes.

18 **Mixed profile, minor comp. 5 of 18 DNA components**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 5 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = MPMC5
(P+)

Complex Mixed DNA profiles (more than 2 contributors) (P+ or PP21)

The following comment should be used when a full or partial mixed DNA profile was obtained from at least two contributors which were unable to be resolved into distinct DNA contributions (e.g. major and minor DNA profiles or conditioned DNA profiles). This may include an indication of a low-level DNA contribution that is affecting the interpretation of the DNA profile (i.e.. it is preventing the DNA

profile from being able to be separated into major and minor DNA profiles). An evidence sample or unknown contributor (e.g. uk m1) could not be excluded as a contributor to this mixed DNA profile. There will always be a name associated with this sample in the *Linked No.* field of the EXR/EXH.

19 **Complex mixed DNA profile – cannot exclude**
This item/sample gave a full or partial mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles) and therefore could not be loaded to NCIDD. The DNA profile obtained from the barcode sent with this exhibit report cannot be excluded as being a possible contributor of DNA to this mixed DNA profile.
Mnemonic = CMPCE
(P+)

The following comment should be used when a full or partial mixed DNA profile was obtained from at least two contributors which were unable to be resolved into distinct DNA contributions (e.g. major and minor DNA profiles or conditioned DNA profiles). This may include an indication of a low-level DNA contribution that is affecting the interpretation of the DNA profile (i.e.. it is preventing the DNA profile from being able to be separated into major and minor DNA profiles). There should be no name associated with this sample in the *Linked No.* field of the EXR/EXH as there are no reference samples/unknown profiles to compare to within the case.

20 **Complex mixed DNA profile. Unable to load to NCIDD**
This item/sample gave a full or partial mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles) and therefore could not be loaded to NCIDD. This complex mixed DNA profile cannot be interpreted further as no reference sample has been received for direct comparison; or alternatively, comparison with additional reference samples may be possible if forthcoming.
Mnemonic = CMPULN
(P+)

The following comment should be used when a mixed DNA profile was obtained from multiple contributors. Due to the unknown number of contributors or the partial nature of the mixed DNA profile, no meaningful interpretation or comparison could be performed. There will be no name associated with this sample in the *Linked No.* field of the EXR/EXH.

21 **Complex mixed profile unsuitable for interp or comparison**
This item/sample gave a complex Mixed DNA profile with multiple contributors. This mixture is not suitable for meaningful interpretation due to either its complexity relating to the unknown and potentially large number of contributors and/or the limited amount of information within the DNA profile.
Mnemonic = CMPU
(PP21 or P+)

No major/minor DNA profiles / Even Mixed DNA profiles (2 contributors) (P+)

The following comment should be used when a full or partial even mixed DNA profile was obtained from this sample which indicated the presence of DNA from two people. The mixed DNA profile could not be separated into major and minor DNA profiles. There should be no name associated with this sample in the *Linked No.* field of the EXR/EXH.

Not Current

22 **Mixed profile, No major/minor. Unable to load to NCIDD**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could not be separated into major and minor DNA profiles and could not be loaded to NCIDD. In the absence of reference samples, no further interpretation can be conducted; or comparison with additional reference samples may be possible if forthcoming.
Mnemonic = MPNMUN
(P+)

The following is comment should be used when a mixed DNA profile was obtained from this sample which could not be separated into major and minor DNA profiles. An evidence sample or unknown contributor (e.g. uk m1) could not be excluded as a contributor to this mixed DNA profile. There will always be a name associated with this sample in the *Linked No.* field of the EXR/EXH.

23 **Mixed profile, No major/minor – cannot exclude**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could not be separated into major and minor DNA profiles and could not be loaded to NCIDD. The DNA profile obtained from the barcode sent with this exhibit report cannot be excluded as being a possible contributor of DNA to this mixed DNA profile.
Mnemonic = MPNMM
(P+)

Conditioned Mixed DNA profiles (P+)

The following comment should be used when a full or partial mixed DNA profile consistent with coming from two contributors was obtained which could not be separated into major and minor contributions. The mixed DNA profile could be conditioned on a known reference sample to determine the unknown contributor. This comment must always be followed by MPRP, MIPPRO, or MPRPAC.

24 **Mixed DNA profile conditioned on**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that the DNA profile obtained from the barcode sent with this exhibit report has contributed to this mixed DNA profile. This result should always be used in conjunction with “Mixed DNA profile. Remaining profile after conditioning”
Mnemonic = MPCO
(P+)

The following comment should be used when a full or partial mixed DNA profile consistent with coming from two contributors was obtained which could not be separated into major and minor contributions. The mixed DNA profile could be conditioned on a known reference sample to determine the unknown contributor. This comment must always follow MPCO, or MIPDNA.

25 **Mixed DNA profile. Remaining profile after conditioning**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the “Mixed DNA profile conditioned on” exhibit report. The DNA

Not Current

profile remaining after the conditioning matches the DNA profile obtained from the barcode sent with this exhibit report.
Mnemonic = MPRP
(P+)

The following comment should be used when a full or partial mixed DNA profile consistent with coming from two contributors was obtained which could not be separated into major and minor contributions. The mixed DNA profile could be conditioned on a known reference sample to determine the unknown contributor. The known contributor to this DNA profile will be uploaded to NCIDD. This comment must always be followed by MPRP, MIPPRO, or MPRPAC.

26 **Mixed DNA profile conditioned on – NCIDD**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that the DNA profile obtained from the barcode sent with this exhibit report has contributed to this mixed DNA profile. This result should always be used in conjunction with "Mixed DNA profile. Remaining profile after conditioning". This DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = MIPDNA
(P+)

The following comment should be used when a full or partial mixed DNA profile which indicates the presence of DNA from two contributors was obtained, which could not be separated into major and minor DNA profiles. The mixed DNA profile could be conditioned on a known reference sample to determine the unknown contributor. The profile remaining after conditioning will be uploaded to NCIDD. This comment must always follow MPCO, or MIPDNA.

27 **Mixed profile. Remaining profile after conditioning – NCIDD**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the "Mixed DNA profile conditioned on" exhibit report. The DNA profile remaining after the conditioning matches the DNA profile obtained from the barcode sent with this report. This DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.
Mnemonic = MIPPRO
(P+)

The following comment should be used when a full or partial mixed DNA profile which indicates the presence of DNA from two contributors was obtained, which could not be separated into major and minor DNA profiles. The mixed DNA profile could be conditioned on a known reference sample to determine the unknown contributor. The profile remaining after conditioning was a partial DNA profile which contained information less than the stringency for reporting a match on NCIDD (less than 12 alleles and greater than 5). This indicates to the QPS DRMU that a partial DNA profile was obtained that could be used for comparison, but does not have enough alleles to obtain a match and be reported as a cold link through Auslab. This sample should not be uploaded to NCIDD. This comment must always follow MPCO, or MIPDNA.

28 **Mixed profile. Remain profile after cond – insuff NCIDD**

Not Current

This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the "Mixed DNA profile conditioned on" exhibit report. The DNA profile remaining after the conditioning was a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This remaining DNA profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this remaining partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = MPRPAC
(P+)

The following comment should be used when a full or partial mixed DNA profile which indicates the presence of DNA from two contributors was obtained which could not be separated into major and minor DNA profiles. The mixed DNA profile could be conditioned on a known reference sample to determine the unknown contributor. The profile remaining after conditioning was a partial DNA profile which has less than 6 alleles and is therefore unable to be loaded and searched on NCIDD. This EXR/EXH line indicates to the QPS DRMU that a partial minor DNA profile was obtained that may have enough information to be compared to other DNA profiles for inclusion or exclusionary purposes. This sample should not be uploaded to NCIDD. This comment must always follow MPCO, or MIPDNA.

29 **Mixed profile. Remain profile after cond– unsuitable NCIDD**
This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the "Mixed DNA profile conditioned on" exhibit report. The DNA profile remaining after the conditioning was a partial DNA profile which contained insufficient information for searching on NCIDD, and therefore is unable to be loaded to NCIDD. This remaining DNA profile may contain enough information to compare to other DNA profiles for either inclusion or exclusionary purposes. Where information was obtained, the DNA components of this remaining partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).
Mnemonic = MPRPC
(P+)

Not Current

4.15 Intelligence Results (PP21 or P+)

These EXR/EXH lines indicate a profile is to be loaded to NCIDD for intelligence purposes only, and further interpretations need to be made in a statement. These comments should only be used when there are no reference samples for a case and should not be used if a better profile exists that can be loaded.

These profiles are loaded to NCIDD in order to provide intelligence information to Queensland Police Service to aid in their investigations. Where possible, an unknown designation should be associated to the Intelligence EXH lines.

1 **Mixture Interp reqd - Intel profile loaded to NCIDD**
This item/sample gave a mixed DNA profile that has been interpreted for intelligence purposes only. This interpretation may not be able to be used for evidentiary purposes. This means that we may have lowered our routine interpretational or NCIDD matching

guidelines in order to assist with the generation of intelligence information. This intelligence DNA profile has been selected for loading to NCIDD and further explanation of the interpretations made will follow in an intelligence report. It should be noted that the interpretation provided within this intelligence report may not meet the stringent court reporting guidelines and therefore wording within an evidential statement may be different. The Intelligence DNA profile loaded to NCIDD will be searched against any DNA profiles currently held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this intelligence DNA profile. It will be outlined in the Intelligence report that this mixed DNA profile may be reported differently in an evidentiary statement.
Mnemonic = MIRIN
(P+)

2 **Partial profile Interp reqd – Intel profile loaded NCIDD**
This item/sample gave a partial DNA profile which contained an indication of DNA at a level less than the laboratorys standard reporting threshold. This profile was submitted for further analysis below QHFSS standard reporting thresholds for intelligence purposes. The subsequent profile has been selected for loading to NCIDD for intelligence purposes only and further explanation of the interpretations made will follow in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution.
Mnemonic = PIRIN
(P+)

3 **Partial profile – Intel profile loaded NCIDD**
This item/sample gave a partial DNA profile which contained insufficient information for NCIDD matching as it was below the QHFSS stringency for reporting a match on NCIDD. This profile may also have indications of DNA at a level less than the laboratorys standard reporting threshold, therefore the profile may have been submitted for further analysis below standard reporting thresholds for intelligence purposes. The profile has been selected for loading to NCIDD for intelligence purposes only and any matches will be reported in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution.
Mnemonic = PPIPL
(P+)

4 **Minor/Remaining DNA profile – Intel profile loaded NCIDD**
This item/sample gave a mixed DNA profile, of which the minor or remaining DNA profile contained insufficient information for NCIDD matching as it was below the QHFSS stringency for reporting a match on NCIDD. The profile has been selected for loading to NCIDD for intelligence purposes only and any resulting matches will be reported in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution.
Mnemonic = MDPIL
(P+)

Not Current

The following comment should be used when the DNA profile obtained cannot sufficiently be explained by an EXH and an Intelligence report is required to be sent to QPS DRMU in order to explain the interpretations made.

5 **Intel report required for further interpretation**
The results for this item/sample require further explanation which will follow in an intelligence report.
Mnemonic = IRRFI
(PP21 or P+)

4.16 Interim Results (PP21 or P+)

The following comments are to be used when initial results are required to be reported to QPS, however reworking is being carried out on the sample.

1 **Interim result- Part profile obtained- NCIDD. Rework Reqd**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a partial DNA profile which has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. Final results are pending.
Mnemonic = INTER1
(P+)

2 **Interim result- Partial profile undergoing rework**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a partial DNA profile. Final results are pending.
Mnemonic = INTER2
(P+)

3 **Interim result- Partial profile -Intel NCIDD. Rework Reqd**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a partial DNA profile which contained insufficient information for NCIDD matching according to standard reporting protocols. After further analysis below standard reporting thresholds the profile has been selected for loading to NCIDD for intelligence purposes only. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. Final results are pending.
Mnemonic = INTER3
(P+)

4 **Interim result- mixed profile obtained. Rework Reqd**
The interim DNA profile obtained from this sample/item indicated the presence of DNA from two or more contributors. This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is

Not Current

repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.
Mnemonic = INTER4
(PP21 or P+)

5 **Interim result- mixed profile - Intel NCIDD. Rework Reqd**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a mixed DNA profile that has been interpreted for intelligence purposes only. This mixed DNA profile indicated the presence of DNA from at least two contributors. An attempt has been made to separate major and minor DNA profiles within this mixed DNA profile in order to load to NCIDD for intelligence purposes only. The major DNA profile has been loaded to NCIDD and further interpretations are required. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. This mixed DNA profile is only reportable by statement in order to clarify interpretation assumptions. Final results are pending.
Mnemonic = INTER5
(P+)

6 **Interim result- no profile obtained- undergoing rework**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is no DNA profile. Final results are pending.
Mnemonic = INTER6
(PP21 or P+)

7 **Interim result- Mixed major comp.- NCIDD. Rework Reqd**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a mixed DNA profile which indicates the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. Where information was obtained, the major DNA profile matched the DNA profile for the barcode sent with this exhibit report. Final results are pending.
Mnemonic = INTER7
(P+)

8 **Interim result- Mixed minor comp.- NCIDD. Rework Reqd**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a mixed DNA profile which indicates the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. Where information was obtained, the minor DNA profile matched the DNA profile for the barcode sent with this exhibit report. Final results are pending.

Not Current

Mnemonic = IRMMC
(P+)

9 **Interim- 9 loci, pos. sub-thresh peaks-NCIDD. Rework Reqd**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a complete 9 loci DNA profile; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. These sub-threshold peaks did not interfere with the interpretation of the reportable DNA components in the 9 loci DNA profile obtained, which has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. Final results are pending.
Mnemonic = IPTPR
(P+)

10 **Interim result – sample undergoing rework**
This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. This rework could be due to: instrument failure, requiring the sample to be re-processed; interpretation difficulties, requiring the sample to be re-run to resolve any issues. Final results are pending.
Mnemonic = IRSUR
(PP21 or P+)

11 **Interim Result- incomplete single source. Rework reqd**
The interim result obtained from this sample/item was an incomplete single source DNA profile. This is not a final result and the sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.
Mnemonic = INTSSR
(PP21)

4.17 Paternity Results (PP21 or P+)

The following comment is to be used in instances where the questioned father contains all of the obligate paternal alleles. This EXR/EXH line is to be placed on a new EXR/EXH barcode with the child barcode in the lab no. field and the questioned father barcode in the linked no field.

1 **Not excluded as biological father**
The DNA profile obtained from the barcode sent with this exhibit report is not excluded as being a biological father of the DNA profile obtained from the exhibit.
Mnemonic = NEXBF
(PP21 or P+)

The following comment is to be used in instances where the questioned father does not contain all of the obligate paternal alleles and is excluded as being the possible father. This EXR/EXH/EXH line is to be placed on a new EXR/EXH barcode with the child barcode in the lab no. field and the questioned father barcode in the linked no field.

Not Current

2 **Excluded as biological father**
The DNA profile obtained from the barcode sent with this exhibit report is excluded as being a biological father of the DNA profile obtained from the exhibit.
Mnemonic = EXBF
(PP21 or P+)

The following comment is to be used in instances where the questioned mother contains alleles that are present in the child's DNA profile. This EXR/EXH line is to be placed on a new EXR/EXH barcode with the child barcode in the lab no. field and the questioned mother barcode in the linked no field.

3 **Consistent with being biological mother**
The DNA profile obtained from this exhibit is consistent with being a biological child of the barcode sent with this exhibit report.
Mnemonic = CWBM
(PP21 or P+)

The following comment is to be used in instances where the questioned mother does not contain alleles that are present in the child's DNA profile and is excluded as being the possible mother. This EXR/EXH line is to be placed on a new EXR/EXH barcode with the child barcode in the lab no. field and the questioned mother barcode in the linked no field.

4 **Not consistent with being biological mother**
The DNA profile obtained from the barcode is not consistent with being a biological mother of the DNA profile obtained from the exhibit.
Mnemonic = NCWBM
(PP21 or P+)

The following comment is to be used only in rare instances where a profile obtained from a crime sample could be a biological child of the barcode in the linked no. field.

5 **Consistent with being child of**
The DNA profile obtained from this exhibit was consistent with being the biological child of the barcode sent with this exhibit report.
Mnemonic = CWBC
(PP21 or P+)

The following comment is to be used only in rare instances where a profile obtained from a crime sample could not be a biological child of the barcode in the linked no. field.

6 **Not consistent with being child of**
The DNA profile obtained from this exhibit was not consistent with being the biological child of the barcode sent with this exhibit report.
Mnemonic = NCWBC
(PP21 or P+)

4.18 Quality control failure Results (PP21 or P+)

The following comment will be used in instances where a failure in one of the quality control processes has resulted in a DNA profile unable to be reported to QPS.

Not Current

1 **Quality control failure – results not reportable**
During the processing of this item/sample, a failure in one of the quality control processes was identified. Investigations into this occurrence were undertaken; however any results for this sample are not reportable.
Mnemonic = QCF
(PP21 or P+)

The comment will be used in instances where a match is obtained to a QPS elimination sample and advice is required from QPS to determine whether results for this sample can be reported. The barcode of the elimination sample will be entered into the warm link number field.

2 **Quality flag identified, on hold awaiting advice from QPS**
During the processing of this item/sample, QHFSS quality control processes indentified the integrity of this sample may be compromised. Advice is required from QPS to determine whether any results for this sample are reportable.
Mnemonic = QFIH
(PP21 or P+)

The following comment will be used in instances where a match is obtained to a QPS elimination sample. The barcode of the elimination sample will be entered into the warm link number field. This line is used when advice has been received from QPS that results for this sample cannot be used.

3 **Quality control failure, refer to QPS**
During the processing of this item/sample, QHFSS quality control processes identified the integrity of this sample is compromised. Results for this sample are not reportable.
Mnemonic = QCFRQ
(PP21 or P+)

The following comment will be used in instances where a failure in one of the quality control processes has been identified and further investigation is being undertaken to determine if the result can be reported to QPS.

4 **On hold, pending further work**
These results are currently subject to quarantine pending the completion of further quality checks. The outcome of these quality checks will be reported once complete.
Mnemonic = OHPFW
(PP21 or P+)

Not Current

4.19 Environmental Monitoring Final results (PP21 or P+)

Note – Environmental monitoring samples are analysed below the limit of reporting (LOR = 50 RFU for P+, 40 RFU for PP21) for intelligence purposes. Environmental samples will be interpreted using P+ assessment techniques for mixed DNA profiles, and will be interpreted through STRmix™ if further statistical interpretation is required.

Environmental samples that match to QPS samples are reported through the EXH as a match. Environmental samples that match to QHFSS staff samples are reported as for crime scene samples – Quality control failure. If no matches are obtained to any staff databases, a further quality search is performed against the DNA Analysis Database (DAD). Any matches to this are reported via an Intelligence report through the Quality and Projects team, with the EXH line "ENVM – additional quality searches conducted". If no matches are obtained, then the profile is assigned as an unknown male or female with no numerical designation, example UK M or UK F, using the following EXH lines:

1 **ENVM – Full DNA profile**
This environmental sample gave a full DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained
Mnemonic = ENFDP
(PP21 or P+)

2 **ENVM –Partial DNA profile**
This environmental sample gave a partial DNA. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained
Mnemonic = ENPDP
(PP21 or P+)

3 **ENVM - Partial profile unsuitable for comparison purposes**
This environmental sample gave a partial DNA profile which was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information obtained. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.
Mnemonic = ENPDPU
(PP21 or P+)

4 **ENVM – No DNA profile**
No DNA profile was obtained from this environmental sample. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.
Mnemonic = ENNDP
(PP21 or P+)

5 **ENVM – Major DNA profile**
This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles, of which the major was a full or partial DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which

Not Current

is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained.
Mnemonic = ENMDP
(PP21 or P+)

6 **ENVM – Minor DNA profile unsuitable for comparison**
This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles, of which the minor DNA profile contained insufficient information for comparison purposes due to the limited amount of information obtained. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.
Mnemonic = ENMDPU
(PP21 or P+)

7 **ENVM – Minor DNA profile**
This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles, of which the minor DNA profile was a full or partial DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained
Mnemonic = ENMIDP
(PP21 or P+)

8 **ENVM- Complex mixture unsuitable for interp or comparison**
This environmental sample gave a complex mixed DNA profile which contained an unknown number of contributors or a limited amount of information. This mixture is not suitable for meaningful interpretation due to either its complexity relating to the unknown and potentially large number of contributors and/or the limited amount of information within the profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.
Mnemonic = ENCMPU
(PP21 or P+)

9 **ENVM - Complex mixed DNA profile**
This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles), and as such, no further interpretation can be conducted as this time. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.
Mnemonic = ENCMDP
(PP21 or P+)

10 **ENVM additional quality search conducted see Intel report**

Not Current

Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. If the profile obtained cannot be matched to a QHFSS DNA Analysis staff or QPS staff member; a second Quality assurance process is used. This search capability is restricted within DNA Analysis to the Managing Scientist and the Quality & Projects Senior Scientist and utilises the DNA Analysis Database (DAD). This quality search is only performed to aid QPS in their investigation of any potential contamination events. In this instance, a match was obtained from this additional quality assurance search. Further information is contained within the intelligence report that will accompany this exhibit report.
Mnemonic = ENAQS
(PP21 or P+)

Not Current

5. Amendment History

Version	Date	Author/s	Amendments
1	May 2005	L Ryan	First Issue
2	Jun 2005	L Ryan	Add changes suggested during review
3	Jan 2006	L Ryan	Addition of new EXR/EXH results
4	Feb 2006	L Ryan	Addition of new EXR/EXH results
5	Sep 2006	L Ryan	Grouping like EXR/EXHs and numbering of results Addition of new EXR/EXH results Seminal Fluid Examination EXR/EXH #s: 12,13 Saliva Examination EXR/EXH #: 5 Hair Examination EXR/EXH #: 3 General Examination EXR/EXH #s:4,13,14,15,16,17 Mixed DNA Profile Final EXR/EXH #s:20,21,22,23 Blood Examination EXR/EXH #s: 5,6
6	Nov 2006	P Taylor	Added Blood Examination EXR/EXH# 7
7	21 Feb 2007	P Taylor	Added Saliva Presumptive EXR/EXH# 6,7
8	11 Dec 2007	P Taylor	Removed unused EXR/EXH lines. Added comments for when to use EXR/EXH lines. Added Paternity EXR/EXH lines. New lines – Intelligence EXR/EXH's; Mixed DNA profile EXR/EXH's #13,16; Seminal Fluid Examination EXR/EXH #7; Saliva Examination EXR/EXH #4; and General Examination EXR/EXH's #13,14,15.
9	05 Aug 2008	P Taylor	Added new EXR/EXH lines: 4.1 (7), 4.2 (13), 4.7 (14,15 and 19), 4.12 Quality Control failure EXR/EXH's and 4.13 Interim EXR/EXH's.
10	25 Jan 2010	P Taylor, E Caunt	Complete re-write of comments and explanations, and revision of EXR/EXH lines.
11	23 Sep 2011	P Taylor	Addition of EXH lines to replace FERRO's, ENVM EXH lines, and some other additional EXH lines. Deactivated some EXH lines that were no longer required. Some minor re-writing of expanded comments.
12	30 Nov 2012	P Brisotto, E Caunt	Update with new EXHs for PowerPlex21 and STRmix

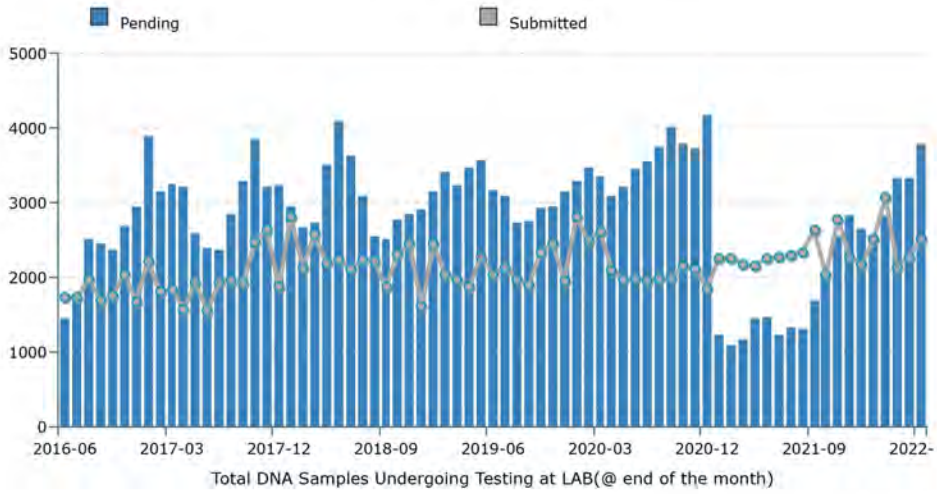
Not Current

Stats Summary - DNA Awaiting Testing

Statistics Report

Current LABAuslab Case Status @ 11/08/2022

Status	Crime Type	Cases	Samples
RECEIVED	MAJOR	2	2
STARTED	MAJOR	533	1819
STARTED	VOLUME	1722	2237



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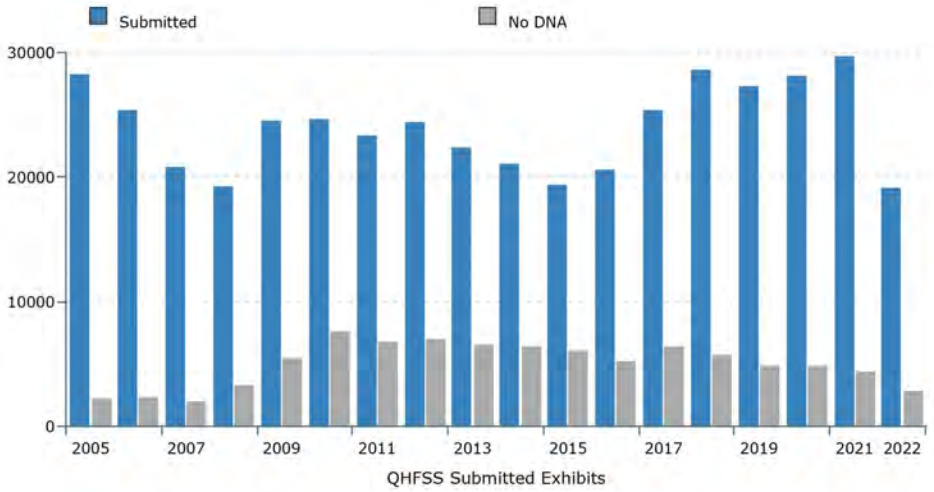
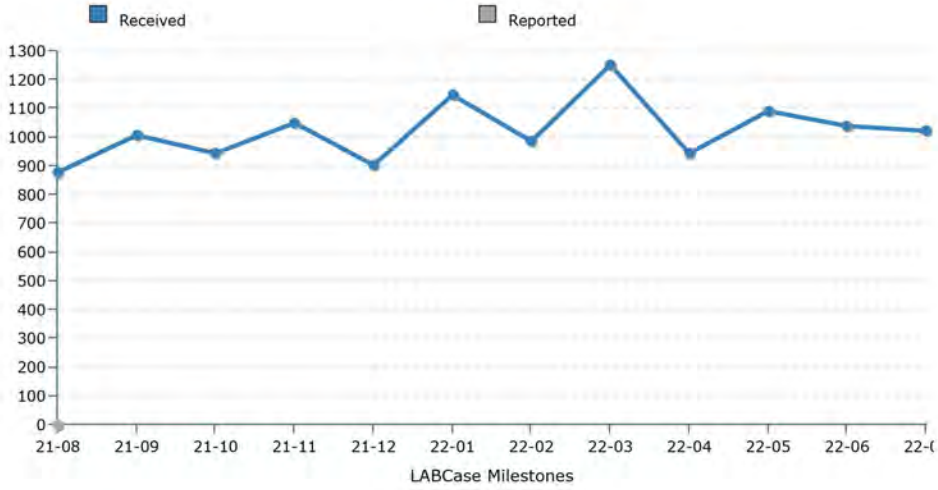
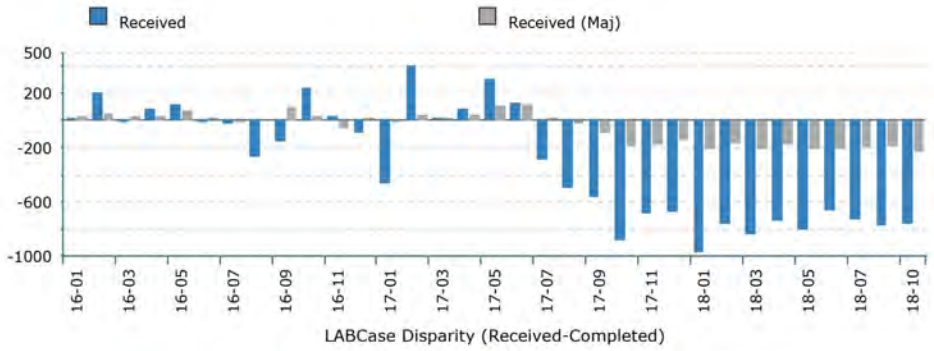
CA-112

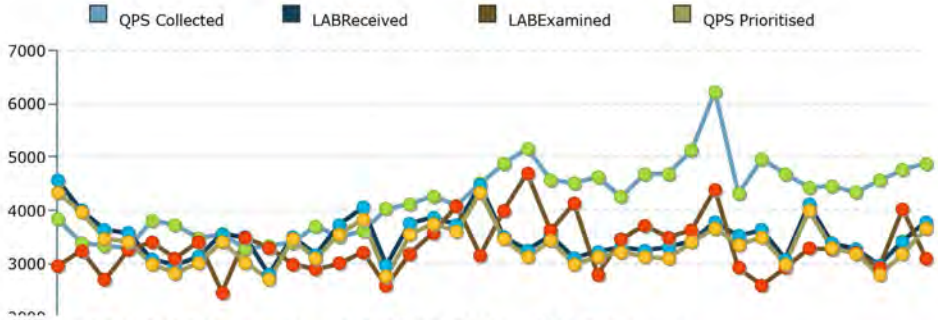
Stats Summary - DNA Performance

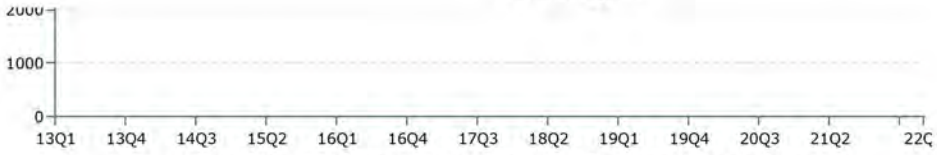
Statistics Report



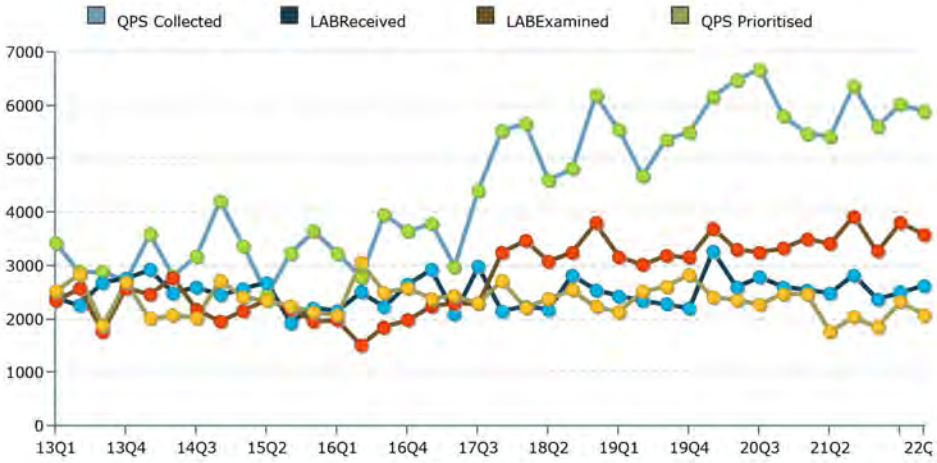








Volume Crime DNA Samples Collected vs Testing Started by LABper quarter



Major Crime DNA Samples Collected vs Testing Started by LABper quarter

440010 (Australia/Brisbane) 2022-08-11 16:17 164.112.251.224

CA-113

Queensland
Government

Forensic Register IP Agreement

Between

The State of Queensland acting through the Queensland Police Service

And

Bdnatec Pty Ltd

ABN 51 149 881 676

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1. Definitions and Interpretation

1.1 Definitions

In this Agreement:

Agreement	means this document, including its Schedules and Annexure 1.
Bdna	means Bdnatec Pty Ltd ABN 51 149 881 676.
Bdna FR	means the Forensic Register as further modified, enhanced, developed and added to after the Effective Date, including any Materials created by or on behalf of, or with the consent of, or otherwise acquired by Bdna, by way of modification, adaptation or translation of, or creation of derivative works based on, the Effective Date FR, and includes any software program (howsoever called) offered commercially by or on behalf of or under licence from Bdna that performs the functions of a forensic laboratory information management system, including any software as a service version. The Bdna FR includes the Consolidated FR and the Commercial Version.
Business Day	means between 9.00 am and 5.00 pm on a day other than a Saturday, Sunday or public holiday in Brisbane, Queensland, Australia (except where another location is specified in the relevant clause).
Claim	includes any claim (whether ascertained or unascertained), action, proceeding, demand, application, enforcement hearing, enforcement order, judgment or investigation of any kind, and includes the allegation of a Claim.
Commencement Date	means the date on which this Agreement is executed by the parties and, if the parties executed on different dates, the later of those dates.
Commercial Version	means a version of the Forensic Register which: (a) meets the minimum specifications set out in clause 7; (b) is able to be deployed and implemented in two or more Australian police jurisdictions without further modification (where such jurisdictions are either QPS or an Existing Licensee); (c) is able to be deployed by licensees within their own network tenancy; and (d) is able to be provided to licensees as software-as-a-service.
Commercialise	means to develop, manufacture, sell, hire or otherwise exploit for financial gain or other advantage, whether directly or through

a third party, and **Commercialisation** and **Commercialising** have an equivalent meaning.

Confidential Information of a Disclosing Party means all information disclosed by or on behalf of the Disclosing Party to the Receiving Party, or acquired or created by or on behalf of the Receiving Party in connection with this Agreement, that:

(a) is by its nature confidential to the Disclosing Party;

(b) the Disclosing Party designates as confidential; or

(c) the Receiving Party knows or ought to know is confidential to the Disclosing Party,

and includes:

(d) information which relates to Intellectual Property Rights of the Disclosing Party and the Disclosing Party's Personnel;

(e) in the case of QPS and QH, information concerning processes, policies, commercial operations, financial arrangements, information technology systems and programs or other affairs of QPS and QH; and

(f) the terms of this Agreement,

whether existing or disclosed to the Receiving Party before or after execution of this Agreement, and includes any information produced by the Receiving Party or any other person derived from or containing any of the Confidential Information, but does not include any information which:

(g) is or becomes public other than through breach of a confidentiality obligation; or

(h) was:

(i) already in the Receiving Party's possession before receipt from the Disclosing Party;

(ii) independently developed by the Receiving Party; or

(iii) received by the Receiving Party from a third party on a non-confidential basis.

Consequential Loss means:

(a) indirect or consequential loss not arising as a natural consequence of a breach or other event giving rise to liability of a party;

(b) any loss of profits, loss of revenue, loss of any contract value, loss of anticipated profit or damages for lost opportunity; or

(c) loss of data.

Consolidated FR	means a version of the Forensic Register which applies the software engineering enhancements in the version of the Effective Date FR developed for the Australian Federal Police to the QPS and QH version of the Effective Date FR while retaining all functionality of the QPS and QH version of the Effective Date FR.
Development Hour	has the meaning given by clause 5.2.
Disclosing Party	means the party disclosing Confidential Information to the other party.
Effective Date	means the date specified in Item 3 of Schedule 1.
Effective Date FR	means the Forensic Register as owned by QPS, being the versions of the Forensic Register in use by or being developed for: (a) QPS and QH as at the Effective Date; and (b) any other Existing Licensee as at the Effective Date while any Existing Licence continues in relation to any adaptations, enhancement or modifications to that version of the Forensic Register, to the extent QPS owns the Intellectual Property Rights in those versions.
Escrow Agreement	means an agreement under which a third party receives the Escrow Materials from Bdna for the delivery to QPS or Bdna on the fulfilment of pre-specified conditions, as further described in clause 6.
Escrow Materials	means: (a) the source code and/or object code of the Bdna FR and all other relevant software programs owned by Bdna, documentation, information, drawings and plans; and (b) a list of any relevant third-party software programs, necessary to enable a competent person skilled in the use of the Bdna FR (and any necessary development tools used to create Bdna FR) to keep the Bdna FR in good order and repair as specified in the Escrow Agreement.
Existing Licence	means a licence concerning the Intellectual Property Right assigned to Bdna under clause 3.1(a) entered into by QPS with an Existing Licensee prior to the Effective Date.
Existing Licensee	means a Government Body identified in Item 5 of Schedule 1.

Final Release Notice	has the meaning given to it in the Escrow Agreement, with respect to the trigger events set out in clause 9.3 of this Agreement.
Financial Year	means each period from 1 July to 30 June of the following year.
Forensic Industry Panel, FIP	means the panel established in accordance with clause 4.4.
Forensic Register, FR	means the software program known as the Forensic Register, and includes the Effective Date FR and, after the Effective Date, the Bdna FR.
Force Majeure Event	means any occurrence, event or omission outside a party's control and, and includes any of the following: acts of god, a physical natural disaster including fire, flood, lightning or earthquake; natural catastrophe; war or other state of armed hostilities (whether war is declared or not), insurrection, riot, civil commotion, act of public enemies, terrorist act, national emergency (whether in fact or in law) or declaration of martial law; national emergency; explosion; epidemic, pandemic, outbreaks of infectious disease, quarantine restriction or any other public health crisis; ionising radiation or contamination by radioactivity from any nuclear waste or from combustion of nuclear fuel; confiscation, nationalisation, requisition, expropriation, prohibition, embargo, restraint or damage to property by or under the order of any government agency; generalised lack of availability of raw materials or energy; law taking effect after the date of this agreement; other governmental acts or omissions; disruption or unavailability of the internet or breakdown of communication facilities; strike, lock-out, stoppage, labour dispute or shortage including industrial disputes that are specific to a party or the party's subcontractors.
FR Support Contract	means a contract between QPS and Bdna, or QH and Bdna, or another Government Body and Bdna, for the provision of support services for the Bdna FR.
Government Body	means any of: (a) a body corporate or an unincorporated body established or constituted for a public purpose by the legislation of the Commonwealth, a State or Territory, or an instrument made under that legislation (including a local authority); (b) a body established by the Commonwealth, a State or Territory through the Governor or a Minister; or

(c) an incorporated or unincorporated body over which the Commonwealth, a State or Territory exercises control.

Insolvent A person or entity is **Insolvent** if:

(a) it is (or states that it is) an insolvent under administration or insolvent (each as defined in the *Corporations Act 2001* (Cth));

(b) it is in liquidation, in provisional liquidation, under administration or wound up or has had a controller appointed to its property

(c) it is subject to any arrangement, assignment, moratorium or composition, protected from creditors under any statute or dissolved (in each case, other than to carry out a reconstruction or amalgamation while solvent on terms approved by the other parties to this agreement);

(d) an application or order has been made (and in the case of an application, it is not stayed, withdrawn or dismissed within 30 days), resolution passed, proposal put forward, or any other action taken, in each case in connection with that person, which is preparatory to or could result in any of (a), (b) or (c) above;

(e) it is taken (under section 459F(1) of the *Corporations Act 2001* (Cth)) to have failed to comply with a statutory demand;

(f) it is the subject of an event described in section 459C(2)(b) or section 585 of the *Corporations Act 2001* (Cth) (or it makes a statement from which another party to this agreement reasonably deduces it is so subject);

(g) it is otherwise unable to pay its debts when they fall due; or

(h) something having a substantially similar effect to (a) to (g) happens in connection with that person or entity under the laws of any jurisdiction.

Intellectual Property Rights includes all copyright, trade mark, design, patents, semiconductor or circuit layout rights, plant breeders rights and other proprietary rights, and any rights to registration of such rights existing anywhere in the world, whether created before or after the date of this Agreement, but excludes Moral Rights.

Item means an item in Schedule 1.

Loss	includes any loss, damage, liability, tax, prohibition, penalty, fine or expense.
Machinery of Government Change	means a transfer of responsibility, function or operations, in whole or in part, from a Queensland Government department or agency or Queensland Government Body to another Queensland Government department or agency or Queensland Government Body.
Material	means any documents, data or information stored or recorded any form, tangible or intangible, including electronic media or devices.
Moral Rights	means the right of integrity of authorship, the right of attribution of authorship and the right not to have authorship falsely attributed, more particularly as conferred by the *Copyright Act 1986* (Cth), and rights of a similar nature anywhere in the world whether existing before, on or after the Effective Date.
New Licence	means a licence concerning the Intellectual Property Right assigned to Bdna under clause 3.1(a) entered into by Bdna with an Existing Licensee after the Effective Date.
New Release	has the meanings given to that term in clause 24.1 of the QITC General Contract Conditions.
Notice to Show Cause	means a notice issued by QPS in accordance with clause 16.1 and 16.2.
Personnel	means officers, employees, agents and contractors of an entity.
QH	means the State of Queensland acting through Queensland Health.
QH Support Contract	means the FR Support Contract referred to in clause 5.1(b).
QITC	means the Queensland Information Technology Contracting framework.
QPS	means the State of Queensland acting through the Queensland Police Service.
QPS Support Contract	means the FR Support Contract referred to in clause 5.1(a).
Receiving Party	means the party receiving Confidential Information from the other party.
Term	means the period specified in clause 2.1.

Trigger Date A	means the occurrence described in clause 17.1.
Trigger Date B	means the occurrence described in clause 17.2.
Update	has the meanings given to that term in clause 24.1 of the QITC General Contract Conditions.

1.2 Interpretation

In this Agreement unless a contrary intention is expressed:

(a) headings do not affect interpretation;

(b) all currency amounts refer to Australian currency;

(c) words in the singular include the plural and vice versa;

(d) other grammatical forms of a defined word or phrase have a corresponding meaning;

(e) a reference to a 'person' includes any legal entity;

(f) a reference to a clause, part, annexure, exhibit or Schedule is a reference to a corresponding part of this Agreement;

(g) a reference to a document (including this Agreement and any laws) includes all amendments or supplements to, or replacements or novations of, that document;

(h) a reference to law includes common law and statutory laws, regulations, orders, subordinate legislation, ministerial directions, directions of relevant regulators and binding codes of conduct;

(i) a reference to a party includes that party's executors, administrators, successors and permitted assignees;

(j) a promise, agreement, representation or warranty by two or more persons binds them jointly and severally;

(k) no rule of construction will apply to a provision of this Agreement to the disadvantage of a party merely because that party drafted the provision or would otherwise benefit from it;

(l) 'include', 'including' and similar words must be read as if followed by the words 'without limitation';

(m) 'documents', 'information' and similar words include information recorded or stored in any form, tangible or intangible, including electronic media or devices;

(n) 'consent' and 'approval' mean prior written consent and prior written approval respectively;

(o) 'agreement' means agreement in writing; and

(p) if anything under this Agreement is required to be done by or on a day that is not a Business Day in the place where the thing is to be done, that thing must be done by or on the next Business Day.

2. Term

2.1 This Agreement commences on the Commencement Date and will continue for a period of 10 years unless terminated earlier pursuant to the provisions of this Agreement.

2.2 The parties may agree to extend the Term.

3. Assignment and Licence of Intellectual Property Rights

3.1 From the Effective Date:

(a) QPS assigns to Bdna all rights, title and interest in the Intellectual Property Rights in the Effective Date FR;

(b) Bdna grants, and will ensure that any relevant third parties grant to QPS and QH, an irrevocable, perpetual (subject to clause 3.2) royalty-free, non-exclusive licence to exercise all Intellectual Property Rights assigned to Bdna under paragraph (a) and all Intellectual Property Rights in or reasonably necessary to use, maintain and develop the Effective Date FR and the Bdna FR (including future copyright), subject to the restrictions in clause 3.3 (provided that, for the purposes of this licence, the Bdna FR is limited to the Bdna FR as provided by Bdna to QPS during the Term of this Agreement); and

(c) Bdna grants, and will ensure that any relevant third parties grant to QPS and QH, an irrevocable, perpetual, royalty-free, non-exclusive licence to access and use the Bdna FR for the functions or operations of QPS and QH, subject to the restrictions in clause 3.4.

3.2 The licence under clause 3.1(b) will terminate if the Term of this Agreement expires in accordance with clause 2.1 and QPS is using the Commercial Version of the Forensic Register, or another version of the Bdna FR (other than a version modified, enhanced, developed, or added to by or on behalf of QPS without the involvement of Bdna).

3.3 The licence in clause 3.1(b) is subject to the following restrictions:

(a) from the Effective Date, the licence:

(i) is limited to using the Intellectual Property Rights for the functions or operations of QPS and QH;

(ii) excludes any right to grant sub-licences, except to any contractor that is providing services to QPS or QH that require the contractor to use the Intellectual Property Rights for the functions and operations of QPS or QH, provided that such sublicence automatically terminates at the end of the period of the service arrangement between QPS/QH and the contractor;

(iii) excludes any right to transfer the licence except on notice to Bdna in connection with a Machinery of Government Change, and subject to the restrictions in this paragraph (a); and

(iv) for the sake of certainty, excludes any right to commercialise the Forensic Register or to sub-license or transfer any rights in relation to the Forensic Register to any entity other than as expressly permitted in paragraphs (ii) and (iii); and

(b) on and from Trigger Date A (if it occurs), the restrictions in paragraph (a) cease and the licence:

(i) is limited to using the Intellectual Property Rights for the functions or operations of:

(A) QPS and QH; and

(B) other Government Bodies in Australia (provided that, for the purposes of this paragraph (B), 'Government Bodies' are limited to such bodies that are not parties to an FR Support Contract);

(ii) excludes any right to grant sub-licences except to:

(A) other Government Bodies in Australia, for their functions and operations (limited to such bodies that are not parties to an FR Support Contract); and

(B) any contractor that is providing services to such Government Bodies in Australia that require the contractor to use the Forensic Register for the functions and operations of the Government Body, provided that such sublicence automatically terminates at the end of the period of the service arrangement between the Government Body and the contractor;

(iii) is transferable to Government Bodies in Australia on notice to Bdna, subject to the restrictions in this paragraph (b); and

(iv) for the sake of certainty, excludes any right to commercialise the Forensic Register or to sub-license or transfer any rights in relation to the Forensic Register to any entity other than as expressly permitted in paragraphs (i), (ii) and (iii).

3.4 From the Effective Date, the licence granted in clause 3.1(c):

(a) excludes any right to grant sub-licences, except to any contractor that is providing services to QPS or QH that require the contractor to access and use the Bdna FR for the functions and operations of QPS or QH, provided that such sublicence automatically terminates at the end of the period of the service arrangement between QPS/QH and the contractor;

(b) without limiting the rights granted under clause 3.1(b), excludes any right to modify, enhance, develop, or add to the Bdna FR;

(c) excludes any right to transfer the licence except on notice to Bdna in connection with a Machinery of Government Change, and subject to the restrictions in this paragraph 3.4; and

(d) for the sake of certainty, excludes any right to commercialise the Bdna FR or to sub-license or transfer any rights in relation to the Bdna FR to any entity other than as expressly permitted in paragraphs (a) and (c).

3.5 On Trigger Date B (if it occurs), Bdna assigns to QPS all rights, title and interest in the Intellectual Property Rights in the Forensic Register, without need for further action by Bdna, subject always to the application of:

(a) sections 415D(1), 434J(1) and 451E of the *Corporations Act 2001* (Cth) (**Ipso Facto Provisions**); or

(b) any process which under any law with a similar purpose to the Ipso Facto Provisions may give rise to a stay on, or prevention of, the exercise of the assignment under this clause 3.5.

3.6 Nothing in this Agreement affects any statutory rights or obligations of the Crown in right of the Commonwealth or a State in relation to the use or exploitation of the IP Assets for the services of the Commonwealth or State, under Commonwealth legislation including the *Copyright Act 1968* and the *Patents Act 1990*.

3.7 Where either QPS or QH exercises its rights under clauses 3.1(b) or 3.2 to modify, enhance, develop, or add to the Bdna FR, or where either QPS or QH breaches clause 3.4(b), the resulting Material (to the extent it is additional to Bdna FR provided by Bdna to QPS or QH) is not Bdna FR.

4. Ongoing collaboration

4.1 Intentions of the parties

The parties acknowledge that:

(a) it is QPS's intention, on and from the Effective Date:

(i) to entrust the Forensic Register and the future development and maintenance of the Forensic Register to Bdna on the terms of the commercial arrangement set out in this Agreement for the mutual benefit of the parties;

(ii) to transition to using the Bdna FR as supplied and supported by Bdna from the Effective Date; and

(iii) not to continue using, maintaining or developing the Effective Date FR in the ordinary course of its operations, or any version of the Forensic Register other than Bdna's commercially released Bdna FR, or to engage any contractor other than Bdna to do any of these things;

(b) it is Bdna's intention to, from the Effective Date, develop and commercialise the Forensic Register, and Bdna recognises that in doing so it is in the interests of Bdna, QPS and QH to maintain the Forensic Register as a product that meets QPS and QH business and operational requirements;

(c) the purpose of the licence in clause 3.1(b) is to manage risk and retain capability and discretion appropriate to a Government Body by ensuring that QPS and QH:

(i) are able to use historical Materials, including records and archival copies of the Forensic Register, without risk of infringing Bdna's Intellectual Property Rights; and

(ii) do not as at the Effective Date immediately forfeit the long-standing legal right and capability to use, maintain and develop forensic register software essential to their operations, and therefore become dependent on Bdna;

(d) the purpose of the right to grant sub-licences to contractors in clauses 3.3(a)(ii) and 3.4(a) is to ensure that QPS and QH can engage contractors to the extent necessary to use the Bdna FR in the course of providing services to QPS or QH and to manage risk and retain the capability and discretion described in clause 4.1(c);

(e) the terms and conditions of this Agreement other than this clause 4.1 set out the rights and obligations of the parties in connection with the Forensic Register and this clause 4.1 does not expand, limit or restrict those rights and obligations, confer any rights or impose any obligations in addition to those rights and obligations, or otherwise have any contractual effect or form or provide any basis for any Claim or other relief.

4.2 Clarification on Bdna obligations

(a) Bdna is not required to continue to support, maintain or develop:

(i) the Effective Date FR, after the date Bdna first releases Bdna FR;

(ii) any version of the Forensic Register other than Bdna's commercially released Bdna FR; or

(iii) compatibility between the Effective Date FR, or any other version of the Forensic Register, and Bdna's commercially released Bdna FR,

unless agreed separately between the parties; and

(b) Bdna will not be required to provide QPS with access to the source code in the Forensic Register after the Effective Date other than in accordance with the Escrow Agreement entered into in accordance with clause 9 of this Agreement.

4.3 Collaboration

QPS will collaborate with Bdna on the ongoing development of the Forensic Register in the form of sharing expertise, knowledge and forensic information, as has taken place historically, including the following ways:

(a) engage in joint research and development centred around the Forensic Register;

(b) engage in forensic process improvement designs with Bdna and participate in design workshops and reviews;

(c) conduct Forensic Register proof of concept trials with Bdna to improve QPS and QH outcomes and Forensic Register capability;

(d) participate in joint industry presentations that promote the Forensic Register, and (at QPS and QH option) also promote the QPS and QH;

(e) provide appropriate access to forensic data for research and product testing; and

(f) provide desk space and access to QPS' offices for Bdna staff members, appropriate to ensuring ongoing engagement between the organisations and Forensic Register support for the QPS. Access by Bdna Personnel to QPS's offices will be subject to usual Personnel requirements including security checks and compliance with site policies.

4.4 Forensic Industry Panel

(a) Bdna will establish and attend to the administration of the Forensic Industry Panel (**FIP**), including maintaining the FIP Terms of Reference, at Bdna's cost.

(b) Bdna will constitute the FIP by:

(i) inviting a senior management representative from each of QPS and QH;

(ii) appointing as chair a senior forensic industry representative nominated by Bdna, subject to paragraph (iii) below; and

(iii) maintaining an open invitation to QPS to nominate either the QPS representative or the QH representative invited under clause 4.4(b)(i), to act as joint chair.

(c) Decisions with respect to the Forensic Register roadmap will be by consensus of the FIP.

4.5 Acknowledgements

The parties acknowledge that:

(a) the objective of the collaborative approach set out in this clause 4 will be to ensure QPS and QH stay at the vanguard of forensic outcomes worldwide and continue to enjoy rapid change to the Forensic Register to help meet the QPS' and QH's operational and regulatory needs; and

(b) while QPS and QH recognise the mutual benefits available, as Government Bodies QPS and QH must ultimately retain discretion and comply with Queensland Government policy concerning collaborative activities with private sector organisations and:

(i) QPS will not be in breach of this Agreement to the extent (if any) it or QH choose not to participate in these activities;

(ii) QPS and QH will not be obliged to incur any expenses, such as travel, accommodation or industry event attendance fees; and

(iii) QPS and QH will not be liable to Bdna for any Claim in relation to any advice or other activities engaged in by QPS and QH representatives in connection with the objectives of the FIP.

5. Support for QPS and QH

5.1 Support Contracts

(a) QPS and Bdna must use their best endeavours to negotiate, agree, enter into and maintain a FR Support Contract (the **QPS Support Contract**) (including obligations to support the Effective Date FR until replaced by Bdna FR).

(b) Bdna must use its best endeavours to agree and enter into a FR Support Contract with QH on terms equivalent to the QPS Support Contract, if required by QH (the **QH Support Contract**).

(c) Bdna will not charge QPS or QH (or require use of Development Hours) for:

(i) installation; or

(ii) maintaining the operation of existing integration points between the Forensic Register and QPS/QH systems at the time the Update or New Release is released,

in relation to Updates or New Releases under the QPS Support Contract or any QH Support Contract.

5.2 **Development Hours**

(a) A Development Hour is one hour of services provided by suitably qualified Bdna Personnel to QPS in relation to the Bdna FR under the QPS Support Contract (or, with QPS's consent, to QH under the QH Support Contract).

(b) At QPS's discretion, Development Hours may be used for:

(i) services in relation to the development of Developed Software under clause 5.5 of QITC–General Contract Conditions;

(ii) ICT Professional Services under clause 5.7 of QITC General Contract Conditions; and

(iii) any other services in respect of which Bdna would be entitled to charge QPS or QH under their respective contracts.

(c) Other than as provided in this clause 5.2, the terms of the QPS Support Contract (and, where applicable, the QH Support Contract) apply to the Development Hours, including any arrangements for estimating, scoping and ordering services.

(d) Bdna will provide to QPS a bank of Development Hours consisting of 750 hours per year for the Term (ie a total of 7,500 hours).

(e) Subject to this clause 5.2(e), QPS will be entitled to 750 Development Hours per year of the QPS Support Contract term, and may not:

(i) bring forward Development Hours from future years, or

(ii) carry over unused Development Hours from past years, provided that QPS may carry over:

(A) up to 100 Development Hours each year; and

(B) any Development Hours requested to be used in a year that are not used due to a breach or delay by Bdna that is not caused by QPS or QH or otherwise excused under the QPS Support Contract or QH Support Contract.

(f) At the end of the QPS Support Contract term, any unused Development Hours will lapse.

(g) Bdna will report to QPS on used and available Development Hours in monthly reports in accordance with the QPS Support Contract.

(h) Bdna will ensure that accurate and proper records are kept in connection with use of Development Hours and provide information from those records to QPS on request.

5.3 **No duplication**

Bdna must not charge QPS or QH or use any Development Hours for any development work in relation to the Bdna FR that it has already completed or has planned or arranged to complete of its own initiative or for another Bdna customer, except where QPS or QH require Bdna to accelerate that development work, after having been informed that the development work is already planned or arranged to be completed by Bdna FR.

5.4 **Updates and New Releases**

(a) During the Term of this Agreement, Bdna will provide Updates and New Releases to QPS and QH in accordance with the applicable FR Support Contract.

(b) After the Term of this Agreement:

(i) Bdna will provide Updates and New Releases to QPS and QH in accordance with any FR Support Contract applicable after the Term; or

(ii) if no FR Support Contract is applicable after the Term, then subject to clause 5.4(c), Bdna will provide Updates and New Releases to QPS and QH if and when Bdna makes them generally available to other customers.

(c) Clause 5.4(b)(ii) does not apply in circumstances where:

(i) Trigger Date A has occurred;

(ii) Trigger Date B has occurred; or

(iii) QPS has sent a Final Release Notice to Bdna in accordance with the terms of the Escrow Agreement, and has ceased to use the Bdna FR (without its own modifications using the Escrow Materials) for production purposes for a period of at least 12 months.

6. Commercialisation

6.1 **Bdna's Activities**

Bdna must, at its own cost:

(a) develop the Bdna FR as a contemporary enterprise standard version of the Forensic Register;

(b) develop and provide the Consolidated FR to the QPS within 18 months of the Commencement Date of this Agreement;

(c) use its reasonable endeavours to:

(i) Commercialise the Bdna FR; and

(ii) release a Commercial Version of the Bdna FR within three years of the Commencement Date of this Agreement (for the sake of certainty, following any such release Bdna must continue to make an equivalent non-software as a service version of the Bdna FR available to QPS and QH during the Term, unless both of those parties opt to transition to a software as a service version); and

(d) advise QPS as soon as practicable if it becomes aware of any adverse matters relating to the Bdna FR, including any significant quality or security failures.

6.2 Marketing and publicity

(a) Bdna must not use or permit use of the names or logos of QPS, QH or the Queensland Government or any other Queensland Government Bodies in connection with the Bdna FR or Commercialisation of the Bdna FR without the prior written consent of QPS or QH (as applicable).

(b) Bdna must cease any breach of 6.2(a) within five Business Days of receiving a notice from QPS requiring it to do so and not repeat the same or similar conduct. This clause 6.2(b) is a material term of this Agreement for the purposes of clause 16.1(i). Any breach by Bdna of clause 6.2(a) or this clause 6.2(b) after QPS has provided ten (10) notices under this clause 6.2(b) will be deemed to be a deliberate or wilful breach of a material term for the purposes of clause 16.1(i).

(c) A notice issued under clause 6.2(b) must:

(i) expressly state that it is a notice issued under that clause; and

(ii) be issued by the QPS Level 2 Representative to the Bdna Level 2 Representative (as set out in or nominated in accordance with clause 19) and comply with the notices procedure set out in clause 22.1.

(d) Neither party may make any public announcement or advertisement relating to this Agreement except where the other party has approved the proposed announcement or advertisement in writing (for clarity, this clause does not restrict QPS, QH or Bdna from making a public announcement or advertisement about the Forensic Register, subject to paragraph 6.2(a)).

(e) Neither party may unreasonably withhold or delay its consent or approval under this clause.

6.3 Reports

Bdna must provide a report to QPS within 20 Business Days of the end of each six months of each Financial Year during the Term. The report must include, in respect of each period, information in relation to Commercialisation progress, including:

(a) summary of key activities completed in relation to the activities referred to in clause 6.1;

(b) estimated completion date for release a software as a service version of the Bdna FR; and

(c) licences granted.

7. Bdna FR minimum specifications

7.1 Subject to clause 7.2, Bdna must ensure that the Bdna FR made commercially available by Bdna:

(a) will conform with:

(i) World Wide Web Consortium (W3C) Web Content Accessibility Guidelines (WCAG);

(ii) Contemporary software industry API best practices, including Department of Home Affairs REST API Standards; and

(iii) OWASP Application Security Verification Standard (ASVS);

(b) will be designed to assist clients to meet the following standards:

(i) ISO 17025; and

(ii) Australian Government Information Security Manual;

(c) is available to QPS and QH in a form that:

(i) retains 100% of the functionality of the Effective Date FR in use by QPS and QH as at the Commencement Date, including in relation to includes all quality management, case management, item management and workflow management functions and associated statistical tools that are specific to the operation of a forensic laboratory; and

(ii) is designed to assist QPS and QH to comply with Queensland Government Enterprise Architecture standards; and

(d) is available to QPS and QH and other Australian customers in a form that can operate fully without transferring or storing any personal information associated with the use of the Bdna FR outside of Australia in any form, temporarily or otherwise (including during provision of support services).

7.2 The requirements in:

(a) clause 7.1(a) and clause 7.1(b) may only be waived or modified in accordance with a decision of the FIP in accordance with clause 4.4.

(b) clause 7.1(c) and clause 7.1(d) may only be waived or modified with the prior written agreement of QPS.

8. Bdna's Undertakings

Bdna warrants that in Commercialising the IP Assets or otherwise exercising its rights or carrying out its obligations under this Agreement, it will not:

(a) infringe any applicable laws;

(b) infringe any third party rights including Intellectual Property Rights or Moral Rights (for clarity, Bdna will not be in breach of this clause where an infringement arises out of the Intellectual Property Rights assigned to Bdna under paragraph 3.1(a));

(c) engage in any conduct which is:

(i) unlawful or in connection with any unlawful activity (and will take reasonable steps to ensure the Bdna FR is not used by any other person in a manner that is unlawful or in connection with any unlawful activity); or

(ii) misleading or deceptive or likely to mislead or deceive; or

(d) do anything or deliberately become involved in any situation which, in the reasonable opinion of QPS, brings QPS, QH or the Forensic Register into public disrepute, contempt, scandal or ridicule, offends public opinion or reflects unfavourably upon QPS, QH or the Forensic Register's reputation.

9. Escrow Agreement

9.1 QPS and Bdna will use their best endeavours to negotiate, agree and enter into an Escrow Agreement substantially in the form of Annexure 1 to this Agreement, adapted to refer to both the QPS Support Contract and this Agreement, and subject to the specific requirements in this clause 9, or such other form reasonably acceptable to the parties.

9.2 The Escrow Agreement will continue for the Term of this Agreement and expire on the date on which both this Agreement and the QPS Support Contract have expired, unless both this Agreement and the QPS Support Contract are terminated earlier, in which case the Escrow Agreement will expire six months after the last termination to occur

9.3 The trigger events in the Escrow Agreement entitling QPS to commence a process for release of the Escrow Materials to QPS, must include circumstances where:

(a) Bdna is Insolvent;

(b) Bdna has ceased for any reason to maintain or support the Bdna FR for all customers. For clarity, a temporary cessation by reason of a Force Majeure Event is not a trigger event;

(c) the QPS Support Contract or this Agreement has been lawfully terminated by QPS for Bdna's breach or other default;

(d) the Escrow Agreement is terminated (other than jointly by QPS and Bdna) and a new Escrow Agreement is not entered into within 30 days on substantially the same terms and conditions as are set out in the original Escrow Agreement, with an alternative escrow agent who is acceptable to both QPS and Bdna. For clarity, it is not a trigger event where:

(i) the alternative escrow agent requires terms and conditions which differ to those of the original Escrow Agreement; or

(ii) failure to enter into the new Escrow Agreement within 30 days is as a result of an act or omission outside of Bdna's reasonable control, provided that Bdna continues to use its best endeavours to negotiate, agree and enter into the new Escrow Agreement (to the extent possible and unless released by QPS);

(e) Bdna makes any assignment or novation in breach of clause 22.11 (Assignment and Novation); or

(f) a Change in Control of Bdna occurs without QPS's prior written consent, in breach of clause 22.12 (Change in Control).

10. Warranties and Acknowledgements

10.1 No Warranty by QPS

Subject to clause 10.2:

(a) except for such warranties on the part of QPS as are expressly set out in this Agreement, there are no other terms or warranties binding upon QPS or between QPS and Bdna;

(b) QPS expressly excludes any representation or warranty in respect of:

(i) the accuracy, currency, correctness, lawfulness, completeness, safety, functionality, compatibility, or marketability of the Forensic Register; and

(ii) the appropriateness or suitability of the Forensic Register for Commercialisation or any other use; and

(iii) whether QPS owns the Intellectual Property Rights in the Forensic Register or is otherwise entitled to grant any rights under this Agreement (subject to clause 10.2); and

(iv) whether the Forensic Register infringes the Intellectual Property Rights or Moral Rights of any other person (subject to clause 10.2).

(c) Bdna acknowledges and agrees that QPS is not responsible for:

(i) updating any part of the Forensic Register;

(ii) informing Bdna if it becomes aware that any part of the Forensic Register is wrong or requires change or correction (other than in accordance with the QPS Support Contract); or

(iii) any Claim, loss or damage howsoever sustained or incurred by Bdna as a consequence of or incidental to the use of the Forensic Register by Bdna or any other person, and Bdna further acknowledges that Commercialisation of the Forensic Register and use of the Forensic Register by Bdna or any person under licence from Bdna is at Bdna's own risk.

10.2 Intellectual property warranties

QPS represents and warrants that, to the best of QPS's knowledge, up to the Effective Date:

(a) QPS owns the Intellectual Property Rights in the Effective Date FR; and

(b) the Effective Date FR does not infringe the Intellectual Property Rights or Moral Rights of any other person.

10.3 Non-Excludable Rights

Nothing in this Agreement is intended to have the effect of excluding any warranties, liabilities or laws that cannot be excluded, restricted or modified by agreement of the parties.

11. PPSA

11.1 PPSA Provisions

The parties acknowledge and agree that the terms of Schedule 2 (PPSA Provisions) are incorporated into, and apply as if they were set out in full in the body of this Agreement.

12. Existing Licensees

12.1 The parties acknowledge that QPS is party to the Existing Licences and that the Intellectual Property Rights assigned by QPS to Bdna under clause 3.1(a) are subject to the rights granted by QPS under the Existing Licences.

12.2 QPS will use its reasonable endeavours to negotiate termination and release of each Existing Licence to bring an end to any ongoing obligations or rights of QPS and any ongoing rights of the Existing Licensees under the Existing Licences that are inconsistent with the future ownership and management of the Forensic Register by Bdna under this Agreement.

12.3 Bdna will use its reasonable endeavours to negotiate a New Licence with each Existing Licensee.

12.4 The parties acknowledge that agreement by each Existing Licensee to termination and release of its Existing Licence will most likely be subject to the Existing Licensee agreeing to a New Licence.

12.5 The parties will cooperate with each other and keep each other informed in relation to the performance of their respective obligations under clauses 12.2 and 12.3, subject to any confidentiality obligations owed to Existing Licensees.

13. Confidentiality

13.1 The Receiving Party:

(a) must not, and must ensure that the Receiving Party's Personnel do not, use or disclose any of the Disclosing Party's Confidential Information without the Disclosing Party's consent, other than in accordance with this clause;

(b) must keep confidential all of the Disclosing Party's Confidential Information and not disclose it unless the disclosure is:

(i) required or authorised by law;

(ii) to the Receiving Party's Personnel to the extent necessary for the performance of this Agreement or the exercise of the Receiving Party's rights under this Agreement;

(iii) with the Disclosing Party's consent; or

(iv) to the Receiving Party's legal or financial advisors;

(c) must not use the Disclosing Party's Confidential Information for any purpose other than for the purposes of performing its obligations or exercising its rights under this Agreement, except to the extent required or authorised by law;

(d) must take all steps reasonably necessary to protect the Disclosing Party's Confidential Information from misuse, loss and unauthorised access, modification or disclosure;

(e) must, where the Receiving Party discloses any of the Disclosing Party's Confidential Information to a third party, inform the third party of the confidential nature of the Confidential Information; and

(f) will be responsible for all use and disclosure of the Disclosing Party's Confidential Information by the Receiving Party's Personnel and legal or financial advisors, and other third parties to whom it discloses the Confidential Information.

13.2 On the termination or expiry of this Agreement (or earlier if requested by the Disclosing Party during the Term), the Receiving Party must deliver or destroy (as directed by the Disclosing Party) all documents, records or files in the Receiving Party's possession or control which contain any of the Disclosing Party's Confidential Information in accordance with the Disclosing Party's instructions, and will notify the Disclosing Party when this has been done. The obligation to return or destroy the Confidential Information includes irretrievably deleting such information in electronic form stored on the Receiving Party's media or devices.

13.3 The Receiving Party may retain a copy of the Disclosing Party's Confidential Information to the extent required or authorised by law, or to the extent necessary to exercise any rights surviving the termination or expiration of this Agreement.

13.4 If Bdna collects or has access to Personal Information in the course of performing this Agreement or exercising its rights under this Agreement, Bdna will comply with the *Privacy Act 1988* (Cth) in relation to that Personal Information, subject to the application (if any) of the *Information Privacy Act 2009* (Qld) (**Information Privacy Act**) in accordance with the QPS Support Contract or QH Support Contract.

13.5 The Receiving Party must immediately notify the Disclosing Party on becoming aware:

(a) of any breach of this clause; or

(b) that a disclosure or use of any of the Confidential Information is required or authorised by law, before such disclosure or use is made.

13.6 Bdna acknowledges that:

(a) the *Right to Information Act 2009* (Qld) (**RTI Act**) provides members of the public with a legally enforceable right to access documents held by Queensland Government Bodies, subject to specified exemptions under the RTI Act;

(b) information relating to this Agreement is potentially subject to disclosure under the RTI Act; and

(c) it should indicate any relevant concerns to QPS at the time of disclosing the information to QPS.

13.7 Despite anything else in this Agreement, QPS may disclose any information:

(a) to Ministers and their advisors, which is relevant to the Minister's role and responsibilities; and

(b) as required under the Information Privacy Act or RTI Act.

14. Liability and Indemnity

14.1 Neither party will be liable to the other whether in contract, tort (including negligence) or otherwise in connection with this Agreement, for any Loss to the extent that the other party (or the other party's Personnel) contributed to the Loss.

14.2 A party who suffers any Loss in connection with this Agreement must take reasonable steps to mitigate its Loss. The other party will not be responsible for any Loss to the extent that the injured party could have avoided or reduced the amount of the Loss by taking reasonable steps to mitigate its Loss.

14.3 To the fullest extent permitted by law, but subject to clauses 14.1 to 14.2, Bdna indemnifies QPS and its Personnel (**those indemnified**) for all Loss suffered or incurred by those indemnified:

(a) resulting from any Claim that may be brought against or made upon or incurred by any of them (whether in contract, tort including negligence or otherwise) in connection with any:

(i) act or omission which amounts to a breach of Bdna's obligations or warranties under this Agreement;

(ii) unlawful or negligent act or omission of Bdna or its Personnel connected with Bdna's actual or attempted performance of Bdna's obligations under this Agreement;

(iii) infringement or alleged infringement of any third party's Intellectual Property Rights or Moral Rights arising out of any use of the Bdna FR; or

(iv) use by any third party of the Bdna FR or any product, process, information, service or other thing derived from the Bdna FR,

and all costs (including legal costs on an indemnity basis) that are reasonably and properly incurred by those indemnified because of any Claim in relation to the circumstances in paragraphs (i), (ii), (iii) or (iv); or

(b) which arises directly or indirectly from a breach of any of Bdna's obligations in relation to Confidential Information or Personal Information under this Agreement.

14.4 To the fullest extent permitted by law, but subject to clauses 14.1 to 14.2, QPS indemnifies Bdna and its Personnel (**those indemnified**) for all Loss suffered or incurred by those indemnified resulting from any Claim that may be brought against or made upon or incurred by any of them (whether in contract, tort including negligence or otherwise) arising out of any modifications, enhancements, developments or additions to the Forensic Register where those modifications, enhancements, developments or additions were carried out by, or authorised by, QPS (and not by Bdna) in circumstances where:

(a) QPS has sent a Final Release Notice to Bdna in accordance with the terms of the Escrow Agreement; or

(b) Trigger Date B has occurred,

and all costs (including legal costs on an indemnity basis) that are reasonably and properly incurred by those indemnified because of any Claim arising out of any such modifications, enhancements, developments or additions to the Forensic Register.

14.5 It is not necessary for those indemnified to incur expense or make payment before enforcing a right of indemnity under this Agreement.

14.6 Subject to clause 10.3, neither party will be liable to the other party for any Consequential Loss suffered or incurred by the other party in connection with this Agreement, howsoever arising.

14.7 To the extent permitted by law, the maximum liability of QPS and QH to Bdna, whether in contract, tort (including negligence) or otherwise in connection with this Agreement, is limited to $1M in the aggregate.

15. Insurance

15.1 Bdna must, at its cost and by the Effective Date, take out and maintain or be insured under the insurance policies specified in Item 4 of Schedule 1 with an insurer authorised and licensed to operate in Australia or otherwise with an insurer with a security rating of A- or better from AM Best (or equivalent rating organisation).

15.2 Bdna must promptly provide notice to QPS if any required insurance policy is cancelled or there is any significant change in any of those policies which may impact Bdna's ability to meet its obligations under this Agreement.

15.3 Bdna must maintain all required insurance policies which are maintained on a 'claims made' basis for a minimum period of four years after this Agreement ends, or such other period specified in Item 4 of Schedule 1.

15.4 Bdna must, on request, promptly provide to QPS:

(a) an insurance certificate of currency confirming that Bdna has effected and renewed or is insured under the insurance policies specified in Item 4 of Schedule 1; or

(b) such other evidence of the required insurances, specified in Item 4 of Schedule 1.

15.5 If Bdna does not organise for the relevant insurances to be taken out and maintained in accordance with this clause 15, QPS:

(a) may take out and maintain the relevant insurances; and

(b) recover the cost of any insurance premiums as a debt due and payable to QPS.

16. Termination

16.1 QPS may, without limiting any right of action or remedy which has accrued or may accrue in favour of QPS, issue to Bdna a Notice to Show Cause if:

(a) Bdna is in breach of any obligation, warranty or term of this Agreement and the breach cannot be remedied, or the breach can be remedied but Bdna has not remedied that breach within 30 days of receiving notice of the breach by QPS;

(b) the QPS Support Contract has been lawfully terminated by QPS in accordance with the following provisions of the QITC General Contract Conditions:

(i) clause 21.1(a) or clauses 21.1(c) to 21.1(g); or

(ii) clause 21.1(b), provided that the Conflict of Interest referred to in that clause is an actual (not just anticipated or perceived) conflict of interest.

(c) Bdna is or becomes Insolvent;

(d) Bdna has indicated to QPS or any other person, expressly or by act or omission, that it is abandoning or no longer intends to Commercialise the Bdna FR, and has not genuinely retracted or corrected this within 30 days of receiving a notice from QPS requesting it to do so;

(e) Bdna makes any assignment or novation in breach of clause 22.11 (Assignment and Novation);

(f) a Change in Control of Bdna occurs without QPS's prior written consent, in breach of clause 22.12 (Change in Control);

(g) QPS and Bdna do not enter into the QPS Support Contract by three months after the Commencement Date, where failure to enter into the QPS Support Contract by such date is as a result of an act or omission of Bdna (excluding acts or omissions arising out of a Force Majeure Event);

(h) QPS and Bdna do not enter into the Escrow Agreement by three months after the Commencement Date, where failure to enter into the Escrow Agreement by such date is as a result of an act or omission of Bdna (excluding acts or omissions arising out of a Force Majeure Event); or

(i) Bdna has deliberately or wilfully breached a material term of this Agreement or the QPS Support Contract, or has committed a fraudulent breach or repudiation of this Agreement or the QPS Support Contract.

16.2 A Notice to Show Cause must:

(a) provide details of the relevant breach or other circumstances in clause 16.1; and

(b) require Bdna within the period specified in the notice, such period being at least five Business Days, to show cause, in writing, why QPS should not terminate this Agreement for the breach or other circumstances.

16.3 QPS may terminate this Agreement immediately by notice to Bdna if:

(a) QPS is not satisfied (at its sole discretion) that Bdna has shown cause in writing within the time specified in a Notice to Show Cause why this Agreement should not be terminated; or

(b) Bdna is or becomes Insolvent, subject always to the application of:

(i) sections 415D(1), 434J(1) and 451E of the *Corporations Act 2001* (Cth) (**Ipso Facto Provisions**); or

(ii) any process which under any law with a similar purpose to the Ipso Facto Provisions may give rise to a stay on, or prevention of, the exercise of QPS' termination right under this clause 16.3.

16.4 QPS may terminate this Agreement at any time for convenience, by notice to Bdna of at least three months.

16.5 Bdna may terminate this Agreement immediately by notice to QPS only if:

(a) QPS is in breach of an obligation under this Agreement which prevents Bdna from substantially:

(i) performing its obligations under this Agreement; or

(ii) exercising its Intellectual Property Rights,

and QPS has not rectified that breach within 45 days of receiving notice of the breach from Bdna.

16.6 Termination of this Agreement under clause 16.3 will:

(a) terminate the QPS Support Contract as if terminated by QPS in accordance with clause 21.1 of the QITC General Contract Conditions; and

(b) forfeit QPS's right to any remaining Development Hours (without limiting any right of QPS to any claim for Loss in respect of those Development Hours due to breach by Bdna of this Agreement or the QPS Support Contract).

16.7 Termination of this Agreement under clause 16.4 or 16.5 will:

(a) not affect the QPS Support Contract; or

(b) forfeit QPS's right to any remaining Development Hours.

16.8 Termination of this Agreement for any reason will not entitle Bdna to any Claim against QPS or QH for any Loss or other compensation.

16.9 Expiry of this Agreement at the end of the Term will, unless otherwise agreed between the parties:

(a) terminate the QPS Support Contract, and the parties may negotiate a new support contract with an associated escrow agreement (provided that if QPS or

QH seek to enter into an FR Support Contract with Bdna after expiry of this Agreement, Bdna will not unreasonably withhold its agreement to provide support services for the Bdna FR on QITC (or its successor) terms for fees that are no less favourable than the fees paid by any other purchaser of support services in similar circumstances, including volumes (where fees are volume dependent), timing, terms and conditions; and

(b) forfeit QPS's right to any remaining Development Hours (without limiting any right of QPS to any claim for Loss in respect of those Development Hours due to breach by Bdna of this Agreement or the QPS Support Contract).

16.10 Expiry or termination of this Agreement will not affect the QH Support Contract unless expressly stated in this Agreement or the QH Support Contract.

16.11 Expiry or termination of this Agreement will not affect the accrued rights and remedies of the parties prior to termination.

16.12 For the purposes of clause 16.1(i), material terms include:

(a) 3.1(b);

(b) 3.1(c);

(c) 4.4;

(d) 5.1;

(e) 5.2(d);

(f) 5.2(e);

(g) 5.2(g);

(h) 5.2(h);

(i) 5.3;

(j) 5.4(a);

(k) 6.2;

(l) 7;

(m) 8;

(n) 9;

(o) 13;

(p) 22.11;

(q) 22.12; and

(r) Schedule 2.

17. Trigger Dates

17.1 Trigger Date A

(a) Trigger Date A will occur if this Agreement is terminated by QPS prior to the Trigger Date A Sunset Date in accordance with clause 16.3.

(b) The Trigger Date A Sunset Date is the date on which all of the following conditions are satisfied:

(i) Bdna has released a Commercial Version of the Forensic Register; and

(ii) the Commercial Version has been implemented and used by QPS for a period of 6 months; and

(iii) during the period of use of the Commercial Version by the QPS, if any, Bdna has resolved all Priority 1 and Priority 2 Defects as defined in the QPS Support Contract.

17.2 Trigger Date B

(a) Trigger Date B will occur if QPS:

(i) provides notice to Bdna to the effect that it is exercising its Trigger Date B rights; and

(ii) is entitled to do so under clause 17.2(b).

(b) QPS will only be entitled to exercise its Trigger Date B rights if:

(i) this Agreement is terminated by QPS in accordance with clause 16.3, where the relevant breach or other circumstances specified in the Notice to Show Cause include one or more of those specified in paragraphs 16.1(d) or 16.1(i); or

(ii) Bdna is Insolvent.

18. Security and Access

18.1 Each party must ensure that its Personnel, when using or attending at the other party's premises or facilities:

(a) comply with all reasonable directions and procedures of the other party including those relating to security and to occupational health and safety which are in effect at those premises or in regard to those facilities;

(b) avoid unnecessary interference with the passage of people and vehicles; and

(c) do not create nuisance or unreasonable noise and disturbance.

18.2 Each party must where reasonable provide access to its premises to Personnel of the other party where the Personnel are attending to engage in business directly related to this Agreement.

19. Contacts and escalation procedure

Without limiting the parties' rights and remedies under this Agreement, either party may raise and escalate issues under this Agreement in accordance with the following table (subject to variation of the representatives from time to time by notice to the other party). A party may escalate an issue to the next level where a satisfactory response has not been provided or a resolution has not been reached within the specified timeframe.

Escalation level	Representatives	Timeframe for Resolution
1	QPS: Project Officer, Forensic Services Group Bdna: Service Delivery Manager	5 Business days
2	QPS: Inspector, Forensic Services Group Bdna: Product Director (Forensics)	10 Business days
3	QPS: Superintendent, Forensic Services Group Bdna: Partner	20 Business days

20. Dispute Resolution

20.1 A party may give notice (**Dispute Notice**) to the other party if a dispute or difference arises between the parties relating to this Agreement or concerning the performance or non-performance by a party of its obligations under this Agreement, including the giving of a notice under clause 16 (other than a notice that effects immediate termination).

20.2 The parties agree to work towards settling any dispute which is the subject of a Dispute Notice as follows:

(a) by negotiation at first instance (to be carried out in good faith);

(b) if an acceptable resolution cannot be achieved within 10 Business Days from delivery of the Dispute Notice (or such longer period if agreed by the parties), by attending mediation; and

(c) the parties will share the cost of the mediator and venue equally

20.3 The mediator and the mediation rules must be:

(a) mutually agreed upon by the parties; or

(b) in the absence of agreement within five Business Days from the end of the period referred to in clause 20.2(b):

(i) a mediator determined by a person appointed by the Chairperson of the Queensland Chapter of the Resolution Institute (ACN 008 651 232, Level 2, 13-15 Bridge Street, Sydney NSW 2000; telephone: [redacted], email: [redacted] or the Chairperson's designated representative; and

(ii) the Resolution Institute Mediation Rules.

20.4 Notwithstanding the existence of a dispute, each party will continue to perform its obligations and may exercise its rights under this Agreement where practicable.

20.5 It is a condition precedent to the right of either party to commence litigation other than for interlocutory relief that it has first offered to submit the dispute to mediation.

21. Force Majeure Events

21.1 A party will not be liable for any delay in or for any failure to perform its obligations under this Agreement to the extent that it is able to demonstrate that such delay or failure has been caused by a Force Majeure Event.

21.2 A party prevented from performing any of its obligations under this Agreement by a Force Majeure Event, must:

(a) notify the other party, as soon as it is affected by the Force Majeure Event, of:

(i) the details of the Force Majeure Event;

(ii) anticipated duration of any delay arising from the Force Majeure Event;

(iii) obligations it is prevented and/or likely to be prevented from performing under the Contract; and

(iv) its plans to work-around or minimise the impact of the Force Majeure Event; and

(b) make all reasonable efforts to minimise the effects of the Force Majeure Event.

21.3 Any provision of this Agreement (other than this clause 21) that excludes a delay or other event or circumstances where it is caused by a Force Majeure Event applies only:

(a) if the affected party complies with clause 21.2;

(b) for the period commencing on the date the affected party provides a notice in accordance with clause 21.2(a); and

(c) for a maximum period of 30 days or such other period agreed in writing between the parties.

22. General

22.1 Notices

(a) Any notice which may be given to or served on a party under this Agreement must be sent or delivered to the address specified for that party in Schedule 1 (as varied from time to time by notice to the other party).

(b) Notwithstanding clause 22.1(a), if Bdna is a company then QPS may serve a notice at any time on Bdna's registered office.

(c) A notice sent to a party will be deemed to be given:

(i) by express post, within one Business Day after the date of posting;

(ii) by any other post, within six Business Days after the date of posting;

(iii) if delivered by hand during a Business Day, on the date of delivery; and

(iv) if emailed, on the date recorded on the device from which the party sent the email, unless the sending party receives an automated message that the email has not been delivered,

except that a delivery by hand or email received after 5.00 pm (local time) on a Business Day at the address of the recipient will be deemed to be given on the next Business Day.

(d) Notices under clause 16 will only be deemed to be given by posting or delivered by hand.

(e) For the purposes of the *Electronic Transactions (Queensland) Act 2001* (Qld), each party consents to the giving of notices by email, subject to clause 22.1(d).

22.2 Waiver

Rights, remedies or powers under this Agreement can only be waived in writing signed by an authorised delegate of a party. Neither party waives a right, remedy or power if it delays in exercising, fails to exercise or only partially exercises that right, remedy or power, or has on a previous occasion waived that right, remedy or power in relation to a particular obligation or breach.

22.3 Severance

If a provision or part of this Agreement is wholly or partly void, illegal or unenforceable in any relevant jurisdiction that provision or part must, to that extent, be treated as deleted from this Agreement for the purposes of that jurisdiction. This does not affect the validity or enforceability of the remainder of the provision or part or any other provision or part of this Agreement.

22.4 Governing Law and Jurisdiction

This Agreement is governed by the laws in force in Queensland, Australia, and the parties submit to the non-exclusive jurisdiction of the courts exercising jurisdiction in Queensland and courts of appeal from them in respect of any proceedings arising out of or in connection with this Agreement.

22.5 Further Assurances

Each party must, at its own expense, do all things and execute all further documents reasonably necessary to give full effect to this Agreement and the transactions contemplated by it.

22.6 Relationship

QPS, QH and Bdna are not and are not to be taken to be in a partnership, joint venture, employment, agency or fiduciary relationship. Nothing in this Agreement gives Bdna authority to bind QPS or QH in any way.

22.7 Remedies Cumulative

Except as expressly provided in this Agreement and permitted by law, the rights, powers and remedies of a party provided in this Agreement are cumulative with and not exclusive of the rights, powers or remedies provided by law or equity independently of this Agreement.

22.8 Entire Agreement

This Agreement constitutes the entire agreement between the parties for its subject matter. Any prior arrangements, agreements, warranties, representations or undertakings are superseded.

22.9 Costs and Expenses

Each party must pay its own costs (including legal costs) and expenses in connection with the negotiation, preparation, execution and stamping of this Agreement.

22.10 Variation

This Agreement may only be varied by agreement between the parties signed by their authorised delegates.

22.11 Assignment and Novation

(a) Bdna must not assign or novate any of its rights or obligations in connection with this Agreement, without the consent of QPS.

(b) QPS must not assign or novate any of its rights or obligations in connection with this Agreement without the consent of Bdna, except in connection with a Machinery of Government Change.

(c) If a party wishes to do any of the things referred to in clause 22.11(a) or 22.11(b), all parties and the recipient of the rights or obligations will execute a deed of novation or any other document reasonably required to effect the novation.

22.12 Change in Control

(a) In this Agreement:

Change in Control means, in relation to Bdna, the occurrence of an event or series of events that result in a person or persons:

(i) that did not have Control of Bdna prior to the event or series of events, having Control of Bdna following that event or series of events; or

(ii) that had Control of Bdna prior to the event or series of events ceasing to have Control of Bdna.

Control in relation to Bdna means the power to determine:

(i) the outcome of decisions about the financial and operating policies of Bdna; or

(ii) the membership of the majority of the board of directors (or members of a governing body having functions similar to a board of directors) of Bdna,

whether or not the power has statutory, legal or equitable force or is based on statutory, legal or equitable rights, and whether or not it arises by means of trusts, agreements, arrangements, understandings, practices, the ownership of any interest in shares or equity interests of Bdna (as applicable) or otherwise.

(b) Bdna must provide reasonable prior notice to QPS of at least 30 days of a potential Change in Control of Bdna, seeking the prior written consent of QPS to that Change in Control. A change in Control is not permitted without the prior written consent of QPS to that Change in Control (which consent must not be unreasonably withheld or delayed).

22.13 Counterparts and Execution

(a) This Agreement may be executed in two or more identical copy counterparts, each of which together will be deemed an original, but all of which together will constitute one and the same instrument.

(b) In the event that the signature of a party executing this Agreement is delivered by email delivery of a scanned '.pdf' format data file or equivalent of the entire Agreement to the other party or its legal representative, the signature will create

a valid and binding obligation of the party with the same force and effect as if the signature were an original.

22.14 **Survival of Clauses**

(a) Clauses 1, 3, 5.2 and 5.3 (unless the Agreement states that Development Hours are forfeited), 5.4(b), 5.4(c), 6.2, 9.2, 10, 13, 14, 15.3, 16.6 to 16.11, 20, and 22 (excluding clauses 22.11 and 22.12) survive the termination or expiration of this Agreement for any reason.

(b) The indemnity contained in clause 14.3 is a continuing obligation, independent from the other obligations of the parties and survives any termination or expiration of this Agreement.

(c) The list of clauses expressed to survive termination or expiration in this clause 22.14:

(i) is not an exhaustive list of the rights and obligations that are intended to survive termination or expiration; and

(ii) does not exclude any rights, remedies and obligations arising by operation of law.

Schedule 1 Details Schedule

1. QPS Details

Name:	State of Queensland acting through the Queensland Police Service
ABN:	29 409 225 509
Address:	Queensland Police Service Headquarters, 200 Roma St Brisbane
Contact name and position, unit/branch/division name:	Senior Sergeant, Project Officer, Forensic Services Group
Telephone:	[redacted]
Email:	[redacted]

2. Bdna Details

Name:	Bdnatec Pty Ltd
ABN:	[redacted]
Address:	
Contact name and position, organisational unit/entity name:	Marty Wauchope Partner
Telephone:	[redacted]
Email:	[redacted]

3. Effective Date (clause 3)

Commencement Date.

4. Insurance (clause 15)

4.1	A public liability insurance policy for not less than 10 million dollars ($10,000,000.00) arising from any one event in respect of accidental death of, or accidental bodily injury to persons, or accidental damage to property.
4.2	Workers' compensation insurance as required by law.
4.3	Professional indemnity insurance for the amount of not less than 10 million dollars ($10,000,000.00) in respect of each claim, and which must be maintained by Bdna for a continuous period of four years after the termination of the Agreement.

5. Existing Licensees (clause 12)

Western Australia Police Force
South Australian Police
Tasmania Dept Police Fire and Emergency Management / Tasmania Police
Australian Federal Police
Department of Defence

Schedule 2 PPSA Provisions

1. Definitions and Interpretation

In this Schedule 2:

Material Adverse Effect	means a material adverse effect: (a) on Bdna's ability to perform any of its obligations under any Transaction Document; (b) on the validity, legality or enforceability of all or any part of a Transaction Document or the Powers of QPS under a Transaction Document or on the perfection or intended priority of any Security; (c) on the assets, business, operations, condition (financial or otherwise) or prospects of Bdna; or (d) on the rights and remedies of QPS under the Transaction Documents.
Permitted Dealing	means any dealing by Bdna with the Secured Property which is permitted under this Agreement, including Commercialisation and the issue of New Licences, subject always to the terms of this Agreement (including but not limited to clauses 2.4 and 2.5 of this Schedule 2).
Power	means any right, power, authority, discretion or remedy conferred on QPS, or a receiver or manager appointed by it, under this Agreement or any applicable law.
PPSA	means the *Personal Property Securities Act 2009* (Cth).
PPSA Law	means: (a) PPSA; (b) any regulation made under or pursuant to PPSA; and (c) any legislation or regulation, or any amendment to any legislation or regulation, at any time made to implement, or as contemplated by or as a consequence of, PPSA or any regulation made under or pursuant to PPSA.
PPSR	means the Personal Property Security Register established under the PPSA.
Secured Obligations	means the obligations of Bdna arising under or in connection with this Agreement, including but not limited to its obligations arising under the Transaction Documents.

Secured Property	means, in respect of Bdna, all of its rights title and interest: (a) in the Forensic Register, including its Intellectual Property Rights in the Forensic Register; (b) in the Escrow Materials; and (c) in, under and in connection with this Agreement and any Transaction Document (but excluding interests in personal property to which PPSA does not apply).
Security	means the Security Interest arising under clause 2.1 of this Schedule 2 and any other Security Interest which may be granted by Bdna to QPS from time to time.
Security Interest	means: (a) an interest or power reserved in or created or otherwise arising in or over an interest in any asset whether under a bill of sale, mortgage, charge, lien, pledge, other security interest or preferential arrangement (including retention of title), trust or power or otherwise by way of, or having similar commercial effect to, security for the payment of a debt, any other monetary obligation or the performance of any other obligation; (b) a 'security interest' as defined in PPSA; or (c) any agreement to grant or create anything referred to in paragraphs (a) or (b) of this definition and any other thing which gives a creditor priority to any other creditor with respect to any asset or an interest in any asset.
Transaction Document	means each of the following: (a) this Agreement; (b) the QPS Support Contract; (c) any QH Support Contract; (d) the Escrow Agreement; (e) any other document or agreement agreed to be a Transaction Document by QPS and Bdna, now or at any time in the future; and (f) any document or agreement entered into or given under any of the above or for the purpose of amending, supplementing or novating any of the above.

2. Security

2.1 Security

Bdna grants to QPS as security for the due and punctual performance of the Secured Obligations a PPSA Security Interest (by way of charge) in the Secured Property.

2.2 Priority

The parties intend that the Security take priority over all other Security Interests of Bdna other than any Security Interest mandatorily preferred by law.

2.3 Attachment and Perfection of Security

(a) Bdna must promptly do all things required by QPS (including by providing information, obtaining or providing consents, supplying information or executing and producing any document):

(i) to ensure that the Security attaches to the Secured Property that is intended to be covered by the Security;

(ii) to ensure that the Security is enforceable and otherwise effective and has the priority it is intended to have under this Agreement;

(iii) to ensure that the PPSA Security Interest granted by this Agreement is, and continues to be, perfected in accordance with PPSA by one or more of registration, possession or control;

(iv) to enable QPS to prepare and register any financing statement or financing change statement or to give any notice in connection with the Security;

(v) to enable QPS to exercise any of its Powers in respect of the Security arising under this Agreement or at law (including to take control of any Secured Property), or perform any of its obligations under PPSA Law or any other applicable legislation.

(b) QPS may, at the cost and expense of QPS, perfect, register or file the Security on the PPSR, for any class or classes of collateral that QPS thinks fit.

(c) Bdna must ensure that the Security and any variation of any of them is registered and filed in all jurisdictions outside Australia and on all registers in, or on, which it must be, or which QPS reasonably requests it to be, registered or filed to ensure the enforceability, validity and priority of the Security and any variation against all persons and to be effective as a security with the priority intended by this Agreement.

(d) Bdna must do all things necessary to ensure that it perfects by registration (and if required by QPS, by control or possession) all PPSA Security Interests granted to, or held by, Bdna in all or any part of the Secured Property and, if it is

granted, or holds, a purchase money security interest within the time necessary to ensure it obtains the priority afforded to a purchase money security interest under section 62 of the PPSA.

2.4 Negative pledge and disposal of assets

(a) Bdna must not create or allow to exist or agree to any Security Interest over any of the Secured Property.

(b) Bdna must not sell, assign, transfer, convey, lease, license or otherwise dispose of, or part with possession of, or make any bailment over, grant any option over or create or permit to be created any other interest in any of the Secured Property, other than (subject to clause 2.4(c) below) a Permitted Dealing made in circumstances where that Permitted Dealing takes effect as:

(i) the grant of a licence to customers, contractors or end users of the Forensic Register and the Intellectual Property Rights in the Forensic Register in the ordinary course of Commercialisation; or

(ii) the grant of New Licences.

(c) For the avoidance of doubt, Bdna must not, during the Term and without the consent of QPS, in a manner which is inconsistent with Bdna's ability to perform this Agreement or which has a Material Adverse Effect:

(i) sell, assign, transfer, convey, lease, license or otherwise dispose of, or part with possession of, or make any bailment over, grant any option over or create any other interest in the Forensic Register or any Intellectual Property Rights in the Forensic Register; or

(ii) grant any rights to any third party to control the Forensic Register or the Intellectual Property Rights in the Forensic Register, or to undertake the Commercialisation of the Forensic Register or the Intellectual Property Rights in the Forensic Register,

including by granting any exclusive licence rights that would have the effect of limiting QPS's exercise of any Intellectual Property Rights in the Forensic Register if it were assigned to QPS under clause 3.5 of the Agreement.

(d) If, by mandatory operation of law, this clause 2.4 may not prevent Bdna creating a Security Interest:

(i) this clause 2.4 does not prevent Bdna creating that Security Interest;

(ii) before that Security Interest is created Bdna must ensure that QPS receives the benefit of a deed of priority granting first ranking priority to each Security Interest granted or arising in favour of it in a form and of substance required by QPS; and

(iii) until that deed of priority is executed and delivered to QPS, QPS is not required to perform any of its obligations under or in connection with this Agreement.

2.5 Undertakings regarding Secured Property

Bdna must:

(a) **maintenance of the Secured Property**:

(i) maintain and protect its Secured Property;

(ii) keep its Secured Property in a good state of repair and in good working order and condition allowing for fair wear and tear;

(iii) remedy every defect in its title to any part of its Secured Property;

(iv) take or defend all legal proceedings to protect or recover any of its Secured Property;

(v) pay on time all rates, taxes and other amounts for which it is liable as owner of the Secured Property; and

(vi) keep its Secured Property valid and subsisting and free from liability to forfeiture, cancellation, avoidance or loss;

(b) **no partnership or joint venture**: not enter into any partnership or joint venture (**Arrangement**) with any other person in relation to its Secured Property without QPS' prior written consent (which must not be unreasonably withheld or delayed but which may be conditional), except:

(i) as part of a Permitted Dealing; or

(ii) in respect of any business venture which is entirely separate to, and in no way connected with the Secured Property (including but not limited to any rights arising under or in connection with the Secured Property) or its Commercialisation in circumstances where the entry into that Arrangement does not have any adverse impact on the Secured Property or QPS' rights, title and interest in the Secured Property under this Agreement or any other Transaction Document

2.6 Personal Property Securities Act

[redacted]

2.3(b)

(a) Subject to clause **~~Error! Reference source not found.~~** everything Bdna is required to do under this clause 2.6Schedule 2 is at Bdna's expense. Bdna agrees to pay or reimburse the costs and expenses of QPS in connection with anything Bdna is required to do under this Schedule 2.

(b) QPS need not give any notice under PPSA (including a notice of verification statement) unless the notice is required by PPSA and cannot be excluded.

(c) A term or expression which is used in this clause 2.6 and which is defined in PPSA has the same meaning in this clause 2.6 as is given to it in PPSA.

2.7 Discharge of the Security

At the written request of Bdna after the expiry or termination of this Agreement, other than where QPS is entitled to exercise its Trigger Date B rights, QPS must:

(a) within 15 Business Days of receiving the written request, discharge the Security by delivering a PPSR release and undertaking in market standard form; and

(b) within 10 Business Days of the discharge of Security referred to in paragraph 2.7(a), do all things necessary (including by executing, producing, and registering any document) to effect the removal of the Security Interest from all registers in all jurisdictions on which it has been registered, including registering a financing change statement on the PPSR.

Signing page

Executed as an agreement on the dates below:

Signed for and on behalf of the **State of Queensland** acting through the **Queensland Police Service** by:

KATARINA CARROLL
Name of authorised representative (print)

[redacted]
Signature of authorised representative

Commissioner
Position title (print)

a duly authorised person, in the presence of:

[redacted]

Rob Fleischer
Full name of witness (print)

28.09.20.
Date (print)

Executed as an agreement in accordance with section 127 of the *Corporations Act 2001* (Cth) by
BdnaTec Pty Ltd ACN 149 881 676

[redacted]
Signature of Director

[redacted]
Signature of Director/~~Company Secretary~~

MARTIN WAUCHOPE
Full name of Director (print)

Ryan Sheppard
Full name of Director/~~Company Secretary~~ (print)

1/10/2020
Date

1/10/2020
Date

Annexure 1 - Draft Escrow Agreement

[Commences overleaf]

Queensland Government

Annexure 2 – Escrow Agreement (QPS96100B)

Forensic Register Services Contract (QPS96100)

AND

Forensic Register IP Agreement (QPS96100)

The State of Queensland acting through the Queensland Police Service

Bdnatec Pty Ltd (ABN 51 149 881 676)

Assurex Escrow Pty. Limited (ABN 64 008 611 578)

General information

No.	Topic	Details
1	**Customer**	Name: The State of Queensland acting through the Queensland Police Service ABN or ACN: 29 409 225 509
	Delivery of notices to the Customer	Physical address: Queensland Police Headquarters, 200 Roma Street Email address: [redacted]
2	**Supplier**	Name: Bdnatec Pty Ltd ABN or ACN: 51 149 881 676
	Delivery of notices to the Supplier	Physical address: Level 9, 231 North Quay, Brisbane, Qld, 4000 Postal address: Level 9, 231 North Quay, Brisbane, Qld, 4000 Email address: [redacted]
3	**Escrow Agent**	Name: Assurex Escrow Pty Ltd ABN: 64 008 611 578; ACN 008 611 578 Street address: Suite 93, Level 5, 330 Wattle Street Ultimo NSW 2007 Postal address: PO Box 8 Broadway NSW 2007 Email: [redacted]
	Delivery of notices to the Escrow Agent	As above
4	**Contracts**	Forensic Register Services Contract (**Support Contract**) Contract Number: [redacted] Date: XXXX Forensic Register IP Agreement (**IP Agreement**) Contract Number: [redacted] Date: XXXX
5	**Escrow Fee**	<<insert>>
6	**Escrow Materials**	means: (a) the source code and/or object code of the Bdna FR and all other relevant software programs owned by Bdna,

No.	Topic	Details
		documentation, information, drawings, release notes, and plans; and (b) a list of any relevant third party software programs, necessary to enable a competent person skilled in the use of the Bdna FR (and any necessary development tools used to create Bdna FR) to keep the Bdna FR in good order and repair.

1. Background

1.1. The Customer and the Supplier are parties to the Contracts.

1.2. The Customer and the Supplier have agreed to appoint an escrow agent and the Escrow Agent has agreed to act as an Escrow Agent and hold the Escrow Materials on the following terms and conditions.

2. Definitions and interpretation

2.1. Definitions

Business Day means between 9.00am and 5.00pm on a day other than a Saturday, Sunday or public holiday at the Customer's address.

Bdna FR has the meaning given to it in the IP Agreement.

Contracts means the agreements between the Customer and the Supplier described in the 'General information' details above.

Customer is specified in the 'General information' details above.

Escrow Agent is specified in the 'General information' details above.

Escrow Agreement means this document titled *'Schedule 5 – Escrow Agreement'*.

Escrow Fee means the fee specified in the 'General information' details above.

Escrow Materials is specified in the 'General information' details above.

Final Release Notice has the meaning given in clause 9.3.

General Contract Conditions means the document titled *'General Contract Conditions – ICT Products and Services'* forming part of the Support Contract.

Harmful Code means any computer program or virus or other code that is harmful, destructive, disabling or which assists in or enables theft, alteration, denial of service, unauthorised access to or disclosure, destruction or corruption of information or data.

A person or entity is **Insolvent** if:

(a) it is (or states that it is) an insolvent under administration or insolvent (each as defined in the *Corporations Act 2001* (Cth));

(b) it is in liquidation, in provisional liquidation, under administration or wound up or has had a controller appointed to its property

(c) it is subject to any arrangement, assignment, moratorium or composition, protected from creditors under any statute or dissolved (in each case, other than to carry out a

reconstruction or amalgamation while solvent on terms approved by the other parties to this agreement);

(d) an application or order has been made (and in the case of an application, it is not stayed, withdrawn or dismissed within 30 days), resolution passed, proposal put forward, or any other action taken, in each case in connection with that person, which is preparatory to or could result in any of (a), (b) or (c) above;

(e) it is taken (under section 459F(1) of the *Corporations Act 2001* (Cth)) to have failed to comply with a statutory demand;

(f) it is the subject of an event described in section 459C(2)(b) or section 585 of the *Corporations Act 2001* (Cth) (or it makes a statement from which another party to this agreement reasonably deduces it is so subject);

(g) it is otherwise unable to pay its debts when they fall due; or

something having a substantially similar effect to (a) to (g) happens in connection with that person or entity under the laws of any jurisdiction.

Supplier is specified in the 'General information' details above.

Trigger Event has the meaning given in clause 9.2.

2.2. Interpretation

Unless it is expressly stated that a different rule of interpretation will apply:

(a) (**agreement**) a reference to an agreement includes any variation or replacement of the agreement;

(b) (**Business Day**) if the due date for any obligation is not a Business Day, the due date will be the next Business Day;

(c) (**currency**) all currency amounts are in Australian dollars;

(d) (**headings**) headings are provided for convenience and do not affect the interpretation of this Escrow Agreement;

(e) (**includes**) "include", "includes" and "including" must be read as if followed by the words "without limitation";

(f) (**corresponding meaning**) if a word or phrase is defined its other grammatical forms have corresponding meanings;

(g) (**joint and several**) agreements, representations and warranties made by two or more people will bind them jointly and severally;

(h) (**law**) a reference to any legislation includes any consolidation, amendment, re-enactment or replacement of legislation;

(i) (**person**) a person includes the person's executors, administrators, novatees and assignees; and

(j) (**construction**) no rule of construction will apply to a provision of a document to the disadvantage of a party merely because that party drafted the provision or would otherwise benefit from it.

3. Duration

Subject to the Escrow Fees being paid in accordance with this Escrow Agreement, this Escrow Agreement is in force until the Escrow Materials are released in accordance with this Escrow Agreement or the Escrow Agreement is otherwise terminated in accordance with its terms.

4. Appointment of Escrow Agent

The Escrow Agent is hereby appointed jointly by the Customer and the Supplier to hold the Escrow Materials and, if the conditions for release under clause 9 of this Escrow Agreement are met, to release the Escrow Materials in accordance with this Escrow Agreement.

5. Supplier's obligations

5.1. The Supplier must deliver to, and deposit with, the Escrow Agent one copy of the Escrow Materials within 7 days of the date of this Escrow Agreement (or such other time as otherwise agreed by the Customer and Supplier).

5.2. The Supplier must:

(a) maintain, amend, modify, update and enhance the Escrow Materials at all times; and

(b) ensure that the Escrow Materials deposited with the Escrow Agent are kept fully up-to-date and accurately reflect the Bdna FR all modifications, amendments, updates and new releases made to, or in respect of, the Bdna FR.

5.3. The Supplier warrants to the Customer that the Escrow Materials are, to the best of the knowledge of the Supplier, free from any Harmful Code which would prevent the Bdna FR from performing its desired function or which would prevent or impede a thorough and effective verification thereof.

6. Escrow Agent's obligations

6.1. The Escrow Agent must accept custody of the Escrow Materials on the date of delivery in accordance with clause 5 of this Escrow Agreement and, subject to the terms and conditions of this Escrow Agreement, must hold the Escrow Materials on behalf of the Customer and the Supplier.

6.2. The Escrow Agent must take all necessary steps to ensure the preservation, care, maintenance, safe custody and security of the Escrow Materials while in the possession, custody or control of the Escrow Agent, including storage in a secure receptacle and in an atmosphere which does not harm the Escrow Materials.

6.3. If the Escrow Materials are lost, stolen, destroyed or damaged while in the possession, custody or control of the Escrow Agent, the Escrow Agent must immediately notify the Customer and the Supplier.

6.4. Unless the Escrow Agreement is terminated in accordance with clause 10.2(b) of this Escrow Agreement, the Supplier must, upon receipt of a notice from the Escrow Agent under clause 6.3 of this Escrow Agreement, promptly deposit a replacement copy of the Escrow Materials with the Escrow Agent.

6.5. Upon receipt of the replacement copy of the Escrow Materials, the Escrow Agent must promptly advise the Customer and Supplier in writing of its receipt of the replacement copy of the Escrow Materials.

6.6. Without limitation to any other rights the Supplier and/or the Customer may have under this Escrow Agreement or at law, where the loss, damage or destruction of the Escrow Materials under clause 6.3 is caused by the negligent, wilful or unlawful act or omission of the Escrow Agent, the Escrow Agent must, at its own expense, reimburse the Supplier for the reasonable cost of replacing the Escrow Materials.

6.7. The Escrow Agent is not obliged to determine the nature, completeness or accuracy of the Escrow Materials lodged with it.

7. Escrow Fee and expenses

7.1. The Customer must pay the Escrow Fee within 30 days of receipt of a correctly rendered tax invoice from the Escrow Agent.

7.2. All expenses and disbursements incurred by the Escrow Agent in connection with this Escrow Agreement will be borne wholly and completely by the Escrow Agent.

7.3. All expenses and disbursements incurred by the Supplier in connection with this Escrow Agreement will be borne wholly and completely by the Supplier.

8. Testing and verification

8.1. The Customer may, in the presence of and under the supervision of the Supplier, analyse and conduct tests in relation to the Escrow Materials to verify that the Supplier has complied with its obligations under this Escrow Agreement.

8.2. The Customer may engage an independent assessor to undertake analysis and tests of the Escrow Materials for verification purposes, on its behalf.

8.3. The Escrow Agent must release the Escrow Materials to the independent party upon presentation of a release form signed by the Customer and the Supplier specifying the material to be released and identifying the person to whom that material may be released.

8.4. The Escrow Materials released pursuant to clause 8.3 of this Escrow Agreement must be returned to the Escrow Agent or its employees or agents and the Customer must ensure that the confidentiality of the Escrow Materials so released is preserved and that the Escrow Materials are not used for any purpose other than verifying that the Supplier has complied with its obligations under this Escrow Agreement.

8.5. All costs that Escrow Agent incurs in assisting the assessment under this clause 8 will be borne by the Customer, and must be paid within 30 days of receipt of a correctly rendered tax invoice from the Escrow Agent.

9. Release of the Escrow Material

9.1. The Escrow Agent must not release, or allow access to, the Escrow Materials except in accordance with the provisions of this Escrow Agreement.

9.2. If:

(a) the Supplier is Insolvent;

(b) the Supplier has ceased for any reason to maintain or support the Bdna FR for all customers. For clarity, a temporary cessation by reason of an Unexpected Event under the Support Contract, or a Force Majeure Event under the IP Agreement, is not a Trigger Event;

(c) either one (or both) of the Contracts has been lawfully terminated by the Customer for the Supplier's breach or other default;

(d) this Escrow Agreement is terminated (other than in accordance with clauses 10.3 or 10.5 of this Escrow Agreement) and, subject to clause 9.3, a new Escrow Agreement is not entered into within 30 days in accordance with clause 10.4 of this Escrow Agreement;

(e) Bdna makes any assignment or novation in breach of clause 21.11 (Assignment and Novation) of the IP Agreement; or

(f) a Change in Control of Bdna occurs without QPS's prior written consent, in breach of clause 21.12 (Change in Control) of the IP Agreement,

(**Trigger Event**) and the Customer wishes the Escrow Agent to release the Escrow Materials to it, the Customer must within 20 Business Days of the Customer becoming aware of the Trigger Event provide written notice to both the Escrow Agent and the Supplier stating which Trigger Event has occurred.

9.3. For clarity, it is not a Trigger Event under clause 9.2(d) where:

(a) the alternative escrow agent requires terms and conditions which differ to those of this Escrow Agreement; or

(b) failure to enter into the new Escrow Agreement within 30 days is as a result of an act or omission outside of Bdna's reasonable control, provided that Bdna continues to use its best endeavours to negotiate, agree and enter into the new Escrow Agreement (to the extent possible and unless released by QPS).

9.4. If the Supplier does not, within 20 Business Days of receiving the notice under clause 9.2 of this Escrow Agreement, rectify the Trigger Event or provide another remedy that is satisfactory to the Customer, the Customer may provide the Escrow Agent with a further written notice confirming that the Supplier has not rectified the Trigger Event in the required time or provided another remedy that is satisfactory to the Customer, and require the Escrow Agent to immediately release the Escrow Materials to the Customer (**Final Release Notice**). The Escrow Agent must release the Escrow Materials to the Customer promptly after receiving the Final Release Notice.

9.5. Except where the Customer has provided a Final Release Notice, where this Escrow Agreement has been terminated under clauses 10.3 or 10.5, or where the Customer has agreed to the release of the Escrow Materials, the Escrow Agent must, upon written request from the Supplier, release the Escrow Materials to the Supplier.

9.6. The Escrow Agent is not obliged to verify or otherwise test the validity of any notice received, or its contents.

9.7. If the Escrow Materials are released to the Customer under this Escrow Agreement, the Customer:

(a) is granted a perpetual, non-exclusive, royalty-free limited licence to:

(i) use and exercise the Intellectual Property Rights in the Escrow Materials:

(A) to the same extent as has been granted to the Customer under the Contracts in relation to the Bdna FR; and

(B) to modify and develop, and to correct any defects or issues in, the Bdna FR in accordance with the rights granted in the IP Agreement; and

(ii) to the same extent as has been granted to the Customer under the IP Agreement, grant a sub-licence of its rights under clause 9.7(a)(i) to any contractor that is providing outsource or support services to the Customer that includes the use of the Bdna FR;

(b) subject to 9.7(c), must use the Escrow Materials subject to all the other terms of the Contracts (as applicable); and

(c) must not use the Escrow Materials for any purpose other than that referred to in clause 9.6(a).

9.8. The obligations under this clause 9 survive the termination of this Escrow Agreement under clause 9.2(d).

10. Termination

10.1. The Escrow Agent may, by giving 3 months' prior written notice to the Customer and the Supplier, terminate this Escrow Agreement subject to a pro-rata refund of any advance payment of the Escrow Fee.

10.2. The Customer and the Supplier may jointly terminate this Escrow Agreement immediately if the Escrow Agent:

(a) is Insolvent; or

(b) is in breach of any obligation under this Escrow Agreement such that there is a substantial failure by the Escrow Agent to perform or observe this Escrow Agreement.

10.3. This Escrow Agreement is terminated as if by mutual agreement by the Customer and Supplier on the date on which both the IP Agreement and the Support Contract have expired, unless both the IP Agreement and the Support Contract are terminated earlier, in which case the Escrow Agreement will expire six months after the last termination to occur.

10.4. If this Escrow Agreement is terminated in accordance with clauses 10.1 or 10.2 while either Contract remains in force, the Customer and the Supplier must enter into a new Escrow Agreement on the same terms and conditions as are set out in this Escrow Agreement, with an alternative escrow agent who is acceptable to both the Customer and the Supplier.

10.5. The Customer and the Supplier may, upon giving 30 days' prior written notice to the Escrow Agent, jointly terminate this Escrow Agreement, however no refund of advance payment of the Escrow Fee will be payable.

11. Confidentiality

11.1. The Escrow Agent must not, except as permitted by this Escrow Agreement, make public or disclose to any person any information about this Escrow Agreement or the Escrow Materials.

11.2. The Escrow Agent must not reproduce, or cause to have reproduced, a copy of the Escrow Materials or any part thereof, except as may be necessary to electronically store (and maintain a backup) of the Escrow Material.

11.3. The obligations under this clause 11 survive the termination of this Escrow Agreement.

12. Compliance with laws

The Escrow Agent shall in carrying out this Escrow Agreement comply with the provisions of any relevant statutes, regulations, by-laws and the requirements of any Commonwealth, State or local authority.

13. Resolution of disputes

13.1. If any dispute arises concerning this Escrow Agreement, it must be resolved according to this clause 13 (other than where urgent interlocutory relief is required).

13.2. Either party may give the other a notice in writing (**dispute notice**) setting out the details of the dispute. Within 5 Business Days after the date on which a party gives the other party a dispute notice (**dispute notice date**), representatives of the parties must meet and use reasonable endeavours to resolve the dispute.

13.3. If the dispute is not resolved under clause 13.2, senior management representatives of the parties must, within 10 Business Days after the dispute notice date, meet and use reasonable endeavours to resolve the dispute.

13.4. If the dispute is not resolved under clause 13.3 within 30 Business Days after the dispute notice date (or such other time as agreed between the parties), the dispute must be referred to mediation according to clause 13.5.

13.5. Where the dispute is referred to mediation, the parties:

(a) will conduct the mediation in Brisbane;

(b) will jointly appoint the mediator, or if the parties cannot agree on the mediator within 5 Business Days of referral to mediation, the Chairperson of the Queensland Chapter of the Resolution Institute will determine the mediator;

(c) may be legally represented at the mediation;

(d) will each bear their own costs concerning the mediation, and will bear the costs of the mediation venue and the mediator equally; and

(e) will continue to perform their obligations under the Escrow Agreement notwithstanding the existence of a dispute.

14. Governing law

14.1. The Escrow Agreement is governed by and is to be construed in accordance with the laws applicable in Queensland.

14.2. Each party irrevocably and unconditionally submits to the exclusive jurisdiction of the courts of Queensland.

15. General

15.1. The Escrow Agreement may only be varied by written agreement between the parties signed by authorised representatives of the parties.

15.2. Clauses and rights in the Escrow Agreement can only be waived in writing signed by the waiving party. Failure or delay of a party in exercising a right under the Escrow Agreement does not waive the party's rights. A waiver will only waive the particular rights in the particular circumstances and will not waive any other rights, or the same rights in other circumstances.

15.3. Neither the Supplier or the Escrow Agent may assign, transfer or novate any of its rights or obligations under the Escrow Agreement without the Customer's prior written consent.

15.4. If any part of the Escrow Agreement is invalid, unlawful or unenforceable, the invalid, unlawful or unenforceable part of the Escrow Agreement (and any parts of the Escrow Agreement which are dependent on those parts) will not apply but the other parts of the Escrow Agreement will not be affected.

15.5. Any notice or other form of communication ("**notice**") which may be given to or served on either the Customer, Supplier or Escrow Agent under this Escrow Agreement must be in writing and must be sent by prepaid postage, delivered by hand or emailed to the addresses specified in the 'General information' details above.

15.6. A notice will be deemed to be given:

(a) if posted:

(i) within Australia to an Australian postal address, 5 Business Days after the date of posting; or

(ii) outside of Australia to an Australian postal address or within Australia to an address outside of Australia, 10 Business Days after posting;

(b) if delivered by hand during a Business Day – on the date of delivery;

(c) if emailed – subject to clause 15.7 below, on the date recorded on the device from which the party sent the email, unless the sending party receives an automated message that the email has not been delivered,

except that a delivery by hand or email received after 5:00pm (local time of the receiving party) will be deemed to be given on the next Business Day.

15.7. A notice under clause 9 or 10 which is sent via email must also be sent by post or hand delivery, and will not be deemed to be given until the notice is deemed to be delivered by post or hand delivery.

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The parties to the Escrow Agreement have executed the Escrow Agreement on the dates set out below.

Execution by Escrow Agent

Date	
EXECUTED for and on behalf of: ..... Name of Escrow Agent by its authorised representative, in the presence of: ..... Signature of witness ..... Name of witness (block letters)	..... Signature of authorised representative By executing this Escrow Agreement the signatory warrants that the signatory is duly authorised to execute this Escrow Agreement on behalf of the Escrow Agent ..... Name of authorised representative (block letters) ..... Position of authorised representative

Execution by Supplier

Date	
EXECUTED for and on behalf of: ..... Name of Supplier by its authorised representative, in the presence of: ..... Signature of witness ..... Name of witness (block letters)	..... Signature of authorised representative By executing this Escrow Agreement the signatory warrants that the signatory is duly authorised to execute this Escrow Agreement on behalf of the Supplier ..... Name of authorised representative (block letters) ..... Position of authorised representative

Execution by Customer

Date .....

EXECUTED for and on behalf of:

.....	)	.....
Name of Customer	)	Signature of authorised representative
by its authorised representative, in	)	By executing this Escrow Agreement the signatory
the presence of:	)	warrants that the signatory is duly authorised to
	)	execute this Escrow Agreement on behalf of the
	)	Customer
.....	)	
Signature of witness	)	.....
	)	Name of authorised representative (block letters)
.....	)	
Name of witness (block letters)	)	.....
		Position of authorised representative

DRAFT

CA-114

Queensland Government

General Contract Details – ICT Products and Services

Forensic Register Services Contract

Contract Number: [redacted]

Queensland Police Service

Bdnatec Pty Ltd

QITC General Contract Details – ICT Products and Services
Issued December 2019 - Version 2.0.0

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1. General Information

The General Contract Conditions - ICT Products and Services apply to these Details.

The definitions and rules of interpretation applicable to these Details are set out in the General Contract Conditions - ICT Products and Services.

1. Customer

Name

The State of Queensland acting through the Queensland Police Service

ABN or ACN

ABN 29 409 225 509

2. Customer contact details

Authorised Representative(s)

Senior Sergeant, Project Officer, Forensic Services Group

For the purposes of clause 23(e) of the General Contract Conditions and any variation to the Contract, the Customer's Authorised Representative is the Superintendent, Forensic Services Group.

Email

[redacted]

3. Supplier

Name

Bdnatec Pty Ltd ("Bdna")

ABN

51 149 881 676

4. Supplier Contact Details

Authorised Representative

Marty Wauchope

Position title / role

Partner

Phone number

[redacted]

Street address

[redacted]

Postal address

(notices preferred by email – see below)

[redacted]

Email

[redacted]

5. Products and Services and documents that form part of the Contract Clause 1.3 and 5

Applicable Products and Services

- ☐ Hardware
- ☐ Hardware Maintenance Services
- ☒ Licensed Software
- ☒ Software Support Services
- ☒ Developed Software
- ☐ As a Service
- ☐ ICT Professional Services

Documents

No additional documents.

6. Additional Provisions Clause 1.4

(a) The following definitions are added to clause 24.1 of the General Contract Conditions:

Consolidated FR has the meaning given in the IP Agreement.

Customer includes Queensland Health to the extent applicable to Queensland Health receiving benefits under this Contract, in accordance with clause 1.4(c).

Enhancement means an extension, alteration, improvement or additional functionality of the Licensed Software included in a New Release, including those requested by the Customer or Queensland Health through the Forensic Industry Panel under the IP Agreement (but not including Developed Software under this Contract).

IP Agreement means the Forensic Register IP Agreement entered into by the parties on or about the date of this Contract.

Production Environment means the Production Environment specified in item 29 of the Details.

Production System means the Supported Software in the Production Environment.

Queensland Health means the State of Queensland acting through Queensland Health.

Queensland Police Service means the State of Queensland acting through the Queensland Police Service.

Release Notes means the Release Notes referred to in item 10 of the Details.

Testing Environment means the Testing Environment specified in item 29 of the Details.

Training Environment means the Training Environment specified in item 29 of the Details.

Unexpected Event means any of the following events provided that they are outside the reasonable control of the affected party and could not have been prevented or avoided by that party by reasonable diligence or reasonable precautions:

(i) an act of God, lightning strike, meteor strike, earthquake, storm, flood, landslide, tsunami, explosion or fire;

(ii) strikes or other industrial action, other than strikes or other industrial action of some or all of the Supplier's Personnel; and

(iii) war, terrorism, sabotage, blockade, revolution, riot, insurrection, civil commotion or epidemic,

but excludes any act or omission of a Subcontractor (except where that act or omission was caused by a an Unexpected Event).

(b) The following new clause 1.4(c) is added to the General Contract Conditions:

Queensland Health is entitled to the benefit of the provisions of this Contract as if it was the Customer, provided that:

(i) Queensland Health is not entitled to provide any notices, approvals or consents in relation to this Contract except to the extent that they apply to Services provided solely to Queensland Health, or Queensland Health's operations, property, premises, Personnel, Confidential Information, Personal Information or Customer Data;

(ii) the Supplier is not required to provide Queensland Health with any notices in relation to this Contract or to seek any approvals or consents in relation to this Contract except to the extent that they apply to Services provided solely to Queensland Health, or Queensland Health's operations, property, premises, Personnel, Confidential Information, Personal Information or Customer Data;

(iii) for the sake of certainty, Queensland Health is not entitled to:

A. incur any fees or charges under this Contract;

B. agree any in statement of work in accordance with clause 7 of the General Contract Conditions; or

B. provide any notices or take any action under clause 21 (Termination), or to take any action to enforce any provision of this Contract,

without the consent of the Queensland Police Service; and

(iv) the Supplier must seek direction from the Authorised Representative of the Queensland Police Service in relation to any concerns or other issues in relation to

the application of this Contract in relation to Queensland Health and defer to the Queensland Police Service in resolving any such issues.

(c) The following new clause 1.4(d) Unexpected Events is added to the General Contract Conditions:

(i) A party will not be liable for any delay in or for any failure to perform its obligations under the Contract to the extent that it is able to demonstrate that such delay or failure has been caused by an Unexpected Event.

(ii) A party prevented from performing any of its obligations under the Contract by an Unexpected Event, must:

(A) notify the other party, as soon as it is affected by the Unexpected Event, of

1 the details of the Unexpected Event;

2 anticipated duration of any delay arising from the Unexpected Event;

3 obligations it is prevented and/or likely to be prevented from performing under the Contract; and

4 its plans to work-around or minimise the impact of the Unexpected Event; and

(B) make all reasonable efforts to minimise the effects of the Unexpected Event (including in the case of the Supplier, by activating its disaster recovery procedures.

(iii) If the affected party is prevented from performing its obligations under the Contract for 30 days or such other period agreed in writing, then the other party may terminate the Contract by notice in writing to the affected party.

(iv) Where the Contract is terminated by a party in accordance with clause (c):

(A) the Supplier will be entitled to payment for all Deliverables which have completed Acceptance Testing (where applicable) in accordance with the Contract up to the date of termination; and

(B) the parties will otherwise bear their own costs and will be under no further obligation to perform the Contract.

(d) The following new clause 5.3(o) is added to the General Contract Conditions:

(o) The Customer and the Supplier will use their best endeavours to negotiate, agree and enter into an escrow agreement in accordance with the IP Agreement. The Customer and the Supplier will maintain the escrow agreement in accordance with the IP Agreement. If for any reason the IP Agreement is terminated or expires while this Contract continues, the Customer and the Supplier will use their best endeavours to negotiate, agree and enter into a substitute escrow agreement substantially in the form of Schedule 5 – Escrow Agreement of the QITC Comprehensive Contract Conditions.

7. Term

Clause 3

Start date

Commencement Date of the IP Agreement.

End date

10 years from the start date.

Extension options

Not applicable

Notice period for extension

Not applicable

8. Policies, codes of conduct, rules, standards and procedures

Clause 4(h)

Site Policies

No further specific policies are required to be stated

Policies, codes of conduct, rules, standards and procedures

No further specific policies are required to be stated.

9. Customer Inputs

Clause 4(k)

Details of Customer Inputs to be provided

The Customer will provide all equipment that is used to host the Production, Test and Training Environments of the Licensed Software.

The Customer will continue to maintain licences for ColdFusion and SQL Server and upgrade these as required to be compatible with the Licensed Software.

10. Documentation

Clause 4(n)

The Supplier must provide Release Notes with each New Release. The Release Notes for each New Release must identify the functionality and provide sufficient instruction on using the functionality that enable the Customer to incorporate into Customer documentation (e.g. operating and work manuals, training materials, etc):

- Customer-requested Enhancements that are included in the New Release;
- Queensland Health requested Enhancements that are included in the New Release; and
- any Developed Software that is included in the New Release.

Context sensitive help must continue to be updated in each Update and New Release.

11. Training

Clause 4(o)

No additional training is provisioned under this Contract.

Rates for additional training

Refer to Schedule 1 – Price and Payment Terms

12. Insurance

Clause 4(q)

Workers compensation insurance as required by law.

Public liability and products liability insurance minimum amount

Public liability:	$10m
Products liability	$10m

Professional indemnity insurance minimum amount

Professional indemnity	$10m

Other insurances

Nil

Minimum period of insurance (for insurance on a "claims made" basis)

Four years

13. Authorisations

Clause 4(r)

Not applicable

14. Security

Clause 4(s)

Not applicable

15. Acceptance Testing

Clause 6

Will testing of Deliverables be required?

☒ Yes

☐ No

Acceptance testing is required for Enhancements to the Licensed Software and Developed Software that is made for the Customer or Queensland Health.

The Customer/Queensland Health will develop the acceptance tests in accordance with the agreed Requirements.

The Customer/Queensland Health will conduct acceptance testing.

16. Subcontractor(s)

Clause 8

No subcontractors will be used

17. Background checks

Clause 8.2(d)

The Customer may request background checks in accordance with clause 8.2 of the General Contract Conditions.

18. Key Personnel

Clause 8.3

No Key Personnel are specified.

19. Price and payment

Clause 9

Maximum price

No maximum Price applies.

The Price will be determined in accordance with Schedule 1 - Price and Payment Terms.

20. Cap on liability

Clause 12 and 13

Supplier's liability cap

Supplier's liability is limited to $10M (liability) and $5M (indemnity) on a per-occurrence basis.

Supplier's liability cap for loss of Customer Data

Supplier's liability is limited to $10M (liability) and $5M (indemnity) on a per-occurrence basis.

Customer's liability cap

Customer's liability is limited to $10M.

21. Intellectual Property Rights in Pre-Existing Materials

Clause 15.1

Pre-Existing Material

No Pre-Existing Materials are specified.

Customer's use of Pre-Existing Material

No additional licence rights apply to Pre-Existing Materials.

Sublicensees and cost

No additional rights to sublicense Pre-Existing Materials apply.

22. Intellectual Property Rights in New Materials

Clause 15.2 and 15.3

New Material

No New Materials are specified.

Ownership of New Material

Will Intellectual Property Rights in the New Material be owned by the Customer or Supplier?

☐ Customer (clause 15.2 of the General Contract Conditions applies).

☒ Supplier (clause 15.3 of the General Contract Conditions applies).

Supplier owned – Customer's use of New Material

No additional licence rights apply to New Materials.

Supplier owned – Sublicensees and costs

No additional rights to sublicense New materials apply.

23. Intellectual Property Rights in Third Party Materials

Clause 15.4

Will any Deliverables incorporate any Third Party Material?

☐ Yes

☒ No

24. Customer Data

Clause 16

The Supplier has no right, title or interest in Customer Data.

25. Confidentiality and Privacy Deed

Clause 17(d)

The Customer may request the Supplier to obtain from its Personnel (including Subcontractors) a signed confidentiality and privacy deed in accordance with clause 17(d) of the General Contract Conditions.

26. Conflict of Interest

Clause 19.2

Nil.

27. Termination for convenience

Clause 21.3

No amount is payable under clause 21.3(b)(ii).

28. Business Hours

Clause 24.1

"**Business Hours**" means the hours 09:00 – 17:00 Australian Eastern Standard Time (GMT +10) on a Business Day.

"**Business Day**" means any day other than Saturday, Sunday or a day that is a Queensland gazetted public holiday.

29. Designated Environment

Clause 24.1

The Licensed Software will operate on the existing hardware and operating environments listed here, that will continue to be maintained by the Customer:

- Production Environment, comprising
  - 2x Web and Application servers, with Internet Information Services and ColdFusion Server
  - Database Server with Microsoft SQL Server
  - 2x Windows storage servers with attached SAS arrays

- Training and Testing Environments (co-hosted), comprising
  - 1x Web and Application server, with Internet Information Services and ColdFusion Server
  - Database Server with Microsoft SQL Server

2. Licensed Software

1. Licensed Software

Name of Licensed Software (including version number and all applicable modules/components)

Product name: forensic-register

Modules: all

2. Requirements

Initially the Customer will continue to use the existing version of the Licensed Software.

At a later date to be mutually agreed, the Customer and Queensland Health will migrate to the new, Consolidated FR.

3. Licence Period

Clause 5.3(b)

The Licence Period is concurrent with the Customer's licence rights in relation to the Licensed Software under the IP Agreement.

4. Use of Licensed Software

Clause 5.3(a)(i)

The Customer's rights to use the Licensed Software include the rights granted under the IP Agreement.

5. Class of Licence

Clause 5.3(a)(i)

Module	Description	Licensing conditions
FR-CI-Core	Core forensic-register Supplied on QPS infrastructure	Unlimited number of users
FR-CI-FP	Fingerprints module	Unlimited number of users
FR-CI-Intel	Intelligence module	Unlimited number of users
FR-CI-Chem LIMS	Chemistry LIMS module	Up to 70 named users
FR-CI-DNA LIMS	DNA LIMS module	Up to 150 named users

6. Sublicensing

Clause 5.3(c)

The Customer's rights to sublicense use of the Licensed Software include the rights granted under the IP Agreement.

7. Additional licence conditions and restrictions

Clause 5.3(e)

There are no additional licence conditions and restrictions under this Contract. Any licence conditions or restrictions under the IP Agreement apply in accordance with the terms of that agreement.

8. Copies of Licensed Software to be provided by Supplier

Clause 5.3(f)

Production, Training and Test Environment installations of the Licensed Software.

Source code is to be provided in escrow in accordance with the IP Agreement.

9. Delivery and installation requirements

Clause 5.3(g)

Site

[redacted]

Delivery Date

n/a – the Licensed Software is already operational.

Is Supplier required to install the Licensed Software?

☒ Yes

If the Supplier is required to install the Licensed Software, specify the requirements for the installation of the Licensed Software:

The Supplier will install the Licensed Software in Production, Training and Test Environments, including all upgrades.

10. Updates and New Releases

Clause 5.3(h)

Specify if the Customer is entitled to Updates and/or New Releases for the Licensed Software (as part of the licence as opposed to part of separate Software Support Services)

☒ Yes

If yes, insert any installation obligations of the Supplier

The Supplier will provide Updates and New Releases in accordance with item 4 of section 3 - Software Support Services.

11. Ancillary services

Clause 5.3(i)

Technical assistance

The Supplier must provide:

(a) technical advice to the Customer and Queensland Health on the appropriate usage and implementation of the Licensed Software; and

(b) other Services identified as additional Products and Services in Schedule 1 - Price and Payment Terms if ordered by the Customer in accordance with the statement of work process in clause 7 of the General Contract Conditions.

User Group representation

The Supplier must provide membership for the Customer's and Queensland Health nominated representatives to any User group for the Licensed Software.

12. Warranty Period

No Warranty Period for the existing Licensed Software; this has been operational with the Customer for over 15 years.

The Supplier must provide 30 days Warranty Period for Enhancements or Developed Software that are made for the Customer and Queensland Health, unless another Warranty Period is specified in an applicable statement of work in accordance with clause 7 of the General Contract Conditions.

3. Software Support Services

1. Supported Software

Name of Supported Software (including version number and all applicable modules/components)

Product name: forensic-register

Modules: all

2. Support period

Clause 5.4(a)

Start of support period

In accordance with the start date of the Term in item 1 of the Details.

End of support period

In accordance with the end date of the Term in item 1 of the Details.

3. Definitions and interpretations

Fix means the correction of a Defect or the resolution of another Issue.

Fix Time means the elapsed time between the time:

(a) the Customer reports the Issue to the Supplier; or

(b) the Supplier identifies the Issue,

and the time the Supplier provides a Fix for the Issue and the Customer provides written confirmation to the Supplier that the Fix has corrected or resolved the Issue.

Issue means a Defect in the Supported Software or another issue included in the FR Support Components that the Supplier is responsible for as defined in Item 4 (Support responsibilities) below.

Issue Update means the written notification/s provided by the Supplier to the Customer during the Fix Time which provide:

(a) an estimate of when a Workaround (if available) will be provided;

(b) an estimate of when a Fix will be provided;

(c) any actions which can be performed by the Customer to mitigate the impact of the Issue on the Customer's operations or use of the Supported Software;

(d) the Supplier's assigned identification number for the Issue;

(e) the current status of the activities being undertaken by the Supplier to provide a Workaround for or to Fix the Issue; and

(f) such other information as reasonably requested by the Customer.

Response means the initial written notification provided by the Supplier to the Customer which:

(a) notifies the Customer of the existence of the Issue; or

(b) acknowledges the Customer's reporting of the Issue, and

Response Time means the elapsed time between the time:

(a) the Customer reports the Issue to the Supplier; or

(b) the Supplier identifies the Issue,

and the time the Supplier provides the Response.

Workaround means a fix or alternative procedure to temporarily address a Defect or other Issue.

Workaround Time means the elapsed time between the time:

(a) the Supplier is notified about the Issue; or

(b) the Supplier identifies the Issue,

and the time the Supplier provides a Workaround for the Issue.

Other capitalised words and expressions used in this document have the meaning given to them in the General Conditions of Contract.

4. General Support

Clause 5.4(b)

Support responsibilities

The Supplier and Customer will bear the following responsibilities:

	Responsible Support Tier		
FR Support Component	Tier 1	Tier 2	Tier 3
FR administration change requests	Customer	Customer	Supplier
FR end-user support			
FR technical support		Supplier	
FR application			
FR database			
Server platform and infrastructure		Customer	Customer
Network, including mobile			

Business hours support

The Supplier must provide support for the Production Environment of the Licensed Software during Business Hours on all Business Days.

After hours support

The Supplier must provide after-hours phone support for Priority 1 faults only.

System monitoring and management

The Customer must monitor the infrastructure that supports the Production Environment, including system alerts, system capacity and availability, to maximise the operational availability of the Production System.

The Supplier must monitor and manage the Production Environment of the Licensed Software, including relevant logs, to attempt to maximise the operational availability of the Production System.

System administration

The Customer will maintain a full-time System Administrator to perform administration functions for the Licensed Software, in support of the users.

The Supplier must provide assistance to the System Administrator for matters that require expert technical intervention.

Issue response and resolution

The Supplier must provide a service desk facility with Priority 1 phone support for the Customer and Queensland Health.

The Supplier must provide an online Issue reporting and management solution and provide access to the Customer's and Queensland Health nominated representatives.

The Supplier must acknowledge, respond to and, where required, resolve Issues that are reported.

The Supplier must assist Customer's and Queensland Health with Issue prioritisation.

The Supplier must provide Issue Updates.

Support location

The Supplier must perform Production System maintenance from a secure support location whenever possible, whether at the Customer's offices or the Supplier's offices.

The Customer and Queensland Health must provide desk space for Supplier Personnel when they provide Support Services from the Customer's site.

Service delivery reporting

The Supplier must provide monthly reports to the Customer and Queensland Health that detail:

- The number of Issues raised in the month, by priority level
- List of Issues that were either closed during the month or remain open
- Numbers of open work items, including Issues and Enhancement requests

Enhancements and Defect resolution

The Supplier must liaise with the Customer and Queensland Health to manage and prioritise the backlog of Defect and Enhancement items, and develop Defect Fixes and Enhancements taking into account Customer priorities.

The Supplier will include Customer and Queensland Health requested Enhancements in the 6 monthly New Releases to the Licensed Software.

Supplier's contact details:

Service Delivery Manager: Andrew Nguyen

[redacted]

5. Updates and New Releases

Clause 5.4(d)

Updates and New Releases to be provided?

☒ Yes

(a) Legacy Customer version of Licensed Software: The Supplier must initially provide Updates and New Releases to the existing Customer and Queensland Health version of the Licensed Software in ad-hoc manner, continuing the operational practice in place prior to this Contract.

(b) Commercial software assurance: After implementation of the Consolidated FR, the Supplier must provide formal New Releases of the Licensed Software to the Customer and Queensland Health on a 6-monthly basis to the Customer, and in accordance with the Customer's entitlements under the IP Agreement.

(c) The Supplier must make available to the Customer any Updates and New Releases no later than when the Supplier makes them generally available to other customers.

(d) In addition to the Release Notes referred to in item 10 of the Details, information that the Customer may require the Supplier to provide includes:

(i) the features of the Update or New Release, and the nature of the improvements and/or corrections contained in the Update or New Release including compatibility of the Update or New Release with the Supported Software;

(ii) any adverse effects that the Update or New Release may be expected to have on the Designated Environment; and

(iii) sufficient information to enable the Customer to determine whether the Update or New Release will suit the Customer's requirements.

If yes, is training to be provided by the Supplier in respect of the Updates and New Releases?

No additional training is provisioned under this Contract.

6. Service Levels

Clause 5.4(f)

Priority / Severity levels - Issues

- **Priority 1 - Critical**: Must be fixed immediately. The Issue is preventing use of the system, there is no Workaround and Customer business processes are being significantly impacted or prevented from completion.
- **Priority 2 - Urgent**: Must be fixed as a priority. Use of the system can proceed but in a degraded mode. There may be a Workaround for the Issue, but it remains a significant risk.
- **Priority 3 – High**: Use of the system can proceed. There may be a low-risk Workaround for the Issue.
- **Priority 4 - Low**: May or may not be fixed, depending on availability of resources. The Issue does not affect operational processes.

Service Level targets – Issues and Defect resolution

The following Service Level times apply to Defects in the Supported Software and other Issues included in the FR Support Components that the Supplier is responsible for as defined in Item 4 (i.e. Support Responsibilities) above.

Priority Level	Response Time	Workaround Time	Fix Time	Service Level Target KPIs
Priority 1 - Critical	15 minutes (All hours)	Within Business Hours: Workaround provided within one (1) Business Hour.	Within Business Hours: Completed within four (4) Business Hours.	95% completed within Service Level (Best Endeavours relating to Fix)
		Outside of Business Hours: Workaround provided within three (3) hours.	Outside of Business Hours: Completed within eight (8) hours.	
Priority 2 - Urgent	1 Business Hour	Provided within four (4) Business Hours	Completed within two (2) Business Days	
Priority 3 - High	2 Business Hours	Provided within two (2) Business Days	Completed within five (5) Business Days	
Priority 4 - Low	1 Business Day	Commence as soon as possible, considering Priorities 1 to 3 and availability of resources	Completed per agreed schedule with client	

Service level reporting

The Supplier must provide monthly reports to the Customer and Queensland Health that detail:

- # Issues received
- # and % of Issues Responded to within target Service Level
- # and % of Issues Fixed within target Service Level

7. Service Credits

Clause 5.4(g)

A True-Up mechanism will be used to record a summary of all incidents and events that may result in either party having an impact on the other.

At the end of each 3-month period the parties will meet and discuss the True-Up content and balance the outcome, which may result in additional time or service provided to a party, if agreed by the parties in writing.

Annexure 1 sets out further information in relation to the True-Up mechanism.

8. Escalation Procedure

Without limiting the Customer's rights and remedies under the Contract, the Customer may raise and escalate Defects and any other Issues under the Contract which adversely impact upon the Customer in accordance with the following table. The Customer may escalate an Issue to the next level where a satisfactory response has not been provided or a resolution has not been reached within the specified timeframe.

Escalation level	Representatives	Timeframe for response
1	Customer: Project Officer, Forensic Services Group Supplier: Bdna Service Delivery Manager	One (1) day
2	Customer: Inspector, Forensic Services Group Supplier: Bdna Forensic Product Director	Two (2) days
3	Customer: Superintendent, Forensic Services Group Supplier: Bdna Partner	Four (4) days

4. Developed Software

1. Developed Software and Design Specification

Description of Developed Software

The Customer may purchase Developed Software from the Supplier during the Term in accordance with the statement of work process in clause 7 of the General Contract Conditions.

Requirements

The Requirements for the Developed Software will be as set out in the applicable statement of work to be agreed between the Parties.

Is Supplier required to prepare a Design Specification?

No, unless specified in the applicable statement of work.

2. Delivery Dates

Clause 5.5(a) and (c)

Delivery dates will be as specified in the applicable statement of work.

3. Delivery and installation requirements

Clause 5.5(c)

Site

As per Licensed Software (Item9).

Is Supplier required to install the Developed Software?

As per Licensed Software (Item9).

4. Ancillary services

Clause 5.5(e)

Ancillary services (if any) will be as specified in the applicable statement of work.

5. Warranty Period

The Warranty Period for the Developed Software will be 30 days from the AAD of the Developed Software, unless otherwise specified in the applicable statement of work.

5. Forming the Contract

Acknowledgements and Certifications

The Supplier:

(a) agrees to provide the Products, Services and other Deliverables to the Customer on the terms described in the Contract.

(b) certifies that it has read, understands, and complies with all the requirements of the Contract.

(c) represents that all the information provided by it and referenced in the Contract is complete, accurate, up to date and not misleading in any way.

(d) acknowledges that the Customer is relying on the information provided by the Supplier and referenced in the Contract in entering into the Contract.

(e) acknowledges that the Customer may suffer damage if any of that information is incomplete, inaccurate, out of date or misleading in any way.

Agreement by Supplier

The Supplier will sign in this section. By signing, the Supplier is offering to enter the Contract on the terms set out in this document. If the Supplier does not execute this document itself, it must (if the Customer requests) provide adequate evidence that the signatory is properly authorised to execute this agreement.

If the parties agree any changes to this document after the date of the Supplier's signature (but before the Customer accepts the Supplier's offer as described below), the Supplier and Customer will prepare a new version of the document incorporating the agreed changes, which will replace this document. The Supplier will sign the new document, offering to enter the Contract on the amended terms.

Date 1/10/2020

EXECUTED for and on behalf of:

BONATEC PTY LTD

Name of Supplier

by its Authorised Representative, in the presence of:

[redacted]

Signature of witness

T S O'MALLEY

Name of witness (block letters)

[redacted]

Signature of Authorised Representative

By executing this agreement the signatory warrants that the signatory is duly authorised to execute this agreement on behalf of the Supplier

MARTIN WAUCHOPE

Name of Authorised Representative (block letters)

DIRECTOR

Position of Authorised Representative

Agreement by Customer

Date 28/09/20

EXECUTED for and on behalf of: The Queensla

KATARINA CARROLL

Name of Customer

by its Authorised Representative, in t

[redacted]

S

Rob Fleischer

Name of witness (block letters)

[redacted]

Signature of Authorised Representative

By executing this agreement the signatory warrants that the signatory is duly authorised to execute this agreement on behalf of the Customer

Katarina Carroll

Name of Authorised Representative (block letters)

Commissioner

Position of Authorised Representative

Schedule 1 – Price and Payment Terms

1.1 Price

Licence fee: No licence fee is payable.

Software Support Services:

Joint Customer and Queensland Health price: $ 687,907 per annum ex GST (See below)

The Customer will receive 56% discount on Software Support Services for the first 10 years of the Contract Term, in recognition of the Customer's contributions of Intellectual Property and Industry Partner assistance to the Supplier.

The discounted price is **$300,000 ex GST per annum**.

1.2 Expenses

Nil

1.3 Price reviews (including during any extension period(s))

Nil

1.4 Payment plan/milestones

The Software Support Services Price for each year of the Term is payable in 12 equal monthly instalments.

The Supplier will invoice all fees monthly in advance. The Customer may request that fees are invoiced annually in advance.

The Customer will pay each correctly rendered tax invoice that complies with clause 10 of the General Contract Conditions within 30 days of receipt.

1.5 Rates for additional Products and Services (if applicable)

Item	Day Rate (ex GST)
Developed Software	$1,300
Extended / urgent enhancements beyond normal inclusions	$1,300
Analysis services	$1,500
Train the Trainer services	$1,300
System Administration	$ 800
User Training courses. Prices will be dependent on course content and length, number of attendees etc.	POA

1.6 Development Hours

The Customer may use its entitlement to Development Hours under the IP Agreement to purchase Services under this Contract.

1.7 Payment methods

Account name: BdnaTec Pty Ltd

BSB: [redacted]

Number:

Swift Code:

Remittance advice to: [redacted]

1.8 Discounts or rebates

See section 1.1 above.

1.9 Address details for invoice

[redacted]

1.9 Other pricing information

Nil

Annexure 1 – True-Up Mechanism

Overview

The True-up is used to record events that have impacted either party and provides a mechanism to balance the impacts on the parties in a collaborative manner. The True-up utilises the concept borrowed from the latin phrase "quid pro quo" that emphasises something is provided or substituted.

The True-up mechanism provides a way to resolve difference in a mutually beneficial way. The register and process enables both parties to continue working on the agreed outcomes with minimal disruption whilst acknowledging events that may have impacted the parties.

The Truing-up will occur each three months.

Method

1. **Recording impact events**
   The Customer representative and the Supplier representative record events that significantly impact on their resources or on service outcomes. Both the Customer and the Supplier record events in the same, shared register. The impact is measured in rectification effort, not the wider impacts on end users.

2. **Periodic Truing up**
   The Customer representative and the Supplier representative meet at the agreed interval to review the events for that period. They discuss and agree the respective impacts in terms of effort and/or a dollar value. Some possible outcomes include:
   - A small number of days is owed to either party, and these are simply carried forward.
   - A significant number of days is owed by the Supplier and the Supplier agrees to provide additional services in the coming period(s) to deliver this.
   - A significant number of days is owed by the Customer and the parties agree to change arrangements appropriately: e.g. to hold other service providers to account to perform their service delivery; or to expand the Supplier's service delivery contract.
   - A significant number of days is owed by the Customer and the Supplier agrees that no action is required, in the spirit of customer-focused delivery and positive relationships.

3. **Escalation**
   In the unlikely event of serious disagreement over a "True-up" event, the Customer or Supplier representative escalates to their respective escalation point.

True-Up example

- Over the course of a 3 month period the Customer's infrastructure failed and the Supplier expended 10 days of additional unplanned effort.
- During the same period the Supplier mistakenly deployed an incorrect module to the Customer's test environment, resulting in a day of wasted test activity involving 6 Customer members, i.e. representing a 6-day impact to the Customer.
- At the quarterly true-up meeting, the balance is calculated as (Supplier 10 days impact) minus (Customer 6 days impact), a net 4 days impact to Supplier.
- The representatives agree to carry the balance over to the next period.

Key Roles

Customer Representative and Customer Escalation point
Supplier Representative and Supplier Escalation point

CA-115

Cathie Allen

From: Cathie Allen
Sent: Friday, 24 June 2022 9:13 AM
To: Lara Keller
Cc: Justin Howes; 'Paula Brisotto'
Subject: Follow-up paper pdf
Attachments: Assessment of Low Quant DNA Samples_June 2022.pdf

Hi Lara

As discussed.

Cheers
Cathie

Cathie Allen **BSc, MSc (Forensic Science) (She/Her*)**
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health

[redacted]

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

*If you're wondering about the use of pronouns She/Her on this signature block, I encourage you to read some resources available here



CA-116

Cathie Allen

From: Cathie Allen
Sent: Friday, 15 July 2022 4:06 PM
To: Lara Keller
Cc: Helen Gregg
Subject: FW: Assessment of low quant DNA samples report
Attachments: Assessment of Low Quant DNA Samples_June 2022.pdf

Importance: High

Hi Lara

It's probably best if you were to address this particular email.

Cheers
Cathie

Cathie Allen BSc, MSc (Forensic Science) (She/Her*)
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health
[redacted]

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

*If you're wondering about the use of pronouns She/Her on this signature block, I encourage you to read some resources available here



From: Helen Gregg <[redacted]>
Sent: Friday, 15 July 2022 3:20 PM
To: Cathie Allen <[redacted]>
Subject: FW: Assessment of low quant DNA samples report

Hi Cathie,

My understanding of this email is that they want to know that we have anticipated the increase in workload that the change in threshold will have, and what we have done about it. DO you agree? If so, I suggest replying that we have anticipated that this change will impact turnaround times, and are actively working on solutions to mitigate this.

Are you happy with this response?

Regards
Helen

From: Pobar.DarrenJ[OSC] <[redacted]>
Sent: Friday, 15 July 2022 12:00 PM
To: Helen Gregg <[redacted]>
Subject: Assessment of low quant DNA samples report

This email originated from outside Queensland Health. DO NOT click on any links or open attachments unless you recognise the sender and know the content is safe.

Good morning Helen

I am currently relieving for a short term in Superintendent Bruce Mcnab's role in Forensic Services Group.

I refer to attached report provided by Acting Executive Director Lara Keller to Supt Mcnab on 24 June 2022 regarding a review assessment of low quant DNA samples and I thank QHFSS for compiling and providing this new report. I note that the success rate in this new review of the micro-concentration process is approximately 25%. This is considerably higher than predicted in the 2018 Options Paper that recommended the removal of the process as a matter of routine. We are still considering the material provided and hope to discuss the options with QHFSS in the near future.

I understand the Health Minister announced on 30 May 2022 the .0088ng/uL processing threshold has been removed and that all samples are now processed as a matter of routine. I am seeking clarification on the current process on testing low quant value samples. If correct that all samples from priority 1 to 3 are being processed despite low quant values, the QPS has concerns how this change will impact anticipated backlogs and turn around times of results. Should this present as a risk, could you also please advise what strategies are in place to mitigate this issue.

Thank you again for providing the report and I look forward to receiving your advice on these queries.

Regards

Darren Pobar | Acting Superintendent
Forensic Services Group
Operations Support Command
Queensland Police Service
[redacted]
200 Roma Street Brisbane
[redacted]



****
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CA-117

Forensic and Scientific Services

Assessment of Low Quantification Value DNA Samples

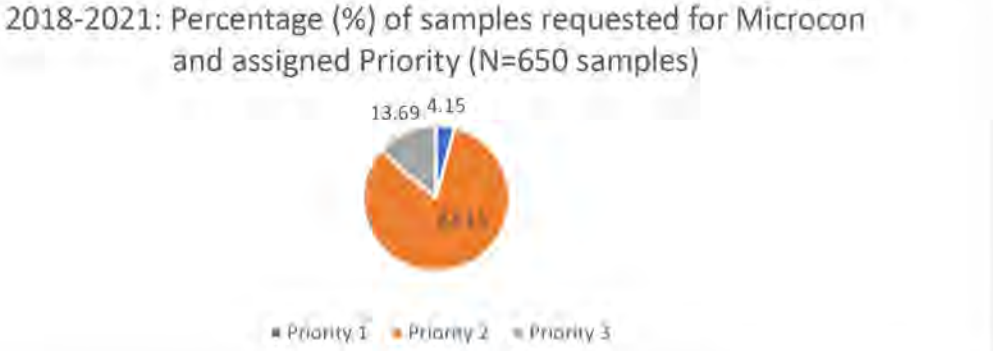
Authors: Cathie Allen, Justin Howes and Paula Brisotto 21 June 2022

Background:

The Queensland Police Service (QPS) implemented a new service model in July 2008, which saw Forensic Officers taking the lead and responsibility for sample selection, examination of some items and case review of forensic results. This change also saw a reduction in case details and case context being supplied to Forensic and Scientific Services (QHFSS). Provision of scientific information to process a sample for DNA profiling remained unchanged. Under this framework, an Options paper was provided to the Superintendent for Forensic Services Group in February 2018 regarding an assessment undertaken to evaluate samples with low quantitation values and subsequent concentration and the DNA profile obtained. The Options paper detailed the assessment of 1449 samples. The QPS selected the option of not DNA profiling samples within a low quantitation range, as a triaging process, and information would be provided electronically on QPRIME (via the Forensic Register) regarding additional work that could be undertaken if requested.

Executive Briefing:

An assessment of all casework DNA samples, with the following criteria was conducted: an initial quantification result of between 0ng/µL and 0.0088ng/µL, underwent a concentration process and reported results issued between 2018 and 2021. This equated to an assessment of 650 DNA samples. The reported DNA result, which may have been completed after one or more amplifications processes, was categorised into two broad categories - 'suitable for comparison purposes' or 'unsuitable for comparison purposes'.



165 DNA samples (25.4%) were categorised as 'suitable for comparison purposes', with most of these samples being major crime samples. 485 DNA samples (74.6%) were categorised as 'unsuitable for comparison purposes' after concentration and amplification processes.

Of the 165 DNA samples categorised as 'suitable for comparison purposes', 41 DNA samples were able to yield a profile suitable for uploading and searching of the National Criminal Investigation DNA Database (NCIDD). This represents 6.3% of total samples selected for processing. This figure is not unexpected as this assessment was based on samples that were actively selected for further processing, determined by either the QPS, QHFSS staff or both organisations using a collaborative approach. This assessment also includes volume crime samples, whereas the previous assessment did not include these samples.

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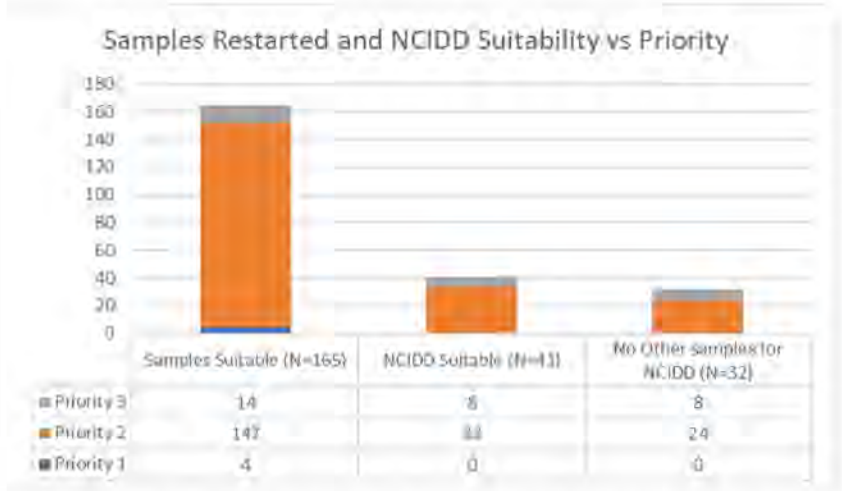

Please note the current dataset is different to the previous dataset due to, but not limited to:

- implementation of the statistical interpretation of four-person mixtures (contributes to 5.5% of the total samples deemed 'suitable for comparison purposes in this dataset),
- all DNA samples were selected in this dataset (the previously assessed dataset only included DNA samples assigned to Major Crime cases),
- active selection of samples for processing by either the QPS or Forensic DNA Analysis staff members based on the context of the case or scientific knowledge with respect to the associated parameters from the quantification process,
- if any new instrumentation or consumables were implemented by either the QPS or QHFSS over that period.

Forensic DNA Analysis staff are mindful of consuming all DNA extract when requesting a concentration step. Technologies available in other jurisdictions or future technologies may be applied to DNA extracts, however if all DNA extract has been exhausted through concentration and amplifications processes, no (or very limited) extract will be available for these technologies or for Defence to request external testing. Forensic DNA Analysis staff have limited scope of the case context and other forensic results for the case.

Observations:

Review of quantitation parameters, other than quantitation value, did not identify a discernible trend, however further monitoring of these parameters will continue.

The value of 0.0088ng/µL is based on assessment of the data (and equates to 132 picograms). Validation studies conducted within the laboratory has shown that stochastic effects become apparent from DNA templates below 0.132 ng (132 picograms) making interpretation of the resultant DNA profile more complex.

If a value of 0.0067ng/µL (equating to 100 picograms) is chosen as the threshold for this triage process, DNA samples with a value of between 0.0067ng/µL and 0.0088ng/µL will not be subjected to a concentration step, which may affect the resulting DNA profile.

It was not unexpected that as the quantitation value increases, the ability to yield suitable profiles for interpretation improved.

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Options for Consideration:

1. Continue with the current workflow:
   a) Priority 1 samples continue to be automatically concentrated prior to amplification if the sample falls into the quantitation range of 0.001ng/µL to 0.0088 ng/µL
   b) Priority 2 and Priority 3 samples are reported as 'DNA Insufficient for Further Processing' if the sample falls into the quantitation range of 0.001 ng/µL to 0.0088 ng/µL (132 picograms) and process upon request by either the QPS or Forensic DNA Analysis staff members. Continue to retain the DNA extract indefinitely, if no request is received.
2. Amend the workflow:
   a) Priority 1 samples continue to be automatically concentrated prior to amplification if the sample falls into the quantitation range of 0.001ng/µL to 0.0088 ng/µL
   b) Priority 2 and Priority 3 samples are reported as 'DNA Insufficient for Further Processing' if the DNA sample falls into the quantitation range of 0.001 ng/µL to a newly determined value and process upon request by either the QPS or Forensic DNA Analysis staff members. If requested, the process would include concentration of the DNA sample prior to amplification. Continue to retain the DNA extract indefinitely, if no request is received. DNA samples with a quantitation value of above a newly determined value will be processed as per routine and will not be subject to a concentration process.
   c) The reasoning for a newly determined quantitation value will be agreed upon and documented, including risks.
   d) This amended workflow will require Forensic Register enhancement prior to use.
3. Amend the workflow:
   a) Priority 1 samples continue to be automatically concentrated prior to amplification if the sample falls into the quantitation range of 0.001ng/µL to 0.0088 ng/µL
   b) All priority 2 samples that fall into the quantitation range of either 0.001ng/µL to 0.0088ng/µL or 0.001ng/µL to the newly determined value will be concentrated prior to amplification.
   c) Priority 3 samples that fall into the quantitation range of either 0.001ng/µL to 0.0088 ng/µL or 0.001ng/µL to the newly determined value will be amplified without a concentration step.
   d) This amended workflow will require Forensic Register enhancement prior to use.
4. Amend the workflow:
   a) Priority 1 samples continue to undergo a concentration step prior to amplification if the sample falls into the quantification range of 0.001ng/µL to 0.0088 ng/µL.
   b) Amplify, without concentration, all Priority 2 and 3 samples above 0.001ng/µL value.

Next Steps:

QHFSS will meet with the QPS representatives to discuss the options provided and discuss risks and implications to reach a collaborative decision on the path forward.

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OQI Number	Title	Subject	Creator	Created Organisational Unit	Actioner	Actioned Organisational Unit	Status	Source of OQI	Date Added
[redacted]	No Title Provided	From Detective Andrew Gillies ,Ferny Grove CIB,who says," ...thank you very much for assisting to make our detective's conference last month quite a success..."(to Leo Freney).	Leo FRENEY	DNA Analysis	Graeme WHITE	Chemical Analysis	Closed Approved	Compliment/Praise	25/02/2003
[redacted]	No Title Provided	compliment (email) from DSgt Adam Simms and DSgt John O'Shea to Snr Forensic Scientists Peter Clausen and Richard Mattner for expert testimony provided during committal and trial re: R v SURREY (Dismembered bodies double Homicide. The email said in part"...it would be remiss of me also not to thank the tenacious and crucial efforts of Peter Clausen and Richard Mattner of the John Tonge Cente. Without the evidence that they presented we would not have had a joint trial to start with, which increased our chances of conviction. ..also thanks to the (Forensic Biology) team who uncovered the most recent DNA profile of ( ) in the backpack with the new technique. Yor professionalism is impressive - Truly great work by you all !"	Pete CLAUSEN	DNA Analysis	Margaret WIEMERS	Radiology Support	Closed Approved	Compliment/Praise	22/09/2003
[redacted]	No Title Provided	Exhibits discarded near scenes of a series of related armed robberies were brought in for forensic testing. These were examined by me and DNA analysed back in 2001. Low level DNA results were obtained. These were challenged vigorously by Damian Walsh (acting for defence) in conjunction with a Laszlo Szabo (NATA technical auditor performing accreditation audit on Qld forensic biology lab/Section Head of the Tasmanian forensic lab.) This evidence was presented by me during a trial, however due to errors committed by another witness the trial was aborted. No re-testing was ever performed by the defence expert so this time the most contested sample had been re-worked. Many of the DNA Analysis scientists were involved in the process but due to the extra effort by Penny Taylor an excellent result was obtained. The improved result was conveyed to the defence and during the second trial the defendant (Kevin Morris) pleaded guilty.	Alice ORWAT	DNA Analysis	Leo FRENEY	DNA Analysis	Closed Approved	Compliment/Praise	30/09/2003

OQI Number	Title	Subject	Creator	Created Organisational Unit	Actioner	Actioned Organisational Unit	Status	Source of OQI	Date Added
[redacted]	No Title Provided	Operation Charlie GAIN. Volume Crime Team recieved thanks from Queensland Police Metropolitan North Region with regard to the efficient supply of results in relation to this operation. "The information supplied by the DNA results helped Detectives involved in convincing these offenders to 'clear up' offences they had committed, even when they were not suspects for most they had been charged with." As a result one offender was charged with 62 B&E offences and a second offender was charged with 12 B&E offences.	Maryanne HADFIELD	Evidence Recovery and Quality	Pete CLAUSEN	DNA Analysis	Closed Approved	Compliment/Praise	5/07/2004
[redacted]	No Title Provided	A Townsville Detective rang to thank the section for the "little bit of extra work" that was done on a rape case from 1999, to isolate an unknown male profile that has this week resulted in a link [redacted] The detective was grateful for the ongoing database work that produced this result. The complainant suffered severe mental trauma after the offence. She has been informed that the possible offender has been identified.	Maryanne HADFIELD	Evidence Recovery and Quality	Vanessa IENTILE	DNA Analysis	Closed Approved	Compliment/Praise	16/03/2006
[redacted]	No Title Provided	Emails received from QPS representatives congratulating QHSS staff on their involvement in the increase of DNA match results produced. Back in 1998, the goal was to develop a laboratory producing DNA results that was able to rival the results from fingerprint matches. The feedback from police it that this is starting to happen. QPS representatives have asked that congratulations and thanks be passed to QHSS Forensic staff for their contribution to solving and preventing crime.	Vanessa IENTILE	DNA Analysis	Vanessa IENTILE	DNA Analysis	Closed Approved	Compliment/Praise	24/03/2006
[redacted]	No Title Provided	Email received from I/O Mark Farrell - "I would just like to pass on my thanks to everyone from your section for your excellent communication and professionalism that you have displayed throughout my inquiries with you all". The I/O had several contacts with FSLU (and FSLU with Volume Crime) regaring the status of a reference sample. It was recieved and reported as an evidence sample, but was only an intelligence sample. This was explained to him and the need to collect an evidence sample for statement purposes. The I/O notified us that the offender plead guilty to the charges.	Maryanne HADFIELD	Evidence Recovery and Quality	Vanessa IENTILE	DNA Analysis	Closed Approved	Compliment/Praise	29/03/2006

OQI Number	Title	Subject	Creator	Created Organisational Unit	Actioner	Actioned Organisational Unit	Status	Source of OQI	Date Added
[redacted]	No Title Provided	rates and progress via operations & links thanks to the work of all Forensic Biology Staff Conviction results for time period 1/7/2005 31/12/2005 Total of 478 suspects nominated as wanted (171% increase on the last six months): Of those, 85% have either been found guilty, have prosecution proceedings commenced or are pending location. For the previous six months conviction results for time period 1/1/2005 30/6/2005 Total of 176 suspects nominated as wanted : Of those, 83% have either been found guilty, have prosecution proceedings commenced or are pending location. For the preceding 12 month period Conviction results for time period 1/1/2004 31/12/2004 Total of 271 suspects nominated as wanted: Of those, 86% have either been found guilty, have prosecution proceedings commenced or are pending location. Its interesting to note that from 2004 to 2005, results received for which we were able to nominate a suspect as wanted increased from 271 to 654 and successful conviction statistics remain high. I think these stats are a valid and significant measure of the operational value of the results that are	Mary GARDAM	DNA Analysis	Mary GARDAM	DNA Analysis	Closed Approved	Compliment/Praise	3/05/2006
[redacted]	No Title Provided	Email received from D Sen Sgt Richard Lacey in response to Operation Echo Motto [redacted] "I dont know if it comes across in the meetings we have, but on behalf of the Oxley Detectives we are very greatful for the efforts that you guys have put in on this job. The ITC cops a pretty fair bagging from time to time (not by us mind you) but the efforts, cooperation and understanding we have had from Sam Cave, Margaret Brian and Katarina Owczarek has been absolutely sensational."	Samantha CAVE	Forensic Reporting and Intelligence	Vanessa KATTIS	DNA Analysis	Closed Approved	Compliment/Praise	10/05/2006

OQI Number	Title	Subject	Creator	Created Organisational Unit	Actioner	Actioned Organisational Unit	Status	Source of OQI	Date Added
[redacted]	No Title Provided	A compliment was received via email from Superintendent, Forensic Services Branch to thank forensic staff in FSLU, Forensic Chemistry and Forensic Biology for their work on Operation Echo Pebble. "I have had some very positive feedback from forensic officers and investigators with respect to the services provided by Queensland Health Scientific Services over the past few days in relation to the incident at Kid Space, Chermside and related matters. Could you please convey my appreciation to (people) involved. Their professionalism, support and enthusiasm has been noted and is greatly appreciated. These incidents can highlight the provision of forensic services and how far we have come in relation to service provision, communication and support to investigators."	Vanessa IENTILE	DNA Analysis	Vanessa IENTILE	DNA Analysis	Closed Approved	Compliment/Praise	14/08/2006
[redacted]	No Title Provided	Robyn, I've just received word of a DNA ident for the school fires, absolutely outstanding work and please give my personal thanks to all those involved on behalf of Metro South Region and the community in general. I'm sure you understand the pressure that's brought to bear with such public offences as these. It's no secret that over the years I've been a critic of QHSS and some of your staff may remember my past outbursts but can I say the past two years have been remarkable in terms of outcomes (volume and major) and significantly in terms of the growing partnership between the two organisations. I've no doubt that there'll be some difficult issues to overcome in the future however I'm sure that we're gaining a better understanding of each others strengths, priorities and organisational goals. This all leads to an excellent working relationship and optimistic future. I certainly look forward to working with you all in 2007. Again, please convey my thanks to all and likewise I'll take this opportunity to wish you all a safe and merry Christmas. ps. just had a snappy conversation with the investigators	Vanessa IENTILE	DNA Analysis	Vanessa IENTILE	DNA Analysis	Closed Approved	Compliment/Praise	3/01/2007

OQI Number	Title	Subject	Creator	Created Organisational Unit	Actioner	Actioned Organisational Unit	Status	Source of OQI	Date Added
[redacted]	No Title Provided	Darren Sargood, Senior Sergeant, Regional Forensic Services Coordinator, Metropolitan North Region, sent an email to me regarding praise for the section. 'I see we received an ident from a smudged fingerprint relating to the above FR number [redacted]. A couple of things. Please express our thanks to the entire volume crime section for the work that is currently being done and the results achieved. Can you also thank whoever was responsible for achieving the result for 300429. Can you tell me if this is a result of new technology you are using or because there may have been a large amount of material deposited.'	Cathie ALLEN	DNA Analysis	Cathie ALLEN	DNA Analysis	Closed Approved	Compliment/Praise	10/05/2007
[redacted]	No Title Provided	Appreciation for DNA analysis work was received from the Crime Scene Co-ordinator from the Far North Region, Snr Sgt Lloyd Arthy regarding the short turnaround time for a particular case, [redacted] This case was processed and results uploaded to NCIDD, which produces a link to a person sample. QPS were then able to investigate the matter further. They were grateful for our efforts.	Cathie ALLEN	Evidence Recovery and Quality	Vanessa ENTILE	DNA Analysis	Closed Approved	Compliment/Praise	24/04/2008
[redacted]	No Title Provided	A compliment was received from Inspector Darren Sargood, Metro North region of QPS. He was appreciative of our efforts regarding a particularly violent case ([redacted] and the short turnaround time we were able to provide to QPS. Inspector Tony Carstensen, officer in charge of the DNA Unit, also passed on his appreciation for our efforts in this case. Results of our testing produces more leads for the investigative team to follow up on.	Cathie ALLEN	Evidence Recovery and Quality	Vanessa ENTILE	DNA Analysis	Closed Approved	Compliment/Praise	24/04/2008

OQI Number	Title	Subject	Creator	Created Organisational Unit	Actioner	Actioned Organisational Unit	Status	Source of OQI	Date Added
[redacted]	No Title Provided	A written compliment has been regarding Case [redacted] This case involved the murder and rape of a woman in Gladstone. Numerous samples were received for this case on a number of different dates and required short turnaround times on each subsequent delivery. This required the DNA Analysis team to work efficiently and effectively with each other and also our client, QPS. Samples were examined, processed and uploaded to the National Criminal Intelligence DNA Database within a timeframe that allowed our client to be able to process the results and execute an arrest warrant. A large number of DNA Analysis staff were required to cooperate with each other and work out of core business hours. The Officer in Charge of the DNA Unit of QPS passed on his appreciation for not only the quick turnaround times but also for the handling of the case and the excellent communication skills displayed by the Case Scientist in a very complex case. Appreciation also came from the lead Forensic Officer and Investigating Officer.	Cathie ALLEN	Evidence Recovery and Quality	Greg SMITH	Public Health Virology	Closed Approved	Compliment/Praise	7/05/2008
[redacted]	No Title Provided	Correspondence received by Detective Superintendant, Homicide, QPS. This emails follows my telephone conversation today concerning the newspaper article at page 17 of the Courier Mail on Friday 27 June 2008. I would appreciate if you could pass on to the relevant sections including Vanessa Ientile, DNA Analysis Manager that State Crime Operations Command and in particular the Homicide Investigation Unit has no issue with the John Tonge Centre relating to any of the matters referred to in the article that are being investigated by the Homicide Investigation Unit. Detective Chief Superintendent Condon requested that I assure the staff at that centre that he was pleased with the assistance being provided in relation to those investigations. The Homicide Squad continues to enjoy a good relationship with the John Tonge centre staff and appreciates the significant assistance provided. Whilst the origin of the story is not known I regret the tenor of the article.	Vanessa IENTILE	DNA Analysis	Vanessa IENTILE	DNA Analysis	Closed Approved	Compliment/Praise	3/07/2008

OQI Number	Title	Subject	Creator	Created Organisational Unit	Actioner	Actioned Organisational Unit	Status	Source of OQI	Date Added
[redacted]	No Title Provided	S/Const M BUCKLE and A/S/Sgt Steve SLADE delivered SOC on the 30/09/08. During the process he described Property Point as being like a 'Well-Oiled Machine' and that service was very prompt and efficient.	Tyson KLEIDON	Quality and Projects	Danielle VAN HEERDEN	Property Point	Closed Approved	Compliment/Praise	30/09/2008
[redacted]	Compliment from QPS on work conducted on DVI matter	QPS Senior Sgt Scott McLAREN, and as part of a 'group thankyou' from Inspector Paul BAKER, and State Coroner Michael BARNES on the work conducted by the DNA Analysis laboratory, in particular the DVI scientists, in reponse to the Mackay car crash DVI (8 February, 2009). The three emails are copied below. Justin, I realise that you received this email, but I wanted to add to the sentiments of Paul in thanking yourself, Ingrid, Tim and I believe Angelina for all the time and effort they have put into getting these identifications completed. Without the support of DNA Analysis during these incidents, this process would be significantly harder. Please pass on my thanks to your team. Scott Scott McLaren Acting Senior Sergeant Quality Management Officer DNA Management Unit Forensic Services Branch Operations Support Command Queensland Police Service All, About 2.50pm on Sunday 8 February 2009 a two vehicle motor vehicle crash occurred on the Bruce Highway some 5 kilometres South of St Lawrence. This resulted in the death of 5 foreign nationals whose bodies were extensively incinerated. Late yesterday afternoon a DVI Identification	Justin HOWES	Forensic Reporting and Intelligence	Cathie ALLEN	DNA Analysis	Closed Approved	Compliment/Praise	3/04/2009
[redacted]	QPS praise	Comment was made during telephone conversation with scientific T'ville that he was very impressed with some of the results that have been coming back for one of his big cases. He was plesently suprised that we had been obtaining DNA profiles successfully from what appeared to be very low DNA sources such as brush marks and hand/fingerprints	Sharon JOHNSTONE	Forensic Reporting and Intelligence	Justin HOWES	Forensic Reporting and Intelligence	Closed Approved	Compliment/Praise	18/09/2009
[redacted]	Praise for liaison work	For case no. [redacted] the Investigating Officer made a special point of passing on thanks to Polly Williams for her liaison work. He said that it was a pleasure working with her and that her work in liaison was excellent.	Justin HOWES	Forensic Reporting and Intelligence	Andrea NORTON	Scientific Services Liaison Unit	Closed Approved	Compliment/Praise	20/10/2009

OQI Number	Title	Subject	Creator	Created Organisational Unit	Actioner	Actioned Organisational Unit	Status	Source of OQI	Date Added
[redacted]	Compliments from DNA Analysis Unit's major client.	The DNA Analysis Unit has received 2 compliments from the Queensland Police Service regarding the reduced turnaround times for results. Compliments have been in relation to turnaround times that have been achieved since the focus has been been on samples submitted after the 1st of September 2009 (considered 'real time' samples). One compliment was from a Regional Forensic Coordinator from a Northen Region and the other compliment was from an Assistant Commissioner for a Brisbane Region. The timeliness of results has meant recent offences are being dealt with more promptly due to intelligence QPS have received from the DNA Analysis Unit.	Cathie ALLEN	DNA Analysis	Greg SHAW	Forensic and Scientific Services (FSS)	Closed Approved	Compliment/Praise	7/04/2010
[redacted]	Qld Public Sector Award	A joint submission by Qld Police Service and DNA Analysis in the category of 'Best Practice in State Government' at the Institute of Public Administration Australia Qld Public Sector Awards was successful. It was awarded on 09 Sept, 2010.	Justin HOWES	Forensic Reporting and Intelligence	Justin HOWES	Forensic Reporting and Intelligence	Closed Approved	Compliment/Praise	10/09/2010
[redacted]	Compliment from Client on Testing and Statement production for Trial	Additional exhibits and reference samples were submitted to DNA Analysis, for urgent testing for a Trial matter. These items were tested and reported within 5 working days of receipt. The Statement was able to be used by the Prosecutor in the Trial matter.	Cathie ALLEN	DNA Analysis	Cathie ALLEN	DNA Analysis	Closed Approved	Compliment/Praise	8/11/2010
[redacted]	Compliment from North Coast Region of the QPS	Insp Carstensen passed along an email from Insp Artie Van Panhuis, Regional Forensic Services Coordinator of the North Coast Region. The email highlighted that the officers were sincerely appreciative of the results achieved and their timeliness through a prolonged investigation for Operation Juliet Solstice [redacted]	Cathie ALLEN	DNA Analysis	Greg SHAW	Forensic and Scientific Services (FSS)	Closed Approved	Compliment/Praise	3/06/2011

OQI Number	Title	Subject	Creator	Created Organisational Unit	Actioner	Actioned Organisational Unit	Status	Source of OQI	Date Added
[redacted]	Compliments on the rapid turnaround time of Missing Person Case	The Coroner from the Northern Coroners Office, the Senior Director and the Chief Pathologist, all passed along their thanks to the DNA Analysis Unit for the rapid turnaround time for a case involving skeletal remains. The skeletal remains were received by the lab on Monday, 6th of June and the report was provided to the Coroner on the afternoon of Friday, 10th of June. Turnaround times for skeletal remains cases are sample dependent and in this case, the remains provided a DNA profile in the first instance. The Coroner was able to release his findings on the afternoon of Friday, 10th of June. The conclusion of this case was truly appreciated by all involved [redacted]	Cathie ALLEN	DNA Analysis	Greg SHAW	Forensic and Scientific Services (FSS)	Closed Approved	Compliment/Praise	10/06/2011
[redacted]	Praise for quick TAT	An urgent FTA sample was received to be profiled and loaded to the NCIDD. The turnaround time from receipt to loading on NCIDD occurred within 24 hours. An email of appreciation from A/Insp Scott McLAREN on 6 July was received for the rapid response to the request. I passed on appreciation to DNA Analysis.	Justin HOWES	Forensic Reporting and Intelligence	Cathie ALLEN	DNA Analysis	Closed Approved	Compliment/Praise	20/07/2011
[redacted]	Appreciation for a fast turnaround time on items from an Assault case	The Regional Forensic Services Co-ordinator (RFSC) from the North Coast Region, Insp Artie Van Panhuis, provided feedback on [redacted] He passed on his sincere thanks for the speedy results and our invaluable support. The case was a vicious assault case in his region. A 5 day TAT was requested for the items. Four items were delivered at 8.30am on the 21st of July 2011, and three items had final results forwarded electronically to QPS at about 11am on the 26th of July (3.5 business days to achieve results). The fourth item's results were forwarded on the morning of the 28th of July (5.5 business days), however this was a sample that required concentration and QPS were made aware of this. It was excellent to receive this positive feedback.	Cathie ALLEN	DNA Analysis	Greg SHAW	Forensic and Scientific Services (FSS)	Closed Approved	Compliment/Praise	1/08/2011

OQI Number	Title	Subject	Creator	Created Organisational Unit	Actioner	Actioned Organisational Unit	Status	Source of OQI	Date Added
	[redacted] Praise for excellent turnaround times for an Urgent Major Crime case	Carstensen, DNA Management Section praising the 'excellent turnaround time and result for an Urgent request' [redacted] The offence occured in Insp Van Panhuis's (Regional Forensic Service Co-ordinator) North Coast Region and he passed on his sincere thanks regarding the result and turnaround time for the item. Insp Carstensen then went on to say that he 'fully endorse those sentiments. There have been some excellent examples recently that demonstrate that this process is working well, both in turn around times and resuls and this is having a real and significant impact in assisting operational police in their investigation of crimes.' The 2 items were received at Property Point at 15:23 on Friday, 20th of April 2012. Interim electronic results were released to the QPS at 11:51 on Thursday, 26th of April (noting that the 25th of April was a public holiday). Link results were released to the QPS at 12.22 on Thursday, 26th of April. The turnaround time for these items was 3 working days, which is what the QPS requested for all items in July 2008. This highlights that all staff have continued to work towards meeting the	Cathie ALLEN	DNA Analysis	Greg SHAW	Forensic and Scientific Services (FSS)	Closed Approved	Compliment/Praise	2/05/2012
	[redacted] Praise for Cold Case work	Certificate of Appreciation given to Thu Nguyen for his assistance and support to the Homicide Investigation Unit of QPS from 2009-2013. Quote: 'Your tenacity and dedication to Homicide Cold Case Forensic Review is highly commendable and your work greatly assisted in the progressing of Cold Case Homicides'.	Justin HOWES	Forensic Reporting and Intelligence	Justin HOWES	Forensic Reporting and Intelligence	Closed Approved	Compliment/Praise	13/08/2013

OQI Number	Title	Subject	Creator	Created Organisational Unit	Actioner	Actioned Organisational Unit	Status	Source of OQI	Date Added
[redacted]	Compliment - Presentation to new QPS Scientific Staff	S/Sgt Jamie Cook requested prenestations from Forensic DNA Analysis and Forensic Chemistry for new QPS Scientific staff. Jamie provided the following positive feedback after the presentation: Gentlemen, Thank you both very much once again for sharing your time and expertise on Wednesday! Your presentations were wonderfully tailored to meet our students? needs and I know they gained a lot from the content of the lectures, your personal insight and also the tours of your facilities. I appreciate the numerous demands on your time and thank you for making yourselves available for our benefit. Cathie, thanks again for providing two of your finest to enlighten our new staff. Kind regards, Jamie Jamie Cook Senior Sergeant Scientific Section Training / QAO / Admin Forensic Services Group Operations Support Command Ph: [redacted] Email: [redacted]	Luke RYAN	Analytical	Cathie ALLEN	Police Services	Closed Approved	Compliment/Praise	13/11/2015
[redacted]	External praise - Forensic DNA Analysis	An urgent FTA sample was received for [redacted] on 15 December, 2016 with a DNA profile obtained, compared to the case, and a result reported to QPS on 16 December, 2016. An email from A/Supt Scott McLaren was received on 16 December, 2016: Cathie, Justin and Paula. I would like to personally pass on my sincere thanks and appreciation for the outstanding response provided to this priority request. I continue to be in awe of the commitment and passion of your staff in advancing active and cold case investigations. Paul, this is an excellent example of the positive symbiotic association that exists between the DNA Management Section and Forensic DNA Analysis. I look forward to extending these cooperative arrangements to our property, reception and liaison teams. Scott McLaren Acting Superintendent	Forensic Services Group	Queensland Police Service [redacted] Ph: [redacted] M: [redacted] Email: [redacted]	Justin HOWES	Forensic Reporting and Intelligence	Cathie ALLEN	Police Services	Closed Approved	Compliment/Praise	16/12/2016

OQI Number	Title	Subject	Creator	Created Organisational Unit	Actioner	Actioned Organisational Unit	Status	Source of OQI	Date Added
[redacted]	Appreciation of work done for [redacted]	of FSS DNA Analysis) gave evidence in Supreme Court in Brisbane in relation to the matter of R vs Newlove. The following email was received by Kylie Rika from Detective Senior Constable Kevin Mawdsley on 14 March 2018: Good morning, On Monday 12 March 2018, Christopher Brian NEWLOVE was found guilty of murder in the Brisbane Supreme Court. The jury deliberated for approximately 3 hours (including lunch break) and asked for clarification on one issue relating to intent. NEWLOVE?s conviction for murder finalises the investigation of Paul Thomas HERON?s death, which occurred on 6 March 2015, at unit 6/126 Gladstone Road, Highgate Hill. Thank you to everyone on this email for your efforts throughout this process, from the initial investigation at the scene, door knocks, witness statements, and the massive amount of forensic testing and analysis which occurred. The level of commitment from everybody to bring this matter to trial cannot be understated. To those people who were required to give evidence at the trial last week, please accept my personal thanks for the evidence each of you gave. I am very	Kylie RIKA	DNA Analysis	Justin HOWES	Forensic Reporting and Intelligence	Closed Approved	Compliment/Praise	14/03/2018
[redacted]	Praise for work conducted - FSS	An email was received, praising the work of Forensic and Scientific Services for the assistance to QPS in achieving an arrest in a 1983 Cold Case (Operation Dolphin).	Justin HOWES	Forensic Reporting and Intelligence	Justin HOWES	Forensic Reporting and Intelligence	Closed Approved	Compliment/Praise	22/08/2018
[redacted]	Praise for work conducted - FSS	An email of praise for work conducted was received from QPS on 3 August 2018 for a 1996 case [redacted] where FSS provided an exceptional service.	Justin HOWES	Forensic Reporting and Intelligence	Justin HOWES	Forensic Reporting and Intelligence	Closed Approved	Compliment/Praise	3/08/2018
[redacted]	External compliment to Forensic DNA Analysis from Cold Case Unit	Email received by Justin Howes from Cold Case Investigation Team (Homicide Group) on 7 August, 2019 detailing appreciation for team's efforts in assisting this unit: Justin, I was just discussing with Thomo that I would like a ?Thank you? button on the FR so I can quickly respond with my appreciation for the info you send over without sending you back another request that you then have to make disappear. Please accept this email as my unending thanks for all the little things and the responses that you guys provide, to both you and your staff. ?? Cheers. Dale	Justin HOWES	Forensic Reporting and Intelligence	Cathie ALLEN	Police Services	Closed Approved	Compliment/Praise	7/08/2019

OQI Number	Title	Subject	Creator	Created Organisational Unit	Actioner	Actioned Organisational Unit	Status	Source of OQI	Date Added
[redacted]	Compliment for work performed in Forensic DNA Analysis	Two complimentary emails were received on 22/08/2019 for [redacted] Emails from S/Sgt Ewen Taylor and S/Sgt Greg Smith thanking the efforts of Forensic DNA Analysis. Matter resolved in Supreme Court.	Justin HOWES	Forensic Reporting and Intelligence	Justin HOWES	Forensic Reporting and Intelligence	Closed Approved	Compliment/Praise	23/08/2019

CA-119

NIFS KEY PROJECT

End-to-End Forensic Identification Process Project

END-TO-END FORENSIC IDENTIFICATION PROCESS PROJECT

Volume Crime

REPORT

Australia New Zealand Policing Advisory Agency
National Institute of Forensic Science
(ANZPAA NIFS)

This report has been produced for the ANZPAA Board and written by Senior Sergeant First Class Cheryl Brown APM, South Australia Police

It shows the aggregate findings and key recommendations arising from the national End-to-End Forensic Identification Process Project conducted across the six states and two territories of Australia.





NIFS KEY PROJECT

End-to-End Forensic Identification Process Project

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NIFS KEY PROJECT

End-to-End Forensic Identification Process Project

Foreword by Alastair Ross

In March 2010, the ANZPAA Board gave approval to *'review the end-to-end forensic processes and develop a national framework for efficient crime scene analysis'.* Following some initial ground work, South Australia Police agreed to second Senior Sergeant First Class Cheryl Brown to the project as the full time Project Officer and this was of significant benefit.

The project was based on the Scientific Work Improvement Model (SWIM Report) conducted in the UK with the key aim to identify bottlenecks and inefficiencies across the end-to-end process and to make recommendations as to how these might be addressed. To this end, the study benchmarked current forensic processes and performance from which the recommendations contained in this report were made.

The study was limited in that it concentrated only on burglary offences and on samples collected for DNA and fingerprint analysis. However, all jurisdictions participated and data was collected for over 8,000 cases nationally. This provided a wealth of data for analysis and some significant results. The project is very much about learning from the best performers and how this learning might be implemented across all jurisdictions. This has the potential to improve efficiency at each stage of the forensic process and result in a more rapid response to criminal investigations.

The report makes recommendations for further aspects of the study to be considered by the Board.

I acknowledge the work conducted by Senior Sergeant First Class Cheryl Brown and the statistical analysis conducted by Ms Robyn Attewell and Professor Michael McFadden which was supported by the Australian Federal Police.

I have pleasure in submitting the report to the Board for consideration.

Executive Summary

During 2011 ANZPAA NIFS, working in partnership with the eight Australian police agencies and a number of relevant DNA Laboratories, conducted a study into the performance of participating sites with regards to the end-to-end processing of volume crime. The study titled 'End-to-End Forensic Identification Process Project' aimed to benchmark current performance specifically for the crime type of burglary and evidence types of fingerprints and DNA. End-to-end processing was defined in this project as the time from the report of a crime through to the arrest of an offender. The process was broken into five distinct stages: attendance, submission, analysis, identification and investigation. This report provides an overview of the project, its findings and recommendations.

Based on data collected from 17sites across Australia for more than 8,000 burglaries reported over a five month period, this study has established that:

- higher arrest rates were achieved for cases where crime scene investigators (CSI) attended and forensic evidence was collected.
- there is wide variation between state jurisdictions across each stage of the forensic process, both in terms of success and lead times.
- 70 percent of burglaries reported to police were attended by CSI with a median response time of 4 hours and a median time spent at the scene of 30 minutes.
- regional areas had higher attendance rates and longer scene examination times than metropolitan areas.
- there was more fingerprint evidence collected compared with DNA (28% vs. 10%). However, there was a higher arrest rate based on DNA identification than fingerprint identifications (50% vs. 37%).
- identification rates were the same for both fingerprints and DNA (23%), although when metropolitan and regional data is compared, it becomes apparent that regional areas achieved higher identification rates through fingerprints.
- at each stage of the end-to-end process, lead times were shorter for fingerprint evidence than DNA evidence, which resulted in a median overall end-to-end process time of 19 days for arrests based on fingerprint identifications compared with 49 days for arrests based on DNA identifications only.
- overall when considered together forensic evidence achieves an end-to-end process time of 29 days.
- analysis and identification lead times tended to be shorter in metropolitan areas than regional areas, particularly with regards to DNA. The longest lead times were for the last stage of the process from identification to arrest.

From consideration of data from a stage by stage basis, there was no consistent evidence to suggest that strong performance at one stage of the process resulted in strong performance for another stage of the process or that there was a link between stages with regards to performance (i.e. for a site that performs well with regards to number of scenes attended does not link to high performance with regards to arrest rates). There was statistically significant variation across the jurisdictions, even in the latter stages where there was less data available to analyse, indicating a potential scope for improvement across all stages of the forensic process. However, as each police agency operates under different legislation and internal

practices vary, it is understood that different strategies may be required in each jurisdiction to improve performance in processing burglary cases.

Table A: Success rates and lead times across the five stages of the forensic process aggregated from 8,179 reported burglary cases in 17 sites across Australia, 2011.

Stage	Success rate*		Lead time (median)	
	Fingerprint	DNA	Fingerprint	DNA
Attendance	70%		4 hrs (and 30 minutes at scene)	
Submission	28%	10%	Same day	5 days
Analysis	100%	98%	1 day	3 days
Identification	23%	23%	Same day	15 days
Arrest	37%	50%	11 days	20 days
End-to-end	2%	1%	19 days	49 days

*success refers to progression to the next stage

Crime Scene Attendance

- 70 percent of burglaries reported were attended by CSI, with statistical variation between the jurisdictions (44% to 83%) and by location (68% to 74%).
- While the attendance lead time nationally is 4 hours, there is statistical variation between jurisdictions (1 hour to 14 hours) but no variation by location.

Evidence Submission

- In 28 percent of scenes attended, fingerprint evidence is collected, with statistical variation between the jurisdictions (17% to 55%) and in 10 percent DNA evidence is collected, again with statistical variation between the jurisdictions (2% to 64%).
- Submission of fingerprint evidence is largely electronic for Australian police agencies and as such, fingerprints are submitted within 24 hours on a consistent basis, a fact that is supported by the fingerprint submission lead time data of same day for this study. The site with the shortest lead time for submission of fingerprint evidence utilises remote image transmission from crime scene to fingerprint bureau.
- Statistical variation still existed between the jurisdictions for submission of fingerprint evidence (0 to 6 days).
- The submission of DNA evidence across the sites surveyed is a manual process requiring physical transportation to the laboratory. As one would expect, where CSI work from the same location as the DNA laboratory, the DNA submission lead time is the shortest.
- The national lead time for submission of DNA evidence is 5 days with statistical variation between jurisdictions (0 to 13 days).

Analysis of Evidence

- In 100 percent of cases, fingerprint evidence submitted for analysis was analysed, yet with statistical variation between the jurisdictions (97% to 100%).
- In 98 percent of cases, DNA evidence submitted for analysis was analysed with statistical variation between the jurisdictions (82% to 98%).

- DNA has longer lead times than fingerprints at the analysis stage particularly for regional sites (3 days as opposed to 1 day).
- Cases with evidence more likely to result in an identification may be prioritised and as such have shorter analysis times. This fact may go towards explaining the shorter lead times for metropolitan DNA cases.
- Overall, 87 percent of fingerprint evidence analysed resulted in a print suitable for upload to the National Automated Fingerprint Identification System (NAFIS) database, compared to only 42 percent of DNA evidence being found suitable for upload to the National Criminal Investigation DNA Database (NCIDD).

Identification

- The overall identification rate for both fingerprints and DNA was 23 percent but there was statistical variation between the jurisdictions with greater variation observed for DNA (fingerprints 10% - 35% and DNA 5% to 53%).;
- There are higher identification rates in fingerprints at regional sites as opposed to metropolitan sites, but no difference for DNA by location.;
- There are significantly longer lead times for DNA identification than for fingerprints. The quality assurance process for DNA identifications may go towards explaining this trend.

Investigation

- For cases in which identification of an offender was made from fingerprint evidence, 37percent resulted in the arrest of the offender. Comparatively, for cases in which identification was made from DNA evidence, 50 percent resulted in an arrest.
- There is significant variation for arrest rates between jurisdictions, with more variation for DNA identifications than for fingerprint identifications (fingerprints 22% to 63% and DNA 21% to 71%).;
- There is no difference by location for both identification rate and lead times.;
- There are longer lead times for DNA based arrests than for fingerprint based arrests and significant differences between jurisdictions for both DNA and fingerprint based arrests (fingerprints 8 to 38 days and DNA 5 to 123 days).;
- The lead time for investigation (i.e. the time from identification to arrest) was longer than the lead time for all other stages put together.

Other Factors

- Jurisdictions with mature NAFIS and NCIDD databases had a greater ability to identify a suspect through the analysis of forensic evidence.;
- Jurisdictions with low rates of identification should consider expanding the scope of law enforcement procedures and legislation to increase the number of reference samples uploaded into the NAFIS and NCIDD databases.

Future Recommendations

This project has not only provided an appreciation of the forensic performance within Australia but has provided an indication of the scope of evaluation that could be carried out.

The project team has made a number of recommendations, including conducting jurisdictional based workshops to examine the findings of this study in detail, identify where improvements could be made and post making changes, conduct a second snapshot study to determine if the changes had a positive impact on performance for the end-to-end forensic process.

Introduction

Background

Although police investigations have traditionally been considered a single process that commences with the report of a crime and ends in the arrest of a suspect, it is in fact possible to consider the process in a number of distinct stages. Each of these stages is performed by a range of personnel performing specific duties, including those performed by general and specialist police officers and scientists.

Property crime has a significant impact on society due to the level of invasiveness of the crime and the effect on the lives of victims (1). Home and business burglaries drastically reduce personal security, peace of mind, and well-being, and the psychological and emotional cost to the victims and potential victims may be much higher than the dollar value. The societal cost of property crime is often underestimated by only evaluating the property value and conversely, the benefit to society in solving volume crime is probably immeasurable.

High property crime rates reflect the low risk of being caught and the relative ease for criminals to commit this type of crime (1). It has been estimated that an average of 38 burglaries are committed per burglar per year and a prolific burglar can commit up to 242 per year. A habitual burglar is an opportunistic criminal who commits not only burglaries but all other types of property crimes including theft of motor vehicles and larcenies (1&9).

It is clear that expediency in the investigation of these crimes and action against these criminals is the key to having a significant impact on the crime rate. Delays in identification and investigation means offenders are likely to be committing further offences during that time. This is little consolation for a victim when it is realised that if the DNA samples had been processed more quickly, the offence committed against them may not have occurred (9).

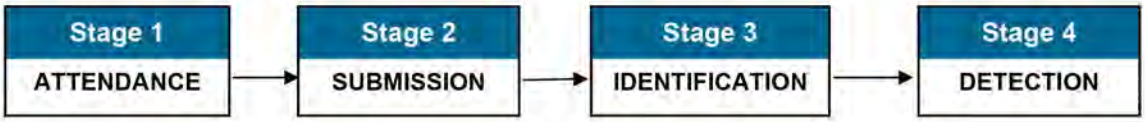
There have been a range of studies performed internationally to evaluate the effectiveness of forensic evidence in an investigation and the associated cost benefits. These reports, particularly from the United Kingdom (UK) Scientific Work Improvement Model (SWIM) report (2), have clearly highlighted the variation of performance at the organisational, work group and individual level. There is anecdotal evidence that the same is true in Australia and as such a need was identified to capture and study relevant data and develop models that would lead to more uniform and improved performance.

The key message from the SWIM report was the need to identify significant leakage points in the process and that systems should be developed to capture and compare relevant data and learn from top performers. The Australia New Zealand Policing Advisory Agency National Institute of Forensic Science (ANZPAA NIFS) End-to-End Forensic Identification Process Project has sought to benchmark current forensic business processes and identify optimal performance to apply as a national model by identifying areas for improvement.

United Kingdom Scientific Work Improvement Model (SWIM)

During 2002 and 2003, the Police Standards Unit piloted a simulation-enabled performance improvement approach for forensic science in Derbyshire Constabulary. The project made recommendations that when implemented, led to increased forensic identification and detection and reduced the end-to-end lead time for forensic led detections (2). The work identified a direct correlation between the time taken from crime occurrence to forensic led detection (lead time) and crime levels. Reducing the lead time can reduce the level of crime. The swiftness of identifying suspects undoubtedly contributed to these forces' overall efforts to reduce crime (2).

The SWIM program of work was developed to replicate the above pilot study and provide a mechanism for implementing performance improvement recommendations to police forces across the UK. The program was the most comprehensive ever performed, running over a two-year period and involving forty-one forces looking at the police and scientific functions in England and Wales. The program focused on the attendance at burglary and motor vehicle theft offences, involving the recovery of DNA and fingerprints and their subsequent use in investigations. The SWIM Report examined four main stages to this process and evaluated the lag time between each of the phases and the success of the case to move through to the next stage.



At each stage, the result was calculated as the proportion of transactions that were transferred to the next stage (2). The lead time was calculated, for each crime report as the earliest activity date at each forensic process stage (2). The success rate was calculated as the percentage of cases that successfully moved to the next stage. The SWIM Report collected data over a 12 month period.

The SWIM Report made 21 common recommendations and 346 force specific recommendations for improvement at all stages of the forensic process.

Denver Colorado Study

In 2004, Denver applied for federal funding to evaluate the effectiveness and cost of DNA technology on high volume crimes such as burglary, auto theft and theft from motor vehicles (1). This study was primarily focused on evaluating the effectiveness of DNA in property crimes and the cost efficiencies realised.

During the target period, 6,538 burglaries were committed in the City and Country of Denver. 400 of these burglaries contained potential biological evidence and were selected for the study as DNA testing was performed as part of the investigation and prosecution of the cases. All 400 cases were analysed, resulting in 340 DNA profiles being obtained and uploaded into the Combined DNA Index System (CODIS DNA database). At the time of publication, the work resulted in 199 CODIS hits. 172 cases were accepted by the Denver District Attorney's Office for prosecution, from which 77 cases were based on CODIS offender hit identification (of

these, 40 were habitual offenders with more than three prior felony convictions) and 53 on new offenders identified only by DNA profiles developed from the evidence left at the crime scene. Only 24 percent of these cases were filed for prosecution based on detection by traditional investigation, yet over 76 percent were filed based on the DNA analysis. The 40 habitual offenders were only arrested due to the DNA evidence located and combined, if not arrested these offenders would have committed an estimated 9,680 crimes within that year.

The study found that aggressive use of advanced DNA forensics in investigation and prosecution resulted in a pronounced reversal in property crimes compared to similar metropolitan areas in the United States, demonstrating the effectiveness of this approach (1). The study went on to demonstrate that much harsher sentences in DNA CODIS hit burglary cases were given to high volume, habitual offenders whose criminal activity had a higher impact on society.

The study further reported that a total of 491 burglaries committed in 2006 files were accepted for prosecution (both traditional based investigations and DNA based investigations). 130 of these cases were based exclusively on the results of DNA analysis of evidence. The rate of prosecution for cases with traditional investigation and no biological evidence was 5.9 percent. The rate of prosecution for burglaries with some type of biological evidence was 32.5 percent, which is an almost 5.5 fold increase in the rate of case prosecution.

The study further conducted a cost benefit analysis and found that the return on investment for every dollar spent with this approach was estimated to be $90 with an actual two year savings to the citizens and the city of Denver of more than $5 million in police costs and $36.8 million in property loss.

The Denver Colorado study recommended an expansion of DNA science in high volume crimes based on the high success rate for prosecution and the value for money return on investment.

New Zealand – Waikato District and Environmental Science and Research: Forensic (ESR Forensic) DNA Project 2010

New Zealand (NZ) Police also reviewed the SWIM Report and as such established the Forensic Work Improvement National System 'FORWINS' to act as a robust case management system designed to capture, monitor and report on all aspects of forensic investigations. At the time of this project, due to IT limitations, 'FORWINS' had not realised its full potential.

In mid-2010, the Waikato Police District in association with ESR Forensic ran a 3 month trial designed to monitor the implementation of quicker turn-around times by ESR Forensic and police for DNA submissions from volume crime scenes. The evaluation was based on the capability of ESR Forensic to implement a 5 working day turn around on volume crime submissions.

17 weeks of data was collected providing information to assess the value of the forensic submissions being made in terms of their likelihood to produce a profile and the value of those links to investigators. Data were also collected relating to the type of crime scene samples

submitted by the Waikato Police District to the ESR Forensic for the purpose of assessing the return on investment.

As a result of the 2010 Waikato DNA Project, there has been a stark improvement in turn-around times by ESR Forensic which significantly increased the value of the forensic results to Police. The prioritising of District volume crime DNA collection and submission and the actioning of forensic identifications has made a significant contribution to volume crime reduction.

The Waikato Project concluded and recommended:

- ESR Forensic Volume Crime Laboratory averaged 5.4 days turnaround time from receipt to result in the laboratory for 78 percent of Waikato submissions over the 3 month trial period, improving significantly on the previous 4 week turn around.
- ESR Forensic has a new contract with New Zealand Police requiring 80 percent of submissions to the Volume Crime Laboratory to be completed in 5 working days, which was demonstrated as achievable through the trial period.
- An increased focus on the importance of the timeliness of DNA sample submissions in the Waikato Police District has seen a reduction in the submission lag from an average of approximately twenty days to six days.
- By ensuring attendance within the same day as a crime is reported, Scenes of Crime Officers (SOCO) were able to see the added value of their forensic results and the effect of their timely response on the current crime environment.
- Investigators identified the benefits of working with rapid identifications both in the potential to recover property and to prevent future offending. Identifying current 'hot' offenders and then applying a targeted approach saw gains in disrupting and influencing the current crime patterns.
- Recommendation of funding and prioritisation for 'FORWINS' and the development of a robust system for the collection and monitoring of forensic data.

The End-To-End Forensic Identification Process Project

Approach

The End-to-End Forensic Identification Process Project (referred to hereafter as the 'End-to-End Project') was developed with a commitment to foster efficiency, effectiveness, continuous improvement and innovation as per the Australia and New Zealand Policing Directions.

The End-to-End Project is a reflection of all four Australia New Zealand Policing Directions (2008-2011), with a strong focus on the community and developing an approach to crime reduction and community safety through operational interoperability between jurisdictions, police agencies and partners (12).

In May 2010, the End-to-End Project was endorsed by the ANZPAA Board. The project was managed and supported by ANZPAA NIFS and consequently was established as an ANZPAA

NIFS Strategic Priority to *'review end-to-end forensic processes and develop a national framework for efficient crime scene analysis'*.

The key objectives were to develop a framework to capture and compare data, to develop a simple performance management model and to develop a national model for the end-to-end forensic process that would provide for maximum efficiency and effectiveness.

Australia 2010 – 2011

	Population	% total Population	Burglaries	% total Burglaries	Burglary rate/100,000
Australia	22,620,600	100%	209,410	100%	925
New South Wales	7,303,700	32%	57,550	27.5%	787
Victoria	5,624,100	25%	44,600	21.3%	793
Queensland	4,580,700	20%	43,024	20.5%	939
Western Australia	2,346,400	10%	35,547	17.0%	1514
South Australia	1,657,000	7.3%	17,577	8.4%	1060
Tasmania	510,600	2.3%	3,802	1.8%	744
Australia Capital Territory	365,400	1.6%	3,464	1.7%	948
Northern Territory	230,200	1.0%	3,846	1.9%	1670

Australian Bureau Statistics March 2012
Police Annual Reports 2010-2011

In November 2010, a small project team was established that consisted of Assistant Commissioner Julian Slater, National Manager Forensic and Data Centres, Australian Federal Police (AFP) as the Senior Project User, Mr Alastair Ross, Director ANZPAA NIFS as the Project Executive and Senior Sergeant First Class Cheryl Brown of South Australia Police as the full time ANZPAA NIFS Project Officer.

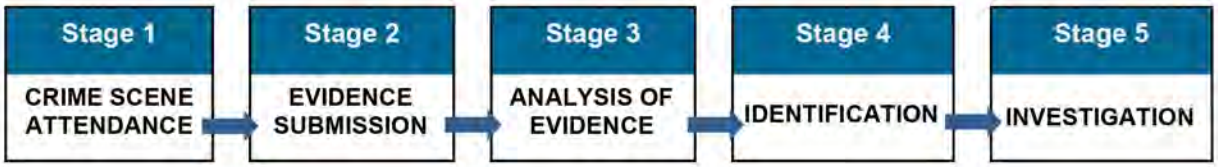
The nature of the project was such that expertise in data analysis was required and the project team was expanded to include Professor Michael McFadden of McFadden Consultancy and Ms Robyn Attewell, Coordinator Performance Analysis, AFP.

Project Scope

The project was originally formulated to follow the methodology applied in the SWIM Report, utilising the same four phases, the same evidence types (DNA and fingerprints), the same crime types (burglaries and motor vehicle theft) and the same measures (lead time and success rate). After further evaluation, however, it was decided to limit the crime type to burglary related offences. This did not overly restrict the scope of the conclusions and made the data collection more straightforward.

Unlike the UK, Australia had not conducted any other national studies of this nature, therefore it was anticipated that there would be significant challenges, particularly with respect to efficient, uniform data collection. Keeping to one crime type would reduce the impact on the officers collecting and collating the data. Burglaries include residential and non-residential premises and represent a significant proportion of the volume crime reported to police each year.

The project team agreed to implement the basic methodology of the SWIM Report and incorporate an additional analysis stage. The performance measures at each stage are described briefly below.



A reference guide to all relevant terminology used within the project (e.g. identification and investigation) is located in Appendix 1.

Lead Time (Duration)

Lead time refers to the time interval between each stage. This was determined through the collection of date/time entries for defined points within the five stages. The project could then measure the time taken for a case to move from one stage to another and ultimately the total time taken to move from the beginning of stage 1 to the end of stage 5.

Success Rate (Proportion)

The success rate measures the progress of a case to the next stage. This was determined by the recording of the date/time entry for the next stage. The only variant was at stage 5 where further descriptors were applied to describe the different possible outcomes for the case.

The unit of observation for this study was a case, not an offender. Two or more arrests based on forensic evidence from one burglary scene were only counted as one successful unit or case as the focus was only on the success of the case, not the number of arrests. This was another point of difference from the SWIM methodology.

Stages

Stage 1: Crime Scene Attendance

This stage relates purely to the response by police personnel to the crime scene.

Stage 1 data relates to the time when a crime was reported, the crime scene examination start time and the crime scene examination end time. From this data the project team is able to determine the following three measures.

Attendance Time

The time lapse between the report of the crime and scene attendance by CSI.

The purpose of this measure is to determine the typical lag time between the victim reporting the crime to the police and CSI attending. The time/date entry for the report of a crime was primarily sourced from business service areas within each police agency to ensure correspondence with corporate reporting data.

Overall Scene Attendance

The proportion of scenes attended by CSI.

Police jurisdictions have differing policy in regard to responding to volume crime, therefore, while attendance at all crimes would be preferable, it is not always deemed feasible. The project endeavoured to evaluate whether increased attendance rate had any significant effect on evidence recovery and the overall success of the investigation.

CSI Time at the Scene

The time spent at a scene by CSI.

This measure determines the optimal time required at a crime scene for the most efficient and effective collection of evidence that maximises success rates through all stages of the process. Good quality evidence collection is required to ensure successful analysis, identification and investigation. Having an appreciation of the average time spent at a volume crime scene can assist jurisdictions in resource planning.

Stage 2: Evidence Submission

From stage 2 onwards, the data is separated into fingerprint evidence and DNA evidence. This stage contains data identifying the collection of DNA and/or fingerprints and the date/time entry for submission to the DNA laboratory or fingerprint bureau. For five jurisdictions, the DNA analysis is conducted by a laboratory external to the police and consequently the collation of data from stage 2 onwards required coordination between two organisations.

Submission Lead time

The time lapse between the fingerprint and DNA evidence being collected at the scene and the time it is submitted to the DNA laboratory or fingerprint bureau.

The date/time entry relates to the time the laboratory or bureau records the case as having been received as opposed to the time when the CSI may send the evidence. There may be a lag time in relation to the submission, but this lag time is not calculated separately as it is included in the time that the CSI has control of the evidence.

Collection Rate

The proportion of scenes attended from which fingerprints or DNA are collected and subsequently submitted for analysis.

While not all evidence collected is submitted, the majority of cases where evidence is collected, it was submitted for analysis.

Stage 3: Analysis of Evidence

Stage 3 includes the date and time that analysis of the evidence was commenced and whether the evidence was suitable for upload on the NAFIS or NCIDD.

Both databases have a national standard for upload, which provides the project with a perspective on the suitability of the evidence for analysis. However, each jurisdiction can analyse and conduct comparisons with internal databases or records, outside of the requirements for NAFIS and NCIDD. Therefore identification may still occur even if the evidence is not suitable for upload according to the national standard.

Analysis Lead time

The time lapse between the time the case file was received for analysis and the time the analysis was commenced.

In some jurisdictions the time the case file was received for analysis is also considered the time the analysis was commenced.

Analysis Rate

The proportion of cases that contained evidence that was analysed.

Suitability Rate

The proportion of cases that contained evidence of a standard suitable for upload to a national database.

Stage 4: Identification

Stage 4 relates to the identification of a suspect from the evidence analysed. The identification might occur as a result of a search on the national database or it may result from a direct comparison between the evidence and a suspect.

Stage 4 contains two date/time entries, one referring to the date/time when the identification was made and the second referring to date/time when the identification was forwarded to the investigating officer (IO). The purpose of the two entries was to allow for an evaluation of the time lapse between the achievement of identification and the transmission of that information for investigation.

Identification Lead time

The time lapse between the analysis commencing and the time identification is achieved;

Identification Rate

The proportion of cases that were analysed that resulted in at least one identification.

Stage 5: Investigation

Stage 5 relates to the investigation of a case file pertinent to the identification of a suspect through the forensic process. It is acknowledged that in many cases a suspect may be arrested prior to the commencement or completion of the forensic analysis as a result of normal investigative procedures or as a result of witness involvement. Furthermore, unlike the other stages, an investigator has to physically locate the suspect to take action that is recorded in this stage.

A large range of actions could be taken against a person identified through the forensic process therefore four action types were identified; Charged, Not Charged, Eliminated and No Action. In many cases a person identified through the forensic process can ultimately be eliminated from the investigation as they may be the victim or complainant with legitimate reasons for their fingerprints or DNA being at the scene. Only data indicating the arrest of a suspect subsequent to the identification was included in this analysis.

The ability of jurisdictions to measure this stage was the most problematic of all, as primarily the personnel collating the data were from forensic areas and their ability to source data from the investigative areas was limited.

Arrest Lead Time

Time lapse between the identification was achieved and the time the nominated suspect was arrested or charged.

Arrest Rate

The proportion of cases where identification is achieved and the nominated suspect was arrested or charged..

Stage 1 – Stage 5: End-to-End Performance

Analysis has also been carried out on the overall performance from the report of the crime to the arrest of the suspect as opposed to the stage by stage analysis. This is represented in the overall forensic performance section of the Findings.

The Study

In December 2010 the project officer through a formal letter of request, approached the Senior Managers Australia New Zealand Forensic Laboratories (SMANZFL) requesting participation in the project. All police jurisdictions and their respective DNA laboratories advised of their willingness to participate.

Participating Agencies

It was the intention of the project team to collate data from policing areas around Australia to provide a national forensic performance perspective. The police jurisdictions were asked to nominate a regional and a metropolitan police area from which to collect data. A comparison between the lead time and success rate for regional areas compared to metropolitan areas was considered a valuable aspect of the project.

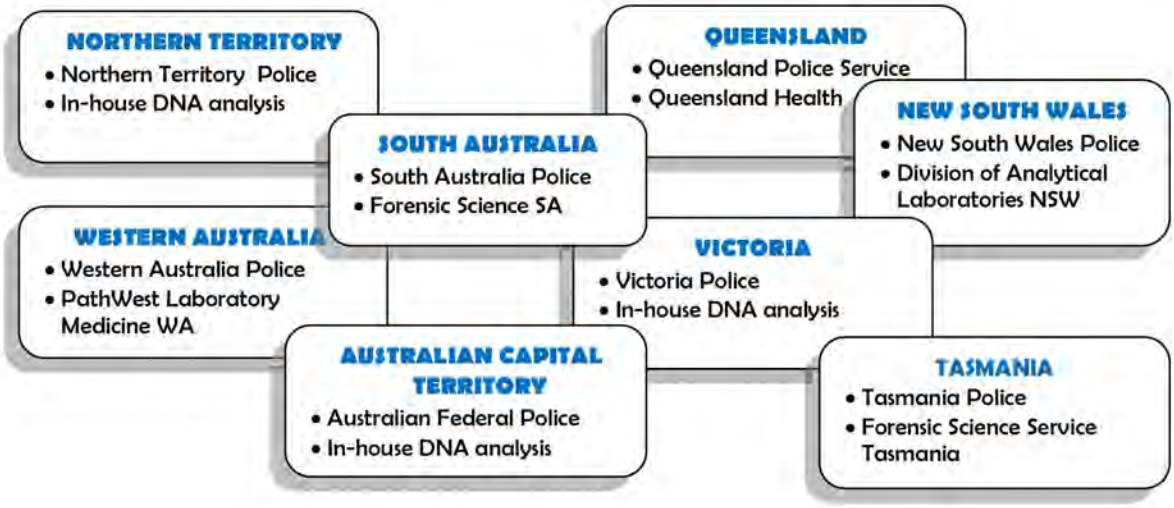
Seventeen policing areas across Australia participated in the End-to-End Forensic Identification Process Project. Of the 17 policing areas, 10 were metropolitan and seven were regional areas. Some jurisdictions utilised police boundaries and provided data from police districts or area commands, whereas some agencies narrowed the field to a defined geographical area.

The population size for the areas ranged from 20,000 in some regional areas to over 340,000 for the largest of the metropolitan sites. This was reflected in the data provided for the respective areas. Likewise the key industries were equally variant including agricultural or residential areas.

All sites had at least one 24 hour police station providing general policing, investigations, criminal justice and crime scene investigation and most contained additional multiple police stations with limited operating hours. Further demographics are located in Appendix 2.

Participating jurisdictions were a combination of police and external forensic laboratories. Fingerprint analysis in all cases is conducted within the police organisations surveyed, whereas in the majority of states the DNA analysis is conducted by an external DNA analysis provider.

The study does not distinguish the external and internal DNA laboratories with regard to performance, as the performance of the DNA laboratory is inclusive of the entire performance for that state or territory.



Contact Officers

Every organisation was requested to nominate a contact officer. In some states there was a contact officer for the police and a contact officer for the external laboratory.

The contact officer performed the following duties:-

- act as a conduit between the organisation and the ANZPAA NIFS Project Officer;
- provide guidance and direction to the participating sites in their state/territory; and
- oversee the collation of the data and completion of the spread-sheet for return to the ANZPAA NIFS Project Officer.

The collation of the data over the data collection period was a significant undertaking by the contact officers who required the assistance of other personnel from a range of areas within their agencies, including business services, Information, Science & Technology (IS&T), fingerprint bureau, DNA laboratory, quality assurance, records management and detectives/investigators.

Data Collection Methodology

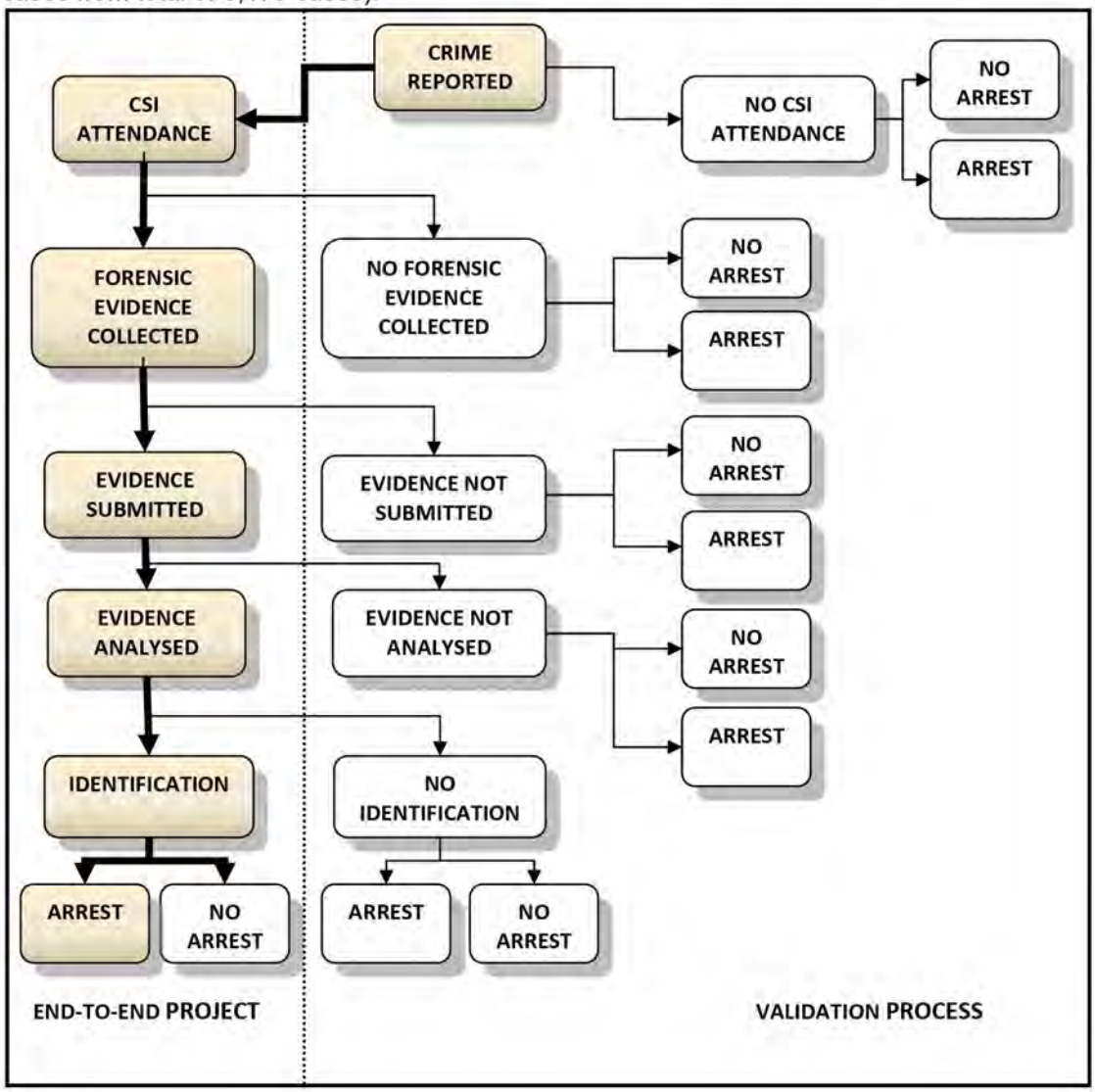
In March 2011 letters were sent to the Commissioners requesting approval for the release of data.

The project collected unit record data at the individual crime level. This enabled both aggregation and statistical modelling.

The additional benefit of having unit data was the potential to make further comparisons on the performance of the individual CSI and to identify trends in the scene examination, evidence collection and submission for each case. Cases were recorded across an Excel spread-sheet requiring date/time entries (dd/mm/yyyy h:min) and information on the success or otherwise of the progress of the case regarding fingerprint and DNA evidence.

Where necessary, comments were added to each stage to explain any anomalies or deviations from the project requirements and to identify at which stage the case was finalised. Data recorded as arrested or charged on the spread-sheet will be referred to as arrested in the Findings.

As per the flow chart, the End-to-End Project only followed up cases through to arrest where there was success at each stage. In a sub-sample of data known as the validation sub-set. all cases were followed up including those for which no forensic evidence was collected (2,418 cases from total of 8,179 cases).



Spread-sheet

A spread-sheet template was created for the purpose of collating the data on a monthly basis. The spread-sheet template is attached as Appendix 3. The spread-sheet contained specific date/time entry requirements that coincided with specific points in the end-to-end process and there was a separate sheet for each participating site within each jurisdiction.

It was the responsibility of the police contact officer to coordinate the collection and collation of the data on the spread-sheet for return to the ANZPAA NIFS Project Officer by the 10th of each month. The data for the month was reviewed by the ANZPAA NIFS Project Officer and anomalies were forwarded to the submitting jurisdiction for resolution.

Each month's data was added to the end of the spread-sheet resulting in a single spread-sheet for each site from the beginning to the end of the data collection period.

Each case was identified through a unique case identifier applied by each jurisdiction. This was later converted to a Project Case ID for the purposes of ensuring the anonymity of each case.

Data Collection Period

The data collection period was originally planned for 1 May 2011 – 31 October 2011. In July 2011 it was decided to close the data set regarding new cases at 30 September and concentrate on following up the 8,179 cases already reported. Follow up continued to 31 January 2012. There were 35 cases that were still ongoing investigations at 31 January, 2012. The final data collection thus spanned a 9 month period and included cases reported in a five month period with follow-up ranging from four months to eight months.

While the data collection was not without its difficulties and was for a shorter period of time than the UK SWIM Report, the data collated was far more comprehensive than that collected for the UK SWIM Report or the NZ Waikato Project.

Analysis Methodology

Data quality

Data quality checks were automated where possible. For example, computer code was written to provide lists of cases with:

- invalid dates and times;
- inconsistencies in time and date sequences across and within stages;
- unexpected missing fields based on information in earlier stages.

It was not feasible to follow up all issues identified. Queries were sent to the jurisdictions for the largest discrepancies and outliers and the database was corrected based on the responses received. In some cases, apparent discrepancies reflected variations in

administrative practices rather than incorrect data entry (for example, lack of exact times, report times after attendance or zero lead times).

Overall, the level of issues was low. For example, 2% of cases had negative or zero lead times for attendance. However, quality varied by site. (See Appendix Data Tables). In particular, lead times in the later stages could at best be calculated on dates only, not times, since some sites (particularly in Jurisdictions C and G) could not supply time data.

There are limitations around the data collected and the methodology applied. The data collected is only across five months and from sites nominated by jurisdictions as opposed to being selected by the project team. This resulted in each state being represented but in an uneven capacity with the majority of data being sourced from metropolitan sites (81%). To obtain a perspective on whether the project was a true national representation, state wide figures were obtained on crime reported and crime attended for the same crime type and reporting period.

The data collection was manually intensive and in most jurisdictions there was little alignment between police and forensic data management systems. This was further exacerbated by the need to collect data from DNA laboratories external to police and from investigative areas of policing.

For most organisations a case could not be tracked through all five stages on one information management system or utilising one central case record system.

Stage 5 data was the most problematic and this was expected from the outset of the project. While four general categories were created, the range of activities that could be performed at investigation was more complex and often did not seem to comply with the categories identified for the project. Additionally, the contact officers were from within forensic areas and in some instances were not aware of how to obtain the stage 5 data from the general or investigative police information management systems. This stage required a manually intensive searching mechanism.

The organisations that were better able to manage the data collection primarily utilised a forensic case management system networked to a police management system. See text box on Forensic Register, a Forensic Case Management System produced by Queensland Police Service (Forensic Services Branch).

The analysis revealed that the CSI were inclined to report the scene examination start and scene examination end times in rounded blocks of 10,15 and 20 minutes.

Data quality tables have been provided in the Appendix Data Tables.

Descriptive statistics

Success rates at each stage and lead times between stages were summarised for each:

- site.
- jurisdiction (aggregating across forensic sites for that State or Territory).
- location (aggregating across all regional sites and across all metropolitan sites).

- overall/national (aggregating across all 17 sites).

The precision in the estimates of success rates (i.e. the percentage of cases progressing to the next stage) was measured by 95% confidence intervals for proportions. The precision decreases from ±1% at Stage 1 to ±5% at Stage 5 overall for arrests due to fingerprint evidence and to ±8% for the corresponding DNA data. This is due to the attrition of data across stages and the smaller rates of DNA collection leading to smaller sample sizes in the later stages of the forensic process.

The lead time data follow particularly skewed distributions. For this reason lead times are summarised using medians rather than means and illustrated with box and whisker plots. The boxes show the 25th, 50th (median) and 75th percentiles and the whiskers show the range (excluding outliers).

Statistical testing

Success rates are compared between jurisdictions and across metropolitan and regional locations using chi-square tests. The corresponding lead time comparisons are performed using non-parametric tests (Mann Whitney and Kruskal Wallis tests).

A series of logistic regression models were fitted to identify factors associated with progression to successive stages of the forensic process. This was to identify whether, for example, shorter lead times or the characteristics of different sites and jurisdictions (such as high attendance rates, or high evidence submission rates) were associated with subsequent success (i.e. higher rates of identification or arrest after identification).

Validation subset

In a small number of sites (four), all cases were followed up regarding final clearance, not just those for which the crime scene was attended and evidence collected. This is referred to as the validation subset. This allows an overall arrest rate to be estimated and for comparisons to be made between clearance rates for cases with forensic evidence and those without.

FORENSIC REGISTER

The Forensic Register is a software application developed by the Queensland Police Forensic Services Branch in 2003 to satisfy the requirements of Australian Standard ISO 17025 and Supplementary Requirements for Accreditation in Forensic Sciences. Moreover there was a need to rationalise many of the separate registers and indices in use by forensic personnel into one system to allow the effective transfer and sharing of information. Additionally the application has been deployed for remote data entry providing a 'paperless' case file solution at the scene of crime.

The Forensic Register application has been licensed at no cost to a number of law enforcement agencies namely Tasmania Police, South Australia Police, Western Australia Police and the Northern Territory Police (installation in progress).

In Queensland the Forensic Register solution integrates seamlessly for real time exchange of information with the Queensland Police Records Information Management Exchange (QPRIME) for reporting and property management from the scene of a crime or disaster. It also offers inter departmental integration with Queensland Health Forensic Scientific Services (AUSLAB) and integration with CRIMTRAC for the National Criminal Investigation DNA Database (NCIDD) and National Automated Fingerprint Identification System (NAFIS) for rapid suspect identification.

The Forensic Register allows for the collection of all forensic case, evidence, examination and scientific information including multimedia elements such as digital images and diagrams into one database. It includes monitoring and management of workflow through a range of highly effective reporting, performance and quality assurance aids.

The Forensic Register records and manages via barcode identification all exhibits under a common case identifier. This allows for exhibit and case records to be shared by all forensic disciplines and interdepartmental laboratories, eliminating repetitive data entry and allows for real time reporting of forensic examinations, identifications and subsequent forensic intelligence reporting and charting.

The Forensic Register (Electronic Case Management & Mobile Data) provided the mechanism for end-to-end performance improvement and was critical in the Queensland DNA and Fingerprint Improvement Strategies.

Courtesy of Troy O'Malley, Queensland Police Service, Forensic Services Branch

Findings

The End-to-End Forensic Identification Process Project has to a certain extent benchmarked current forensic process performance standards, in many cases for the first time in Australia. Many jurisdictions have existing performance measures in place but have not been in a position to benchmark their performance on a 'national' basis, noting of course the limitations of the data collected in this study with regards to timeframe of the study and representative nature of data.

The findings are a summary of actual data from recent cases that have occurred within Australia and with some follow on work could provide an opportunity to learn from top performers across all stages of the forensic process.

In the following charts, the identification of individual jurisdictions and/or sites has been removed. Each jurisdiction participating in the End-to-End Project has been provided with their own performance information relative to the overall results. The reference codes shown on the graphs have been applied by the project team and are unique to this report.

The findings have been produced in the following categories:

- Data Overview Nationally.
- Results by Stages.
- Overall Forensic Performance;

and refer to the two main measures being the lead time and success measures.

Analysis is provided on the national performance, the jurisdictional performance, metropolitan and regional areas, DNA and fingerprint data individually and combined. Each graph is followed by key points and an interpretation.

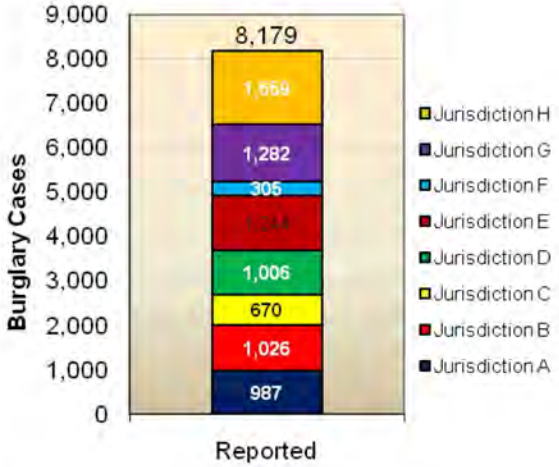
Appendix Data Tables from which the analysis was drawn have been provided with this report.

NIFS KEY PROJECT

End-to-End Forensic Identification Process Project

Data Overview Nationally

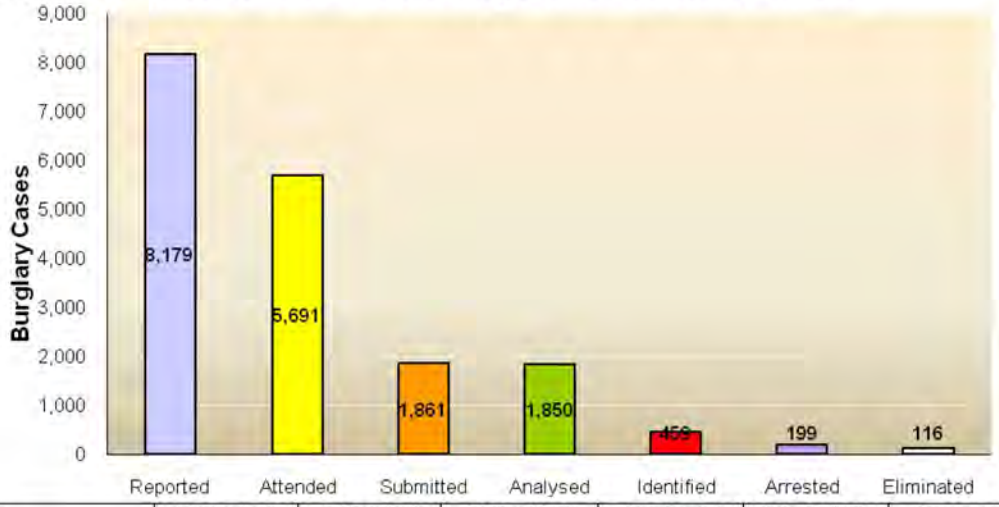
Figure 1: Distribution of Data



Key Points:

- 8,179 burglary cases were reported in the five month period in 2011.
- 17 sites (10 metro, 7 regional).
- 43 cases reported per day (metro sites).
- 10 cases reported per day (regional sites).
- Each State/Territory is represented.
- The majority of cases are in metropolitan locations (81%).

Figure 2: Attrition of Cases across Stages of the Forensic Process



Stage	Reported	Attended	Submitted	Analysed	Identified	Arrested	Eliminated
Cases	8,179	5,691	1,861	1,850	459	199	116
Per 100 reported	100	70	23	23	6	2.4	1.4
Per 100 attended		100	33	33	8	3.5	2.0

Key points:

- There is attrition at all stages of the process.
- Arrests prior to forensic identification or arrest at the scene are excluded.
- 33 percent of cases for which CSI attend the scene have forensic evidence collected.
- Almost 25 percent of forensic evidence analysed results in an identification.
- 2.4 arrests are linked to forensic evidence out of 100 reported burglary cases.
- There is an additional 1.4 elimination per 100 reported burglary cases.
- 3.5 arrests are linked to forensic evidence out of 100 attended burglary cases.

Figure 3: Attrition of Cases across Stages of the Forensic Process: By Jurisdiction

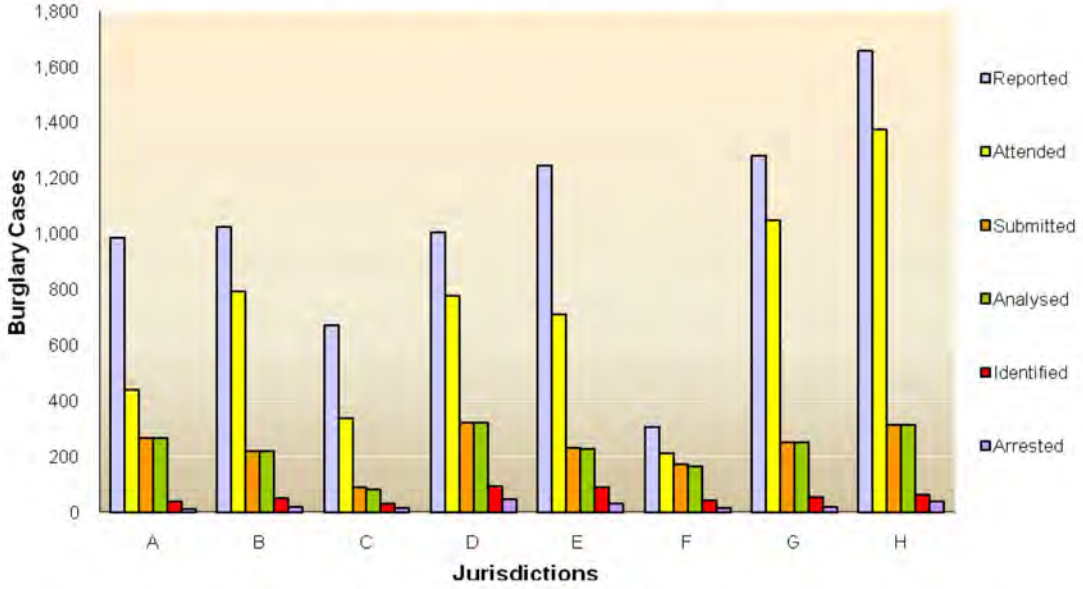


Figure 3.1: Attrition of Fingerprint Cases

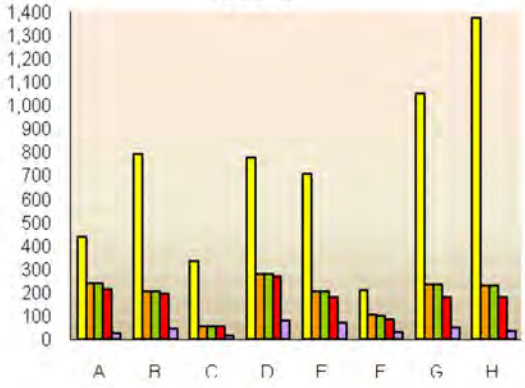
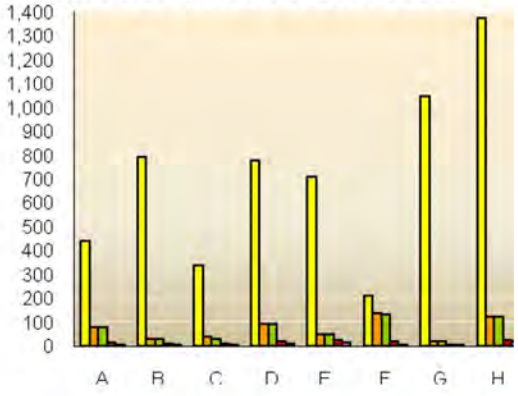


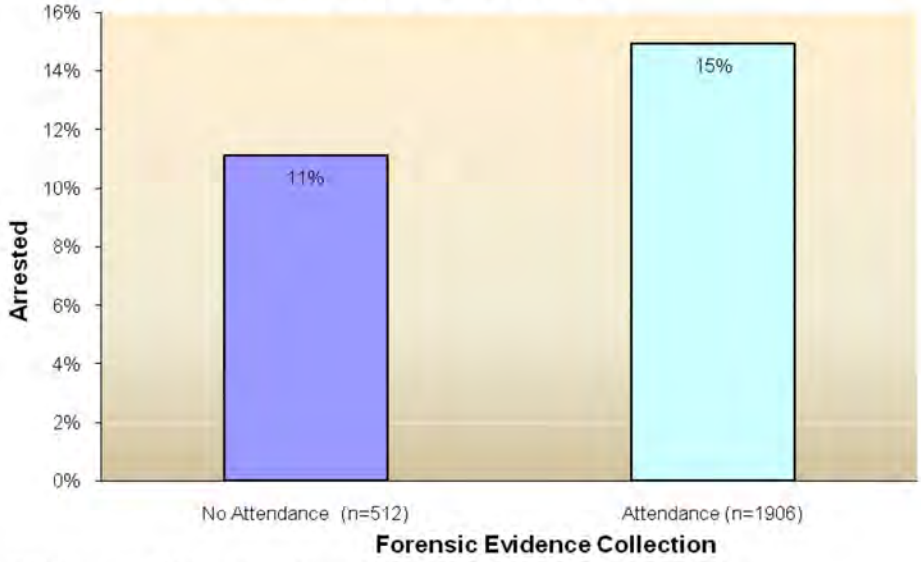
Figure 3.2: Attrition of DNA Cases



Key Points:

- Attrition is at different rates in different stages across different jurisdictions.
- Overall DNA collection rate is lower than fingerprints (10% as opposed to 28%).
- Refer to Table 1 below and Appendix Tables for further details.

Figure 4: Validation Data: Overall Arrest Rates: Reported

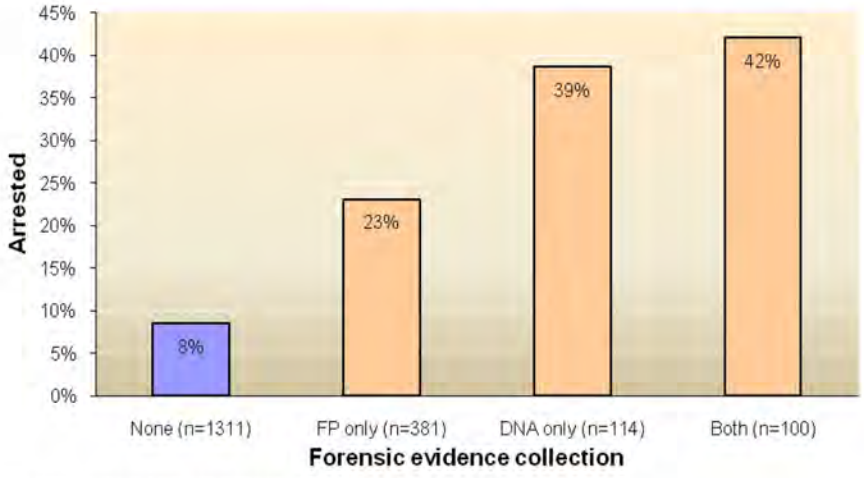


Validation subset. Note: statistically significant differences p= 03

Key Points:

- There is a higher overall arrest rate when CSI attend the scene than for cases where there was no CSI attendance.

Figure 5: Validation Data: Overall Arrest Rates: Attended



Validation subset. Note: statistically significant differences p<0.001

Key Points:

- Where forensic evidence is collected there is a higher overall arrest rate than cases where no forensic evidence is collected.

Results by Stage

Table 1

	Stage 1 Attendance		Stage 2 Evidence Submission		Stage 3 Analysis		Stage 4 Identification		Stage 5 Investigation	
Success Rate			FP	DNA	FP	DNA	FP	DNA	FP	DNA
Description	Attended / Reported		Submitted to Lab / Attended		Analysed / Submitted to Lab		Identification / Analysed		Arrest/ ID	
Cases	5691/8179		1569/5691	581/5691	1564/1569	571/581	362/1564	134/571	135/362	67/134
National mean	70%		28%	10%	100%	98%	23%	23%	37%	50%
95% CI	69%-70%		26%-29%	10%-11%	100-100%	97%-99%	21%-25%	20%-27%	32%-42%	42%-58%
Lowest, highest	44%, 83%		17%, 55%	2%, 64%	97%,100%	82%, 98%	10%,35%	5%, 53%	22%, 63%	21%,71%
Metro, Regional	68%, 74%		28%, 27%	10%, 10%	100%,99%	92%, 98%	21, 30%	24%, 23%	39%, 32%	53%, 37%
Significance										
by jurisdiction	***		***	***	***	***	***	***	*	*
by location	***		NS	NS	NS	NS	***	NS	NS	NS
Lead Time										
Description	Attendance lead time	At scene	Days from attendance to submission to lab		Days from receipt to analysis		Days from analysis to ID		Days from ID to arrest	
Units	hrs	min	d	d	d	d	d	d	d	d
National mean	11	38	2	8	3	14	4	21	23	29
Lowest, highest	5,19	29,58	0, 8	0, 21	0, 15	0, 49	0, 13	4, 42	11, 40	10, 123
Metro, Regional	10, 14	37, 44	1, 3	8, 10	3, 4	12, 24	4, 4	18, 34	22, 28	26, 43
National median	4	30	0	5	1	3	0	15	11	20
Lowest, highest	1,14	21,50	0, 6	0, 13	0, 11	0, 57	0, 12	4, 32	8, 38	5, 123
Metro, Regional	4, 4	30, 30	0, 1	5, 5	1, 1	3, 9	0, 0	15, 16	11, 14	20, 45
Cases	5621	4896	1567	581	1564	571	362	132	135	67
Significance										
by jurisdiction	***	***	***	***	***	***	***	***	***	***
by location	NS	***	***	*	NS	***	NS	NS	NS	NS

Notes:

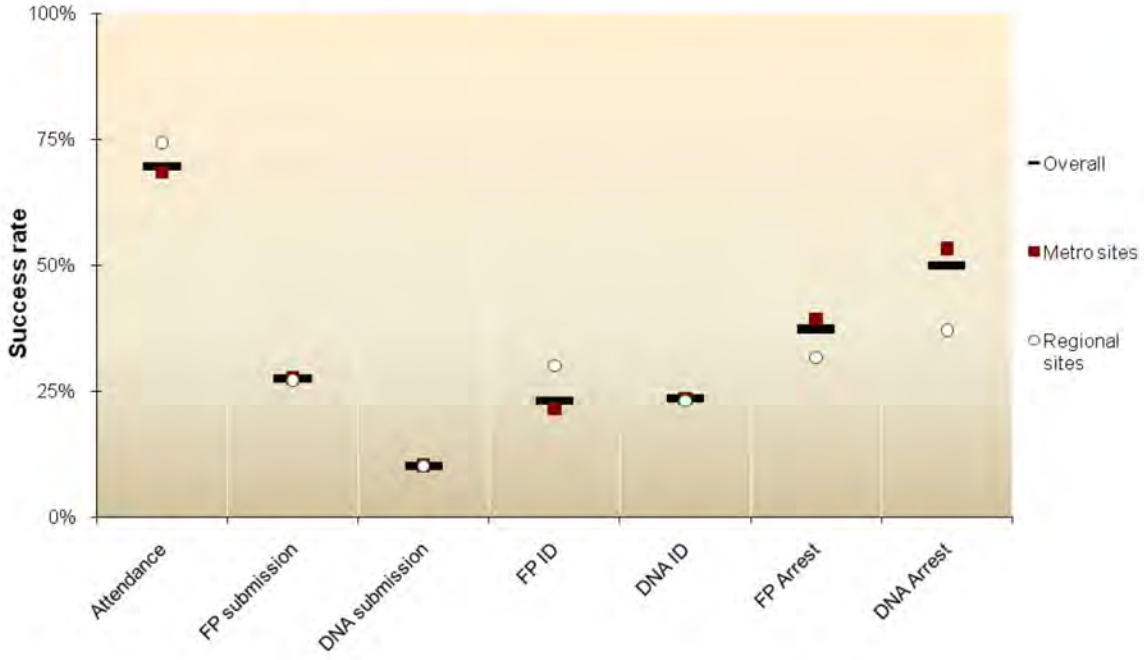
- The national mean is the overall mean across all sites in the study.
- Lowest, highest are the lowest and highest aggregated means across each of the 8 jurisdictions.
- Statistical significance denoted by *(***=p<.001;**=p<.01;*=p<.05;NS=p≥.05 considered not statistically significant).

Key Points:

- This table provides success rate and lead times across each stage of the forensic process. It also shows the variation in the measures across jurisdictions and across locations.
- Statistical testing shows significant differences for all measures across jurisdictions.
- Metropolitan and regional results generally show differences in the early stages.
- These results will be discussed in greater detail in subsequent sections.
- 95% confidence intervals around the national success rates shows that the precision of the estimates is greater in the earlier stages as the data decreases with the attrition. For example the width of the 95% confidence interval for stage 1 is 1% and for stage 5 is 8%. Note also the precision is higher for fingerprint results than DNA for the same reason.
- Refer to Appendix Data Tables for data relevant to each Jurisdiction.

Success

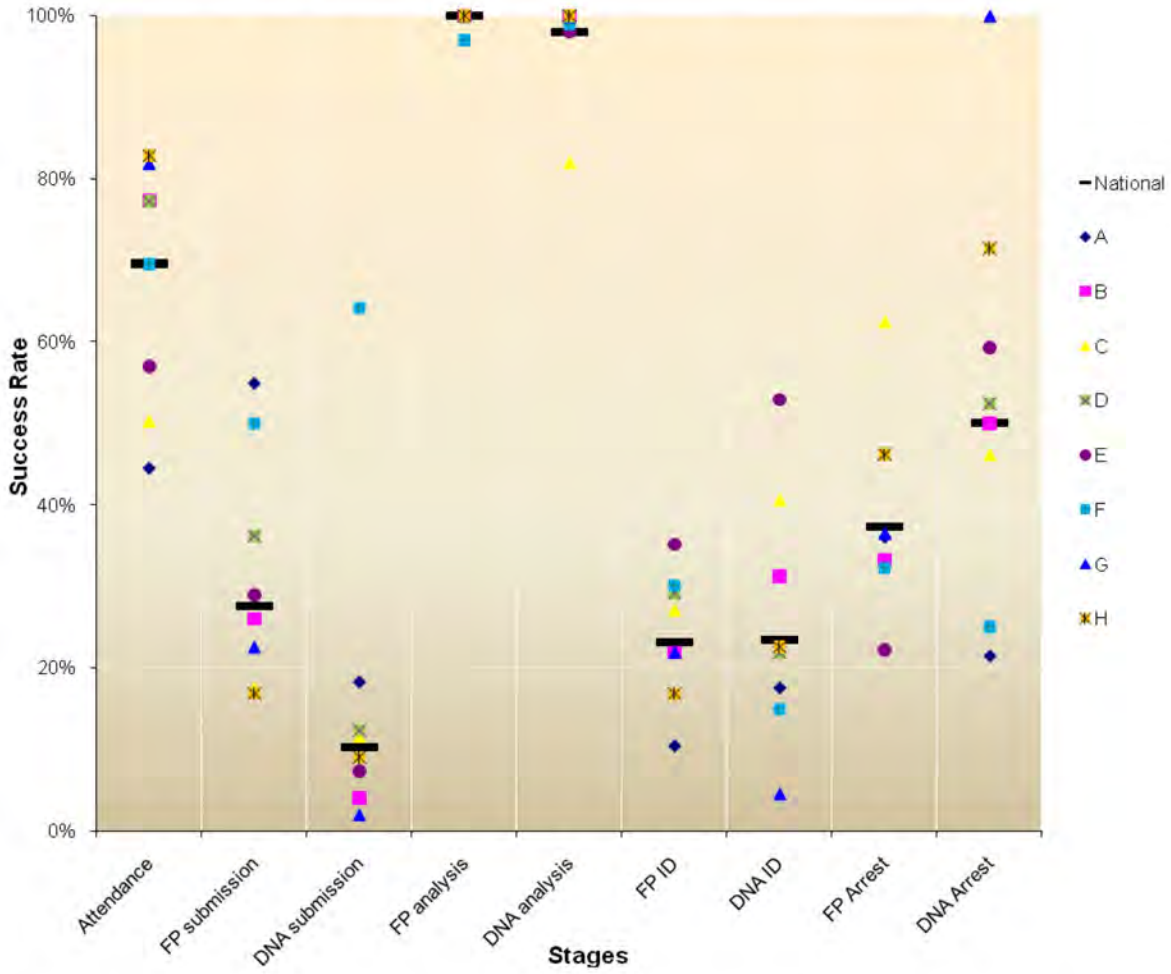
Figure 6: Success by Stage: By Location



Key Points:

- The results by location are mixed across the stages.
- The only differences that are statistically significant are the higher attendance rates for regional sites and higher fingerprint identification rate for regional sites.
- Refer to Table 1.

Figure 7: Success by Stage: By Jurisdiction with National



Key Points:

- Note the accuracy of the jurisdictional estimates in the later stages is less than the earlier stages.
- The extreme attrition of DNA for Jurisdiction G has resulted in only 1 case for stage 5.
- Refer to Table 1.

Stage 1 (Attendance)

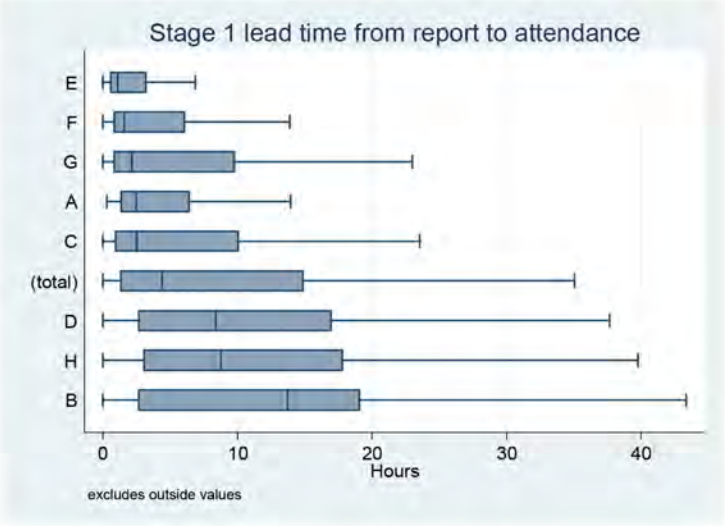
Table 2

	Stage 1 Attendance	
Success rate		
Description	Attended/Reported	
Cases	5691/8179	
National mean	70%	
95% CI	69%-70%	
Lowest, highest	44%, 83%	
Metro, Regional	68%, 74%	
Significance		
by jurisdiction	***	
by location	***	
Lead Time		
Description	Attendance lead time	At scene
Units	hrs	min
National mean	11	38
Lowest, highest	5,19	29,58
Metro, Regional	10, 14	37, 44
National median	4	30
Lowest, highest	1,14	21,50
Metro, Regional	4, 4	30, 30
Cases	5621	4896
Significance		
by jurisdiction	***	***
by location	NS	***

Key Points:

- Overall 70% of burglary cases reported are attended by CSI. There is statistically significant variation across the jurisdictions and by location.
- There is a higher attendance rate in regional areas. The mean lead time is 11 hours but the median lead time of four hours better reflects the performance.
- There are statistically significant differences in the response times between jurisdictions but not by locations.
- There is a median of 30 minutes for time spent at the scene. There are statistically significant differences between the times across jurisdictions and by location. The difference by location is illustrated in the next figure.

Figure 8: Attendance Lead times: By Jurisdiction with National (Median)



Key Points:

- Median lead time varies from 1 hour to 14 hours.

Figure 9: Time at the Scene: By Jurisdiction

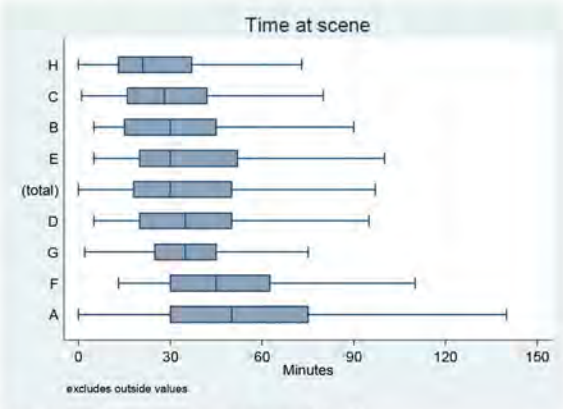
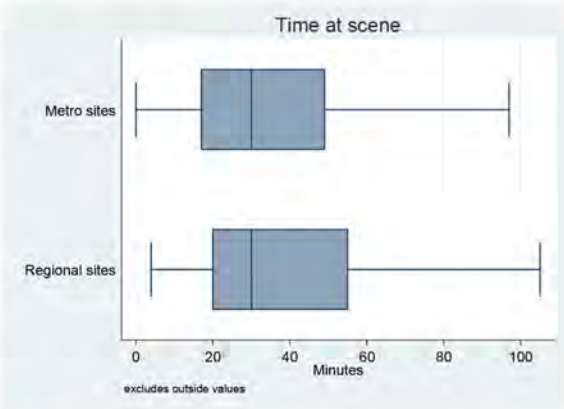


Figure 10: Time at the Scene: By Location



Note: scale different between figure 9 & 10

Key points:

- the median time at the scene ranges from 21 minutes to 50 minutes with the national median of 30 minutes.

Key points:

- longer times spent in regional sites.

Stage 2 (Submission)

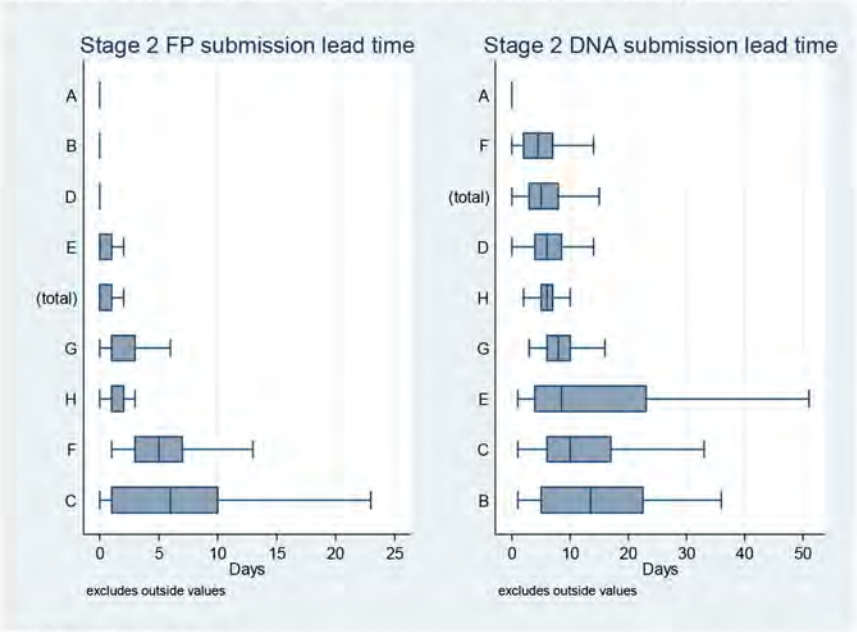
Table 3

	Stage 2 Evidence submission	
Success rate	FP	DNA
Description	Submitted to Lab / Attended	
Cases	1569/5691	581/5691
National mean	28%	10%
95% CI	26%-29%	10%-11%
Lowest, highest	17%, 55%	2%, 64%
Metro, Regional	28%, 27%	10%, 10%
Significance		
by jurisdiction	***	***
by location	NS	NS
Lead Time		
Description	Days from attendance to submission to Lab	
Units	d	d
National mean	2	8
Lowest, highest	0, 8	0, 21
Metro, Regional	1, 3	8, 10
National median	0	5
Lowest, highest	0, 6	0, 13
Metro, Regional	0, 1	5, 5
Cases	1567	581
Significance		
by jurisdiction	***	***
by location	***	*

Key Points:

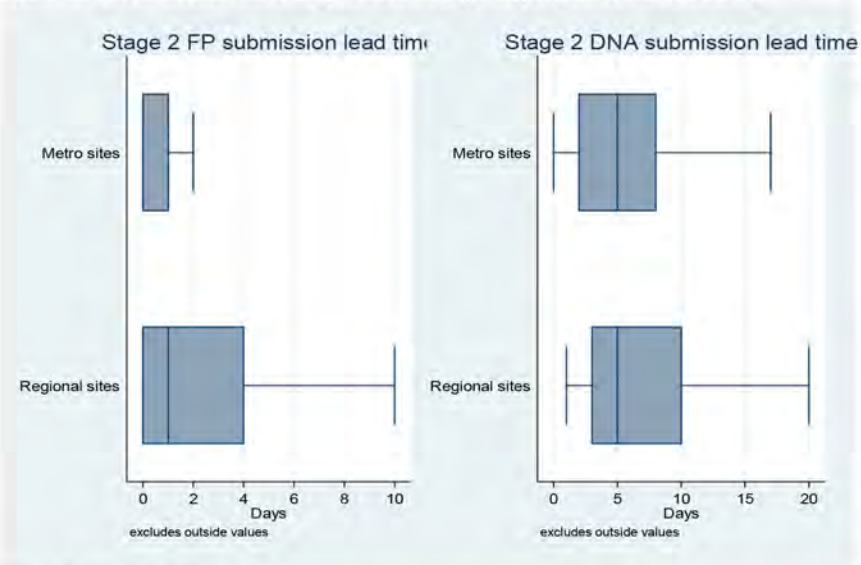
- Note that zero lead time indicates submission on same day as attended.
- Fingerprint evidence was submitted in 28% of cases where CSI attended.
- This varied from 17% to 55% across jurisdictions.
- The jurisdictions with the highest attendance rate did not necessarily have the highest fingerprint submission rate or highest DNA submission rate. Refer to Figure 7.
- Fingerprints have a substantially shorter submission lead time than DNA.
- There is no difference in the submission rate by location.
- The submission rate was lower for DNA (10%) with a large variation across the jurisdictions but not by location.
- Jurisdiction F has over three times the DNA submission rate of the next highest jurisdiction, but this is due to different procedures at the time data was collected.

Figure 11: Submission Lead time: By Jurisdiction with National (Median)



Note: scale different between two plots

Figure 12: Submission Lead time: By Location (Fingerprints and DNA)



Note: scale different between two plots

Key Points:

- These plots illustrate the longer lead times for DNA than fingerprints, longer lead times in regional areas and substantial variation by jurisdiction.

Stage 3 (Analysis)

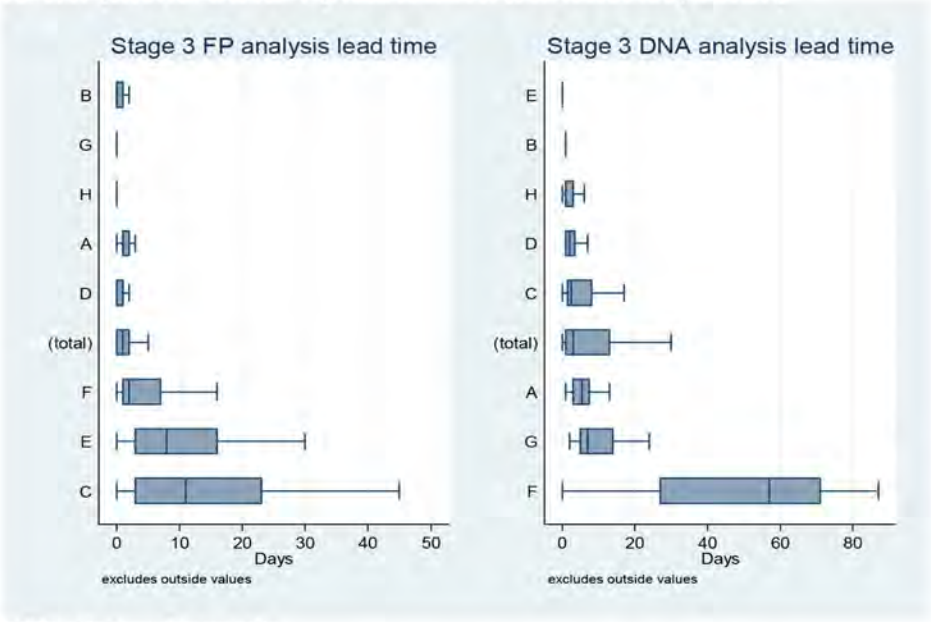
Table 4

	Stage 3 Analysis		Stage 3 Analysis (FP & DNA Suitability)	
Success rate	FP	DNA	FP	DNA
Description	Analysed / Submitted to Lab		Suitable for upload to NAFIS database / Submitted to Lab	Suitable for upload to NCIDD database / Submitted to Lab
Cases	1564/1569	571/581	1367 / 1569	241/ 581
National mean	100%	98%	87%	42%
95% CI	100-100%	97%-99%		
Lowest, highest	97%,100%	82%, 98%	76%, 96%	26%, 78%
Metro, Regional	100%,99%	92%, 98%	87%, 89%	42%, 41%
Significance				
by jurisdiction	***	***	***	***
by location	NS	NS	NS	NS
Lead Time				
Description	Days from receipt to analysis		As per left column	
Units	d	d		
National mean	3	14		
Lowest, highest	0, 15	0, 49		
Metro, Regional	3, 4	12, 24		
National median	1	3		
Lowest, highest	0, 11	0, 57		
Metro, Regional	1, 1	3, 9		
Cases	1564	571		
Significance				
by jurisdiction	***	***		
by location	NS	***		

Key Points:

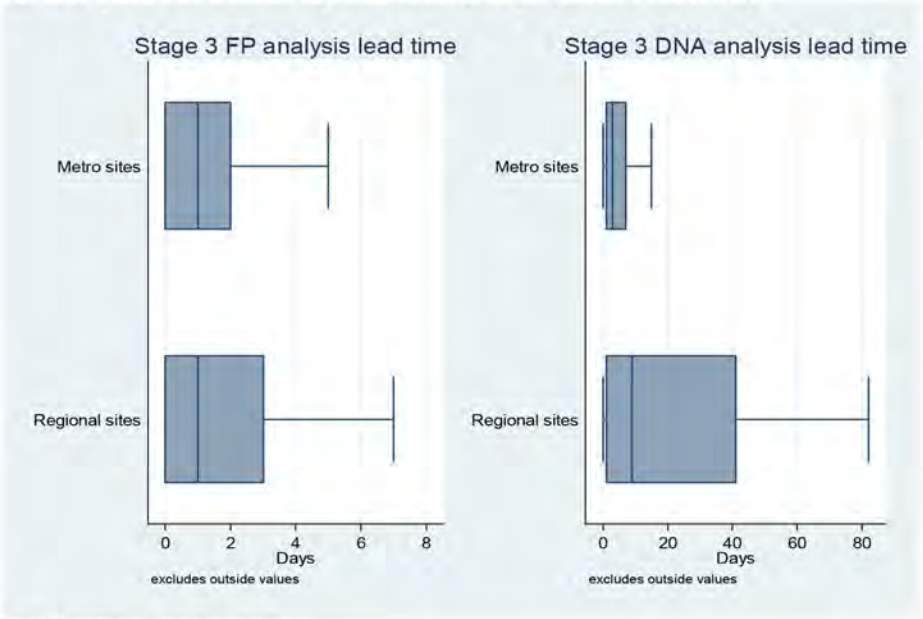
- Virtually all fingerprint evidence is analysed. This is the case in all except one jurisdiction.
- Overall 98% of DNA evidence is analysed.
- There is some variation by jurisdiction.
- Fingerprints have a shorter analysis lead time than DNA (median 1 vs. 3 days).
- There is significant variation across jurisdictions in lead time for both fingerprints and DNA.
- The ranking is different between fingerprints and DNA.

Figure 13: Analysis Lead time: By Jurisdiction with National (Median)



Note: Scale different between the two plots

Figure 14: Analysis Lead time: By Location (Fingerprints and DNA)

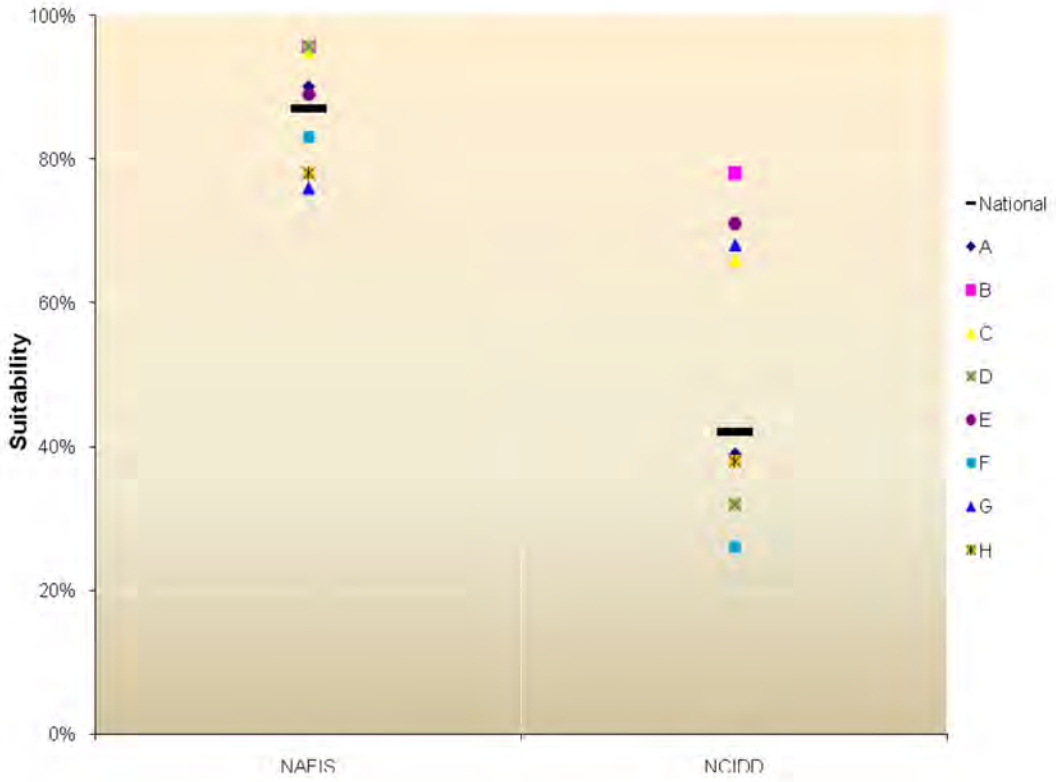


Note: Scale different between the two plots

Key Points:

- There is no significant difference by location for fingerprint analysis lead time but there is a longer DNA lead time for regional sites.

Figure 15: Success: Profile Suitability for upload to Databases



Key Points:

- Overall the percentage of cases with a profile suitable for upload to the NAFIS database is 87% and the corresponding percentage of cases with a profile suitable for upload to the NCIDD database is 42%.
- There is significant variation across jurisdictions in these percentages but no difference by location.
- There is a greater variation in DNA than in fingerprints.
- Some of the DNA variation may be due to the interpretation of database suitability by the contact officers during the data collection period.

Stage 4 (Identification)

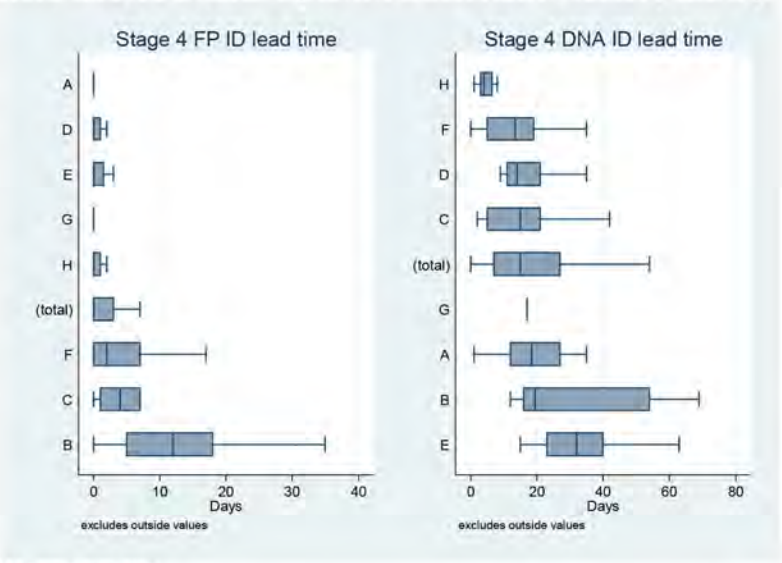
Table 5

	Stage 4 Identification	
Success rate	FP	DNA
Description	Identification / Analysed	
Cases	362/1564	134/571
National mean	23%	23%
95% CI	21%-25%	20%-27%
Lowest, highest	10%,35%	5%, 53%
Metro, Regional	21, 30%	24%, 23%
Significance		
by jurisdiction	***	***
by location	***	NS
Lead Time		
Description	Days from analysis to ID	
Units	d	d
National mean	4	21
Lowest, highest	0, 13	4, 42
Metro, Regional	4, 4	18, 34
National median	0	15
Lowest, highest	0, 12	4, 32
Metro, Regional	0, 0	15, 16
Cases	362	132
Significance		
by jurisdiction	***	***
by location	NS	NS

Key Points:

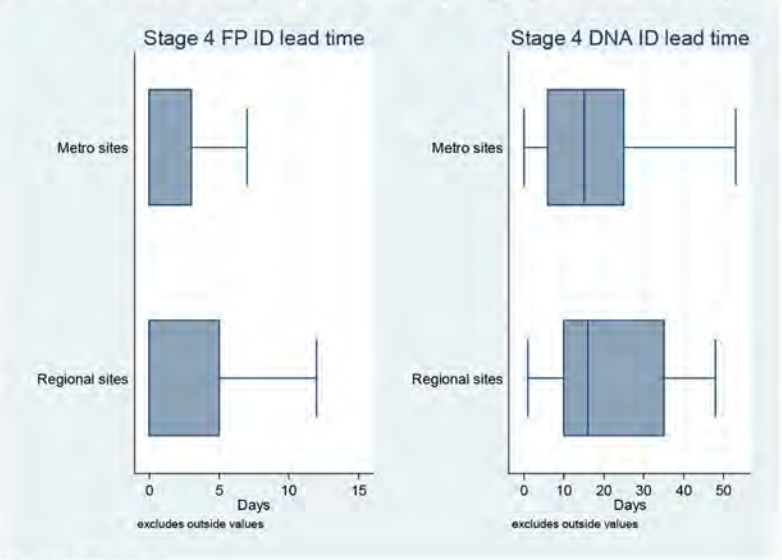
- Overall identification rate for both fingerprints and DNA is 23%.
- There are statistical differences across jurisdictions but there is more variation for DNA identification rates (5% to 53%).
- There are higher identification rates in fingerprints at regional sites, but no difference for DNA.
- The jurisdictional ranking is different between fingerprints and DNA.
- The DNA data available is from a smaller sample than for fingerprints.
- Jurisdiction G has only one case with a DNA identification.

Figure 16: Identification Lead time: By Jurisdiction with National (Median)



Note: scale different between two plots

Figure 17: Identification Lead time: By Location (Fingerprints and DNA)



Note: scale different between two plots

Key Points:

- There are statistically significant differences across jurisdictions in the lead time for both fingerprints and DNA, but metropolitan and regional sites are similar.
- There are longer lead times for DNA than fingerprints (median 15 days vs. same day for fingerprints).

Results: Stage 5 (Investigation)

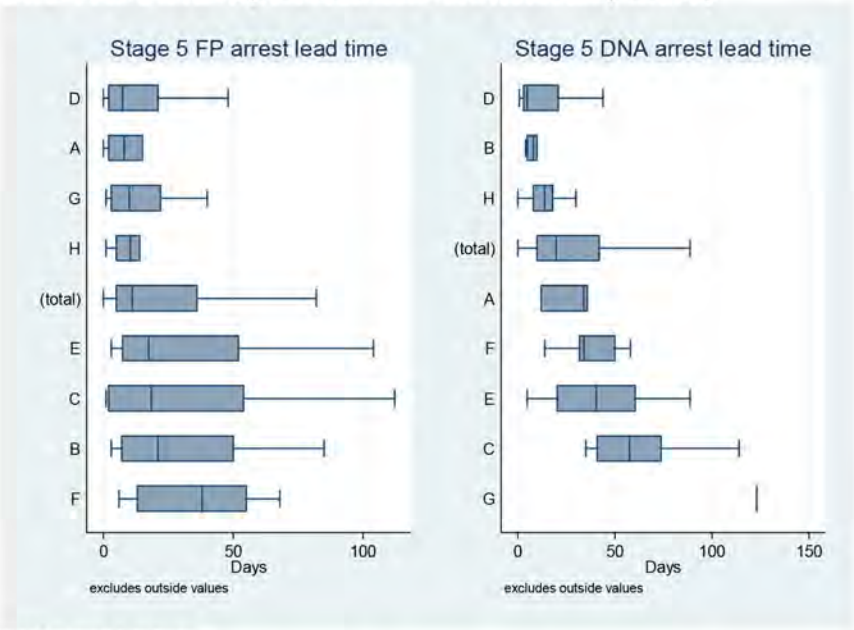
Table 6

	Stage 5 Investigation	
Success rate	FP	DNA
Description	Arrest / ID	
Cases	135/362	67/134
National mean	37%	50%
95% CI	32%-42%	42%-58%
Lowest, highest	22%, 63%	21%,71%
Metro, Regional	39%, 32%	53%, 37%
Significance		
by jurisdiction	*	*
by location	NS	NS
Lead Time		
Description	Days from ID to arrest	
Units	d	d
National mean	23	29
Lowest, highest	11, 40	10, 123
Metro, Regional	22, 28	26, 43
National median	11	20
Lowest, highest	8, 38	5, 123
Metro, Regional	11, 14	20, 45
Cases	135	67
Significance		
by jurisdiction	***	***
by location	NS	NS

Key Points:

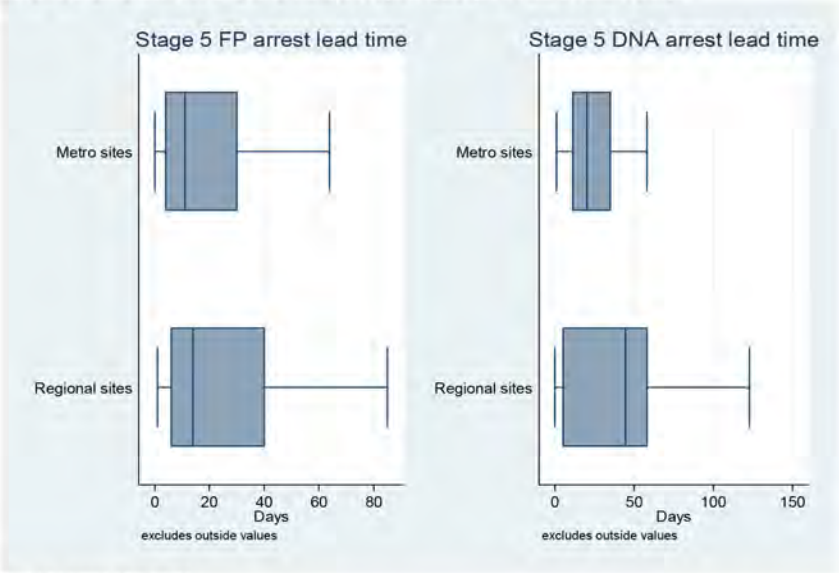
- The overall arrest rate after fingerprint identification is 37% and 50% after DNA identification.
- Significant variation is observed by jurisdiction but there is more variation for DNA identification than fingerprints.
- There is no difference by location.
- Note that the DNA data available is a smaller sample than for fingerprints.
- Jurisdiction G was excluded from the DNA comparisons due to it being represented by only one case.

Figure 18: Arrest Lead time: By Jurisdiction with National (Median)



Note: scale different between two plots

Figure 19: Arrest Lead time: By Location (Fingerprints and DNA)



Note: scale different between two plots

Key Points:

- No significant differences are observed between Metropolitan or Regional sites.
- Longer lead times are seen for DNA than fingerprints.
- Significant differences are observed between jurisdictions.

Overall Forensic Performance

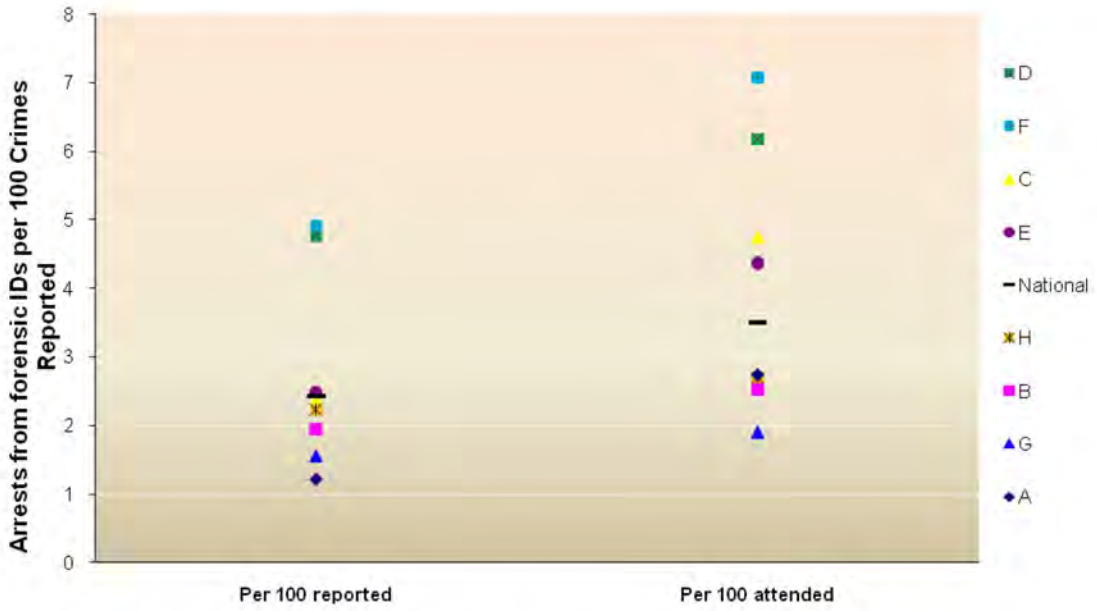
Table 7

	Stage 1 - Stage 5 Investigation			Stage 1 - Stage 5 Investigation		
Success rate	FP	DNA	FP and/or DNA	FP	DNA	FP and/or DNA
Description	Arrest/Reported			Arrest/Attended		
Cases	135/8179	67/8179	199/8179	135/5691	67/5691	199/5691
National mean	1.7%	0.8%	2.4%	2.4%	1.2%	3.5%
95% CI	1.4-2.0%	0.6-1.0%	2.1-3.0%	2.0-2.8%	0.9-1.5%	3.0-4.0%
Lowest, highest	0.9,3.8%	0.1,1.6%	1.2,4.9%	1.3, 4.9%	0.1, 2.4%	1.9, 7.1%
Metro, Regional	1.6,1.9%	0.9,0.6%	2.4,2.5%	2.3, 2.6%	1.2, 0.9%	3.5, 3.4%
Significance						
by jurisdiction	***	**	***	***	**	***
by location	NS	NS	NS	NS	NS	NS
Lead Time						
Description	Days from report to arrest			As per left column		
Units	d	d	d			
National mean	33	60	41			
Lowest, highest	13, 72	25,158	22, 83			
Metro, Regional	31, 40	55, 85	39, 51			
National median	19	49	29			
Lowest, highest	9, 52	26, 158	14, 87			
Metro, Regional	16, 29	42, 92	28, 39			
Cases	135	67	199			
Significance						
by jurisdiction	***	***	***			
by location	NS	NS	NS			

Key Points:

- When the arrests are related back to the number of crimes reported the overall success rates are 1.7% for fingerprints (or 1.7 per 100 crimes reported) and 0.8% for DNA.
- There are statistically significant differences across jurisdictions but not by location.

Figure 20: Results Overall: By Jurisdiction



Key Points:

- There are significant differences by jurisdiction but more variation exists per attendance due to the wide range in attendance rates.
- Note that Jurisdiction C is obscured, but has the same value as the national rate per crimes reported. Jurisdiction H is partly obscured, but has the same value as jurisdiction A as per crimes attended.

Figure 21: Arrests from DNA vs. Fingerprints per 100 Crimes Reported: By Jurisdiction

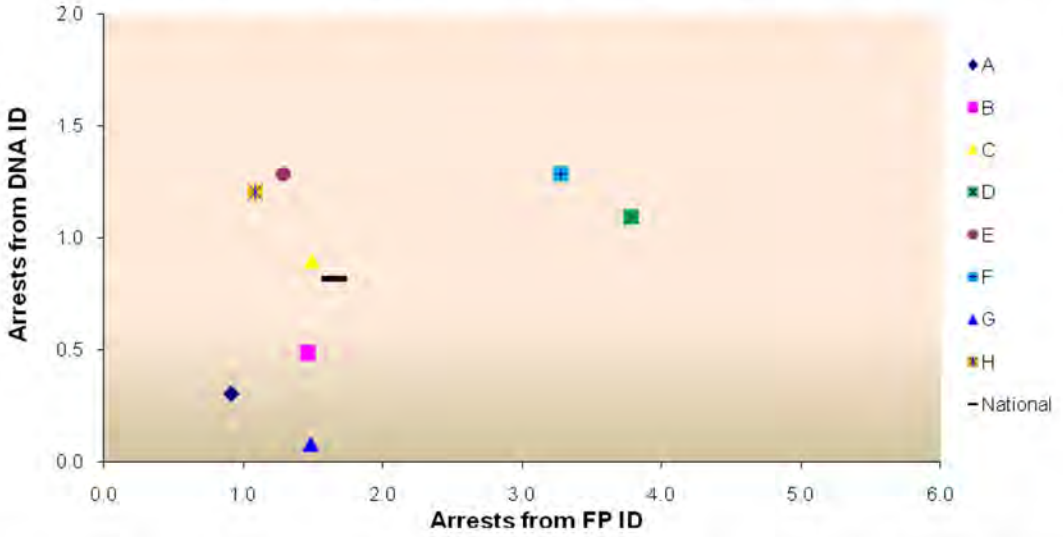
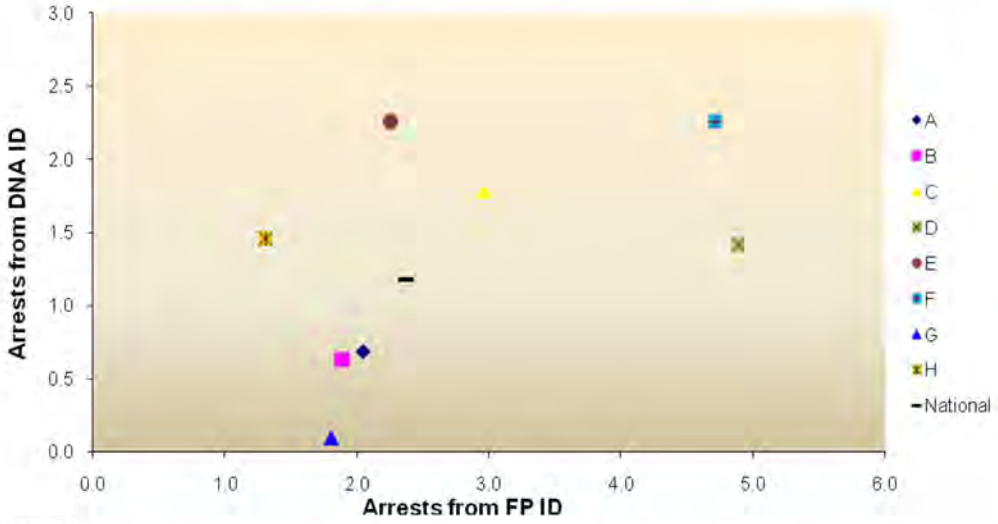


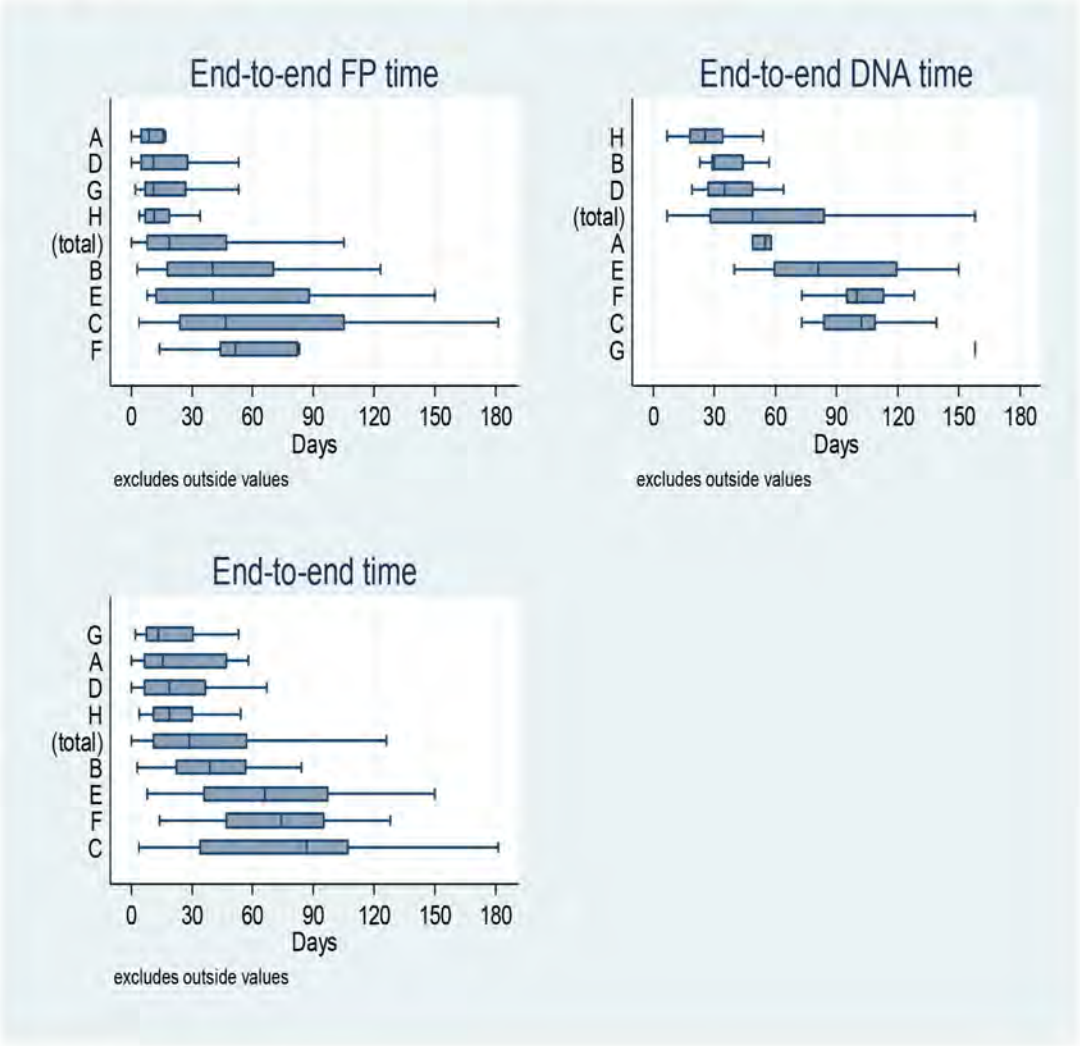
Figure 22: Arrests from DNA vs. Fingerprints per 100 Crimes Attended: By Jurisdiction



Key Points:

- These graphs compare the relative jurisdictional performance for DNA vs. fingerprints.
- There is less variation in the DNA results across jurisdictions and overall lower arrest rates.
- Some jurisdictions achieve twice the fingerprint arrest rate than the national median.
- There is not a strong correlation between performance regarding DNA and fingerprint evidence, but the jurisdictions with the highest overall arrest rates from fingerprints also have DNA arrest rates above the aggregate national figure.

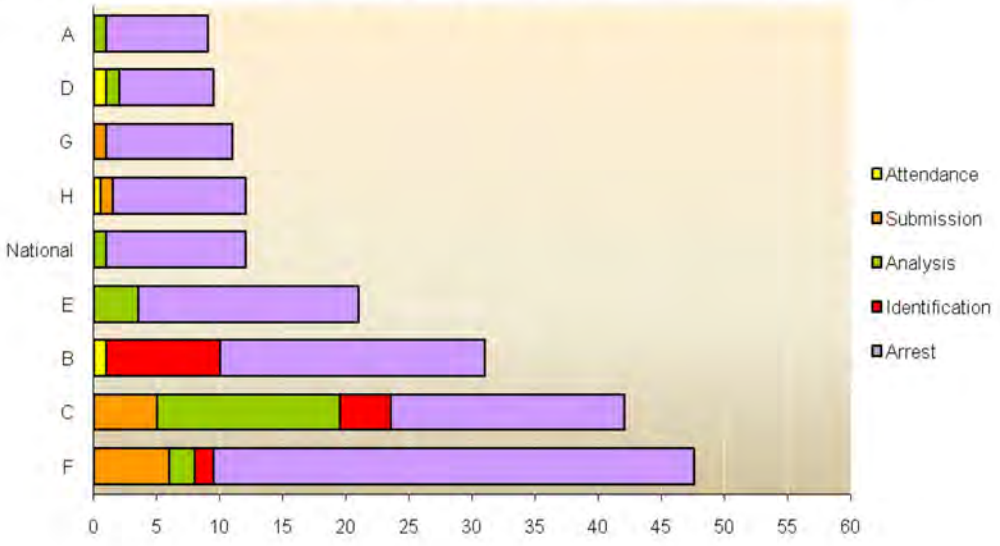
Figure 23: Overall End-to-End Lead times: By Jurisdiction



Key Points:

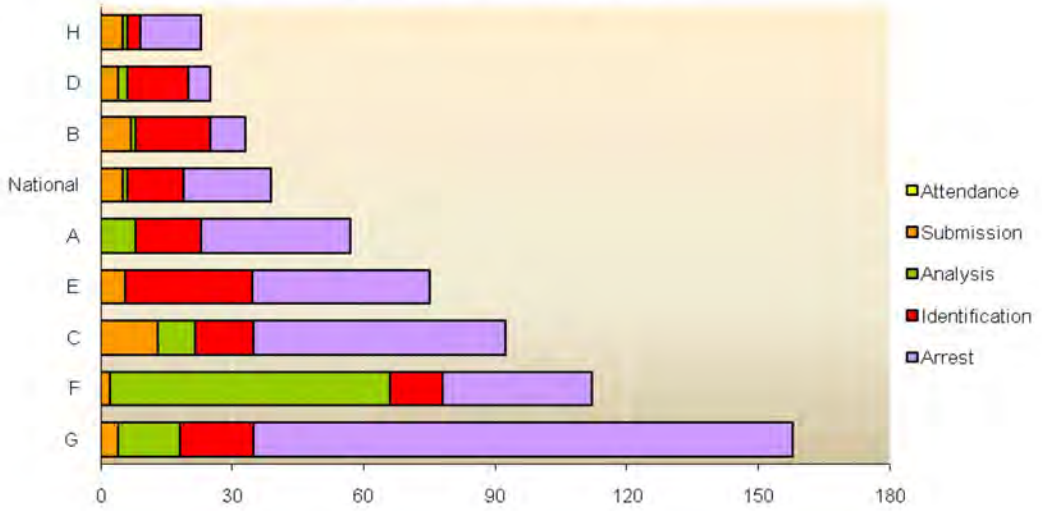
- Overall median lead times across all sites were 19 days for fingerprints and 49 days for DNA evidence. The fastest times achieved were a median of 9 days for fingerprints (Jurisdiction A) and 26 days for DNA (Jurisdiction H).
- When fingerprint and DNA information was considered together, the fastest times were achieved in Jurisdiction G (but this jurisdiction collected very little DNA evidence).
- The median lead time for the cases with arrest from the report to arrest, regardless of evidence type and not by stage is 29 days.

Figure 24: Lead times (Median in each Stage): By Jurisdiction (Fingerprint)



Days (based on median FP lead time at each stage, successful cases only)

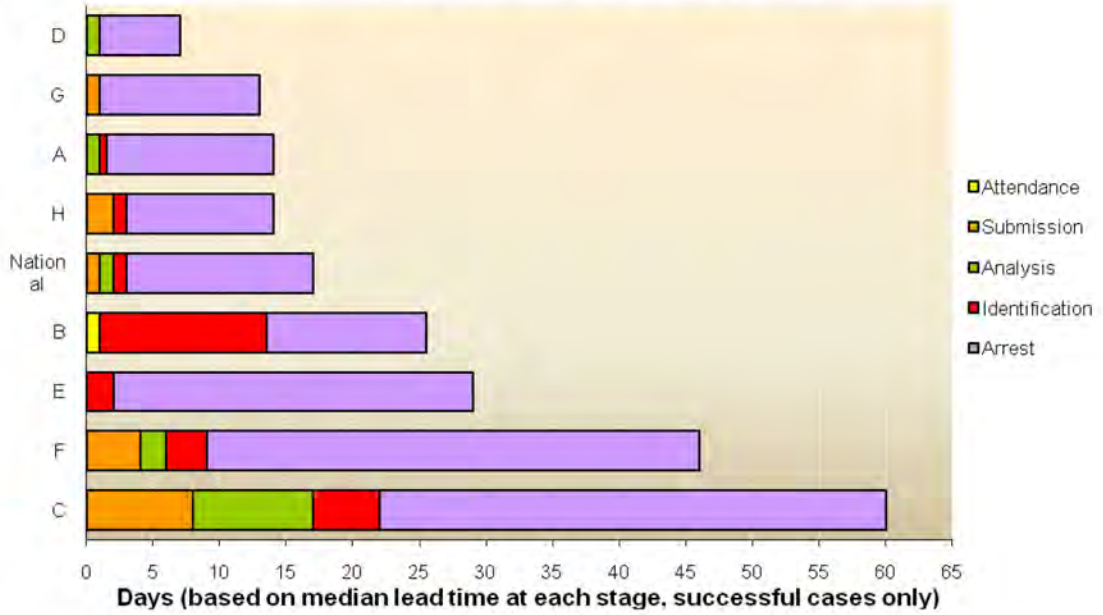
Figure 25: Lead times (Median): By Jurisdiction (DNA)



Days (based on median DNA lead time at each stage, successful cases only)

Note: the lead time scale for figure 25 is three times longer than the lead time scale for figure 24

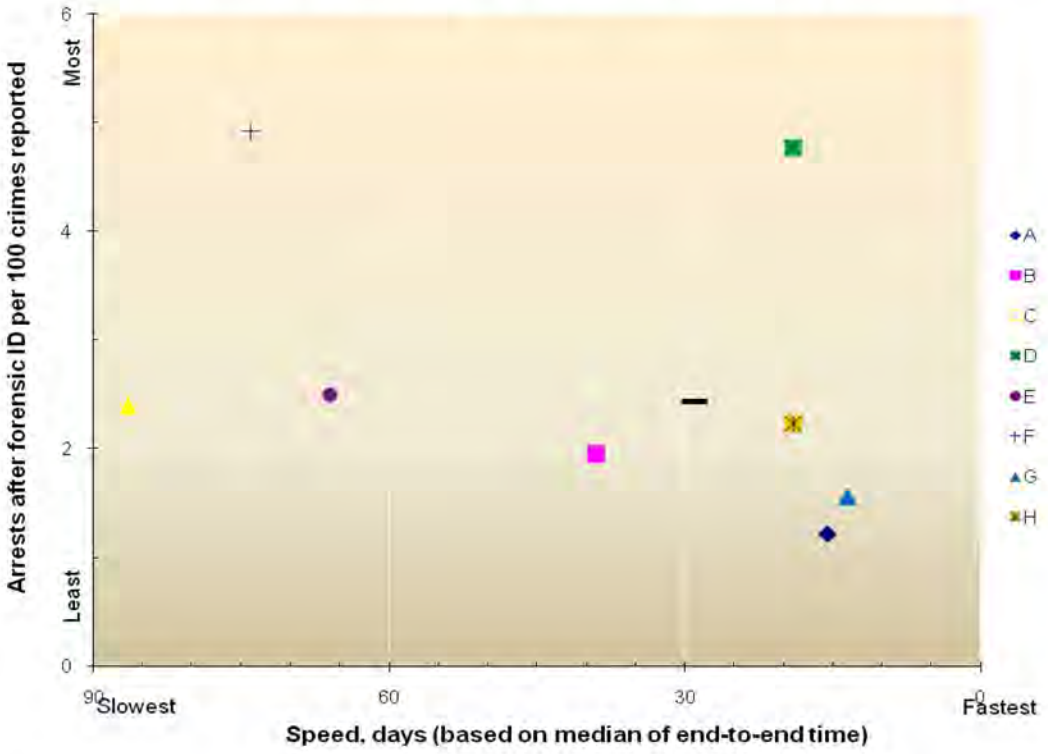
Figure 26: Lead times (Median): By Jurisdiction (Forensic Evidence)



Key Points:

- These graphs illustrate the relative length of each stage in contributing to the overall end-to-end lead time. This may assist in identifying where it may be possible to improve efficiency in the various jurisdictions.
- The last stage dominates the overall time in almost all jurisdictions.
- Longer identification lead times for DNA contribute to the longer overall lead times for DNA compared with fingerprints.

Figure 27: Success vs. Time (Median) per 100 Crimes Reported: By Jurisdiction



Key Points:

- This graph provides an overall performance summary plotting end-to-end effectiveness (arrest rates) against end-to-end efficiency (lead time). The scale is adjusted so that the top right area of the graph indicates best performance in both dimensions.
- The overall arrest rate is 2.4 per 100 crimes reported with a median lead time of 29 days (on evaluation of only the data for the 199 cases that successfully completed all stages).
- There is statistically significant variation in the arrest rates and lead times across jurisdictions.
- However, there is no consistent correlation between these two measures. The jurisdictions with the fastest lead times are not necessarily the ones with the highest arrests.).
- From an overall forensic performance perspective, the top performer is jurisdiction D.
- Jurisdiction F achieved similar arrest rates but with longer lead times.

NIFS KEY PROJECT

End-to-End Forensic Identification Process Project

Multivariate Model Results

		Outcome for each logistic regression model			Explanatory variables									
					Site		1			2		3	4	4
Model	Cases	Stage	Outcome success	Forensic evidence	Loc-ation	Juris-diction	Attend-ance rate	Attend-ance lead time	Time at scene	Sub-mission rate	Sub-mission lead time	Analysis lead time	ID lead time	ID-IO lead time
1	[redacted]	2	Sub-mission	FP	NS	***	NS	NS	***					
2				DNA	***	***	NS	NS	***					
3				FP/ DNA	NS	***	NS	NS	***					
4		3	Suitability	NAFIS	NS	***	NS	NS	***	NS	NS	NS		
5				NCIDD	NS	***	NS	NS	*	NS	NS	NS		
6		4	ID after sub-mission	FP	NS	***	NS	NS	***	NS	NS	NS		
7				DNA	NS	**	NS	NS	**	NS	NS	NS		
8				FP/ DNA	NS	***	NS	NS	***	NS	NS	***		
9		5	Arrest after ID vsID'd	FP	NS	*	*	NS	NS	**	NS	NS	NS	NS
10				DNA	NS	*	NS	NS	NS	NS	NS	NS	*	NS
11				FP/ DNA	NS	*	NS	NS	NS	**	NS	NS	NS	NS
12		5	Arrest after ID vs. Reported	FP	NS	***	*			NS				
13				DNA	NS	*	NS			NS				
14				FP/ DNA	NS	***	NS			NS				
15		5	Arrest after ID vs. Attended	FP	NS	***	*	NS	***	*				
16				DNA	NS	NS	NS	NS	***	NS				
17				FP/ DNA	NS	***	NS	NS	***	*				

Notes:

- Each model has different amounts of data (cases) depending on the stage of the process
- Statistical significance of explanatory variables denoted by*
- (***=p<.001; **=p<.01; *=p<.05; NS=p≥.05 considered not statistically significant)
- Grey shaded regions indicate where the explanatory variable is not relevant to the model

Key Points:

- Higher submission rates are associated with longer time at the scene (models 1-3).
- Higher DNA submission rates are observed in metropolitan sites (model 2).
- Higher suitability rates are associated with longer time at the scene (models 4-5).
- Higher ID rates are associated with longer time at the scene (models 6-8) and shorter analysis lead time (model 8).
- Higher arrest rates after fingerprint identification are associated with higher attendance rates (models 9, 12, 15) and lower submission rates (models 9, 11, 15, 17).
- Higher arrest rates after DNA identification are associated with shorter DNA identification lead times (model 10).
- Jurisdictional differences remain statistically significant across all stages even when these other associations are adjusted for.

Discussion

The effectiveness of forensic science is a function of both the quality of the scientific analysis and the timeliness with which that analysis is provided, while efficiency is associated with attempts to minimise costs without negatively impacting quality (4). Effectiveness requires an evaluation of the trade-off between cases reviewed and cases delayed (backlog). Greater investment in the review of cases increases the quality but simultaneously reduces effectiveness due to an increase in time to process those cases as well as delays in processing other cases (backlog) (4).

Case backlogs can grow to the point where, the analysis achieves very little benefit or result, court proceedings are delayed and public criticism in the media can result. Where there is a delay in analysis and therefore a delay in the identification of a suspect, particularly prolific offenders, the organisation carries a risk of delaying justice. The cost of analysis cannot be evaluated on a case by case basis to the exclusion of others, as each individual case may not be cost effective but the process is one that must exist.

INTERFACES BETWEEN SCIENCE, MEDICINE AND LAW ENFORCEMENT PROJECT (NIFS KEY PROJECT)

NIFS in association with the University of Tasmania has undertaken the Interfaces between Science, Medicine, Law and Law Enforcement Project. The project is designed to explore how medical practitioners, pathologists, forensic scientists, police officers, lawyers and sexual assault centre personnel work together during homicide and/or sexual assault cases. It is clear that forensic science plays a significant role in the criminal justice system whether that is to assist prosecutors to help establish the guilt of an accused person or allowing investigators to quickly establish whether persons of interest are more than likely to be innocent (6).

Courtesy of Professor Roberta Julian, University of Tasmania

While quality evidence collected will have a higher probative value and give better results, a balance needs to be met in regard to ensuring that when trying to expedite the process we are not sacrificing quality. Poor quality evidence will only waste the time of the experts and divert them from analysing evidence with a high probative value.

The elimination or investigation of a suspect in a timeframe of close proximity to the perpetration of the offence can focus an investigation and provide a greater likelihood of a successful justice outcome.

Attrition points exist in the forensic process and identifying means by which such points can be reduced will ensure a better flow for the forensic process. Overall police organisations have been able to reduce the attrition points for fingerprints with the conversion to digital imaging and the subsequent transmission of fingerprint evidence electronically. There is still room for improvement with technology such as remote data entry.

Significant work has been undertaken within the DNA laboratories to streamline processes, improve on policies surrounding the submission of samples and reduce backlogs for volume crime. There is still room for improvement in regard to reducing the lead time for submission of samples and lead time for distribution of identification details to investigators.

As stated, forensic science facilities have actively been developing strategies to improve service delivery for some time, but these strategies have not extended to the investigation stage.

The investigation stage has the longest lead time, in fact a lead time longer than all 4 previous stages put together. There are a variety of reasons why the lead time at this stage is long and these can include the inability of the investigators to locate the suspects due to their transient nature, high workloads associated with a range of investigations and the lower priority applied to volume crime investigations.

QUEENSLAND – FINGERPRINT PROCESS IMPROVEMENT STRATEGY

The aim of the Fingerprint Process Improvement Strategy was to design and implement an improved, quality-assured process for fingerprint identification which would be highly efficient, providing front line police with a rapid means of offender identification. This new end-to-end process, building upon in-house technological initiatives, has produced a dramatic reduction in reporting times.

The Fingerprint Process Improvement Strategy has been successful in designing and implementing an end to end workflow which enables latent fingerprints located at the scenes of crime to be examined, searched and reported upon with unprecedented speed and without compromise to the quality and reliability of results. The Strategy has built upon technological solutions developed in-house by QPS Forensic Services. These include the Forensic Register (case management system) and the Remote Data Entry Project. The latter allows digital images of latent fingerprints to be wirelessly transmitted to the Fingerprint Bureau directly from the crime scene.

A dramatic and novel redesign of workflows within the fingerprint laboratory, including the creation of paperless case files and the introduction of on-screen examinations, has resulted in the time taken to examine and report on latent fingerprints being reduced from an average of 10 to 14 days to 24 hours. Indeed, a large proportion of latent fingerprints are actually being identified within the same shift in which they are received. This means that many offenders are being identified and can be stopped before they reoffend.

The fingerprint initiative won a QPS Award for Excellence in Corporate and Support Services, the Remote Data Entry Project earned the Queensland Police Service the 2009 Premiers Award for Excellence in Public Service Delivery.

Courtesy of Queensland Police Service, Forensic Services Branch

While forensic science continues to develop strategies to improve service delivery, police organisations correspondingly need to apply strategies to develop means to improve the investigation stage.

QUEENSLAND - DNA IMPROVEMENT STRATEGY, SUB-SAMPLING AT VOLUME CRIME

The DNA Improvement Strategy was a joint initiative between the Queensland Police Service, Forensic Services Branch and Queensland Health Forensic and Scientific Services aimed at reducing DNA analysis turnaround times.

Prior to the initiative prioritised samples took 13 to 16 weeks to be analysed. This delay gave opportunity for offenders to commit further crimes which in turn create more victims.

The end to end process of DNA sampling and analysis was examined to determine where efficiencies could be gained. This revealed that the initial screening and sampling of physical exhibits caused the greatest delay. Other delays included transport of exhibits to the laboratory and reporting of results.

Efficiencies could be gained if:

- the screening and sub-sampling of whole items was performed by QPS crime scene officers in the field;
- sub-samples were reduced to a form that could be directly introduced to automated laboratory platforms;
- sub-samples were forwarded to the laboratory by secure registered post; and
- the reporting of results was streamlined through interface of the Laboratory Information Management Systems used by the two organisations.

Sampling resources were developed that would enable field collected sub-samples to be placed into automated analytical platforms. Over 300 officers were provided training on how to target and sample items for DNA whilst preventing loss or contamination. In July 2008 the QPS began to take sub-samples in the field.

As a result of this initiative, under normal laboratory conditions all samples are now able to be analysed within two to three weeks of receipt. Police are now able to use DNA results to direct investigations.

QPS Forensic Services through the Forensic Register and good intelligence alliance practices is able to then link the DNA analysis to any fingerprint analysis and also to any other linked crime or suspect and provide the Investigating Officer with a Linked Chart for intelligence purposes.

The DNA Improvement Strategy won the 2010 QPS Gold Award for Excellence in Policing Operations and the IPAA Prime Ministers Awards for Excellence in Public Sector Management and Collaboration.

Courtesy of Queensland Police Service, Forensic Services Branch

NEW SOUTH WALES – DNA SUB-SAMPLING STRATEGY

As a result of an increasing backlog of DNA samples and identification that there was duplication between the sampling performed by field investigators and subsequent re-examination by laboratory biologists in the preparation of DNA samples, New South Wales Police in conjunction with Division of Analytical Laboratories (DAL) implemented the following strategies:-

- Automated analysis via robotics to streamline the DNA analysis process (installation of a state-of-the-art robotic solution and associated new chemistry);
- Field-based sub-sampling for all items requiring DNA analysis. This involves the production of robot-ready samples in the field which are submitted directly to DAL, effectively removing the duplicate examination by laboratory staff.

At the peak of the backlog in late 2010, DAL had 3,500 unstarted cases for both major and volume crime. The turn-around times for volume crime at this stage was 2 – 3 years.

Prior to the implementation of sub sampling, a number of other solutions were first implemented. The first was sending out letters to the Local Area Commands (LACs) and where there was no response (after a third letter), the exhibits were forwarded back to the LACs, where if necessary they could be re-submitted. This reduced the backlog to 1500 and was followed by the deployment of the robotic solution in the Laboratory.

The second strategy was implemented in mid-2011 where biologists from the Police Forensic Laboratory at Pemulwuy were seconded to DAL to assist with processing the cases. This resulted in the unstarted cases at DAL being reduced to zero.

The sub-sampling roll out timeline in NSW involved training of personnel and implementation for all volume crime in late 2011 and training and implementation for complex major crime is underway.

At a non-complex (volume crime) examination, generally undertaken by a SOCO, the items will be examined for fingerprints, recorded and sub-sampled at the scene and generally not retained as evidence.

The decision of what and where to sample rests with the examiner and should be based on a critical analysis regarding the probative value of the item/sample. The examiner gives consideration to which samples will contribute to and advance the investigation and which samples have the greatest chance of yielding evidence i.e. a useable DNA profile.

Sub-samples to be analysed are forwarded to DAL via a security satchel on the day of collection or on the first business day after collection. All sub-samples submitted to DAL as analysis ready will be DNA tested without question. Samples are not submitted 'for completeness' and therefore, where a suspect has made admissions in regard to handling or being in contact with the scene, the samples will not be submitted in the first instance as this only increases the backlog, causing delays in turnaround times.

Currently the turn-around-times from submission of the robot ready samples to when a result is available is 8 days.

Courtesy of New South Wales Police, Forensic Services Group

Impact of Immature DNA and Fingerprint Databases on Success Rate of Forensic Identification Process

The development and expansion of the NAFIS and NCIDD databases in Australia has greatly enhanced law enforcement's ability to solve cases using DNA profiles and fingerprints. Through the partnership between CrimTrac and Australia's police agencies, these databases store tens of thousands of potential offender and suspect reference DNA profiles and fingerprints, against which DNA profiles and fingerprints collected from crime scenes can be compared.

Given the recidivistic nature of many crimes, the likelihood exists that the individual who committed the crime being investigated was previously convicted of a similar crime and already has his or her DNA profile or fingerprints in the respective database. Moreover, NAFIS and NCIDD also permit the cross-comparison of DNA profiles and fingerprints developed from evidence found at crime scenes. Even if a perpetrator is not identified through the database, crimes may be linked to each other, thereby aiding an investigation, which may eventually lead to the identification of a suspect.

AUSTRALIAN CAPITAL TERRITORY – FORENSIC INTELLIGENCE CASE STUDY

As part of the Australian Federal Police (AFP) Forensic and Data Centres' new Forensic Intelligence initiative, ACT Crime Scenes reviewed their procedures and now attend all reported burglaries for the purpose of ensuring all evidence and intelligence is harvested from such scenes. This case study highlights the use of forensic intelligence in the form of shoeprints initiating the identification and arrest of one unknown offender and the clearance of 15 burglaries in the ACT.

Through utilisation of the Shoeprint Image Capture and Retrieval (SICAR) database as a forensic intelligence tool, similar shoeprints were observed at four burglaries within a two month time period. On interrogation of the evidence associated with these cases and liaison with relevant forensic disciplines, a number of further scene to scene linkages were introduced resulting in ten linked burglary cases. Whilst these scene linkages included two known persons, they also included the fingerprints of an unknown person of interest (POI) at seven of the ten cases. The AFP intelligence analyst embedded within the Forensic Intelligence team nominated a suspect for the unknown POI based on their knowledge of the associates of the two known persons.

The Forensic Intelligence team subsequently developed an intelligence package that was utilised by AFP investigators to support their successful application for a Magistrate's Order to obtain the nominated suspect's fingerprints and DNA. Collection of the suspect's fingerprints (no DNA was collected) resulted in the identification of the unknown POI as the nominated suspect for the seven cases, as well as the POI's fingerprints being identified at an additional eight unsolved burglaries. A pair of shoes matching the sole pattern of the original shoeprints were also recovered a couple of days later during a search warrant executed on the residence of the POI's brother.

Courtesy of the Australian Federal Police, Forensic and Data Centres

The more reference and crime scene data contained in the NAFIS and NCIDD, the more powerful a tool they become for law enforcement, especially in their application to unsolved case investigation. In jurisdictions where the databases are relatively immature, the identification rate for crime scene DNA profiles and fingerprints is reduced. The reasons for under populated databases may include education and training for frontline police officers, where there is a lack in understanding of potential impacts on clearing unsolved cases through collection of reference samples, or there could be a policy or legislation issue constraining their ability to collect such evidence as a part of the routine processing of suspects and offenders.

For jurisdictions with low rates of identification, the population of the DNA and fingerprint databases should be an area for consideration.

Future Applications of the Project

The project team has given consideration to future applications of the End-to-End Project as follows.

End-to-End Forensic Identification Process Project – Implement Recommendations

The End-to-End Project has benchmarked the forensic process in Australia for the first time on a national basis. Much like the SWIM Report, this project was a pilot program. However, the data strongly indicates that there is an opportunity to learn from the best performers in each of the five phases studied. Once this learning has been identified and implemented, the project should be repeated to benchmark any improvements that have been realised.

End-to-End Forensic Identification Process Project – Judicial System

The current End-to-End Project considered the final stage for the forensic process as the arrest or charge of a suspect. Much can happen with a prosecutorial case and as such, value would be gained by tracking the success and lead time measures through the further stages of prosecution, trial, conviction and sentencing. Anecdotal evidence from the jurisdictions indicates that at the time of prosecution, cases may be dropped due to lack of value being placed on the forensic evidence.

There are 199 cases where an arrest occurred within this data collection period, with 35 ongoing cases that should now have a stage 5 result. This project could provide a largely historical review of these cases tracked through the judicial system, resulting in a comprehensive review of the data from reported crime to the final possible outcome for the case.

Crime Scene Investigator Skills and Attributes Project

The SWIM Report provided a range of information relating to performance of individual crime scene investigators (CSI). The report indicated that the performance of CSI as it relates to identification was not linked to the average time spent at the scene and that the quality of evidence was not guaranteed simply by spending longer at a scene (2). However, indicators

suggest that success at the identification stage relates closely to the skills of the CSI to gather high quality evidence.

The Identifying the Skills and Attributes of Good Crime Scene Personnel Project conducted by the University of Tasmania has identified key CSI attributes and a small number have been noted earlier in the report (refer to page 11).

While the End-to-End Project has not conducted an evaluation on the individual performance of the CSI participating in this project, the project officer does have the relevant data (5,691 cases).

Analysis of the individual CSI and the effectiveness of their practices at collecting evidence for comparison against the key attributes identified by Dr Sally Kelty would be a means to test both theories and demonstrate the interaction between the two key NIFS projects.

Validation Process Project

The End-to-End Project evaluated the effectiveness of forensic evidence at the conclusion of the forensic process but, as can be seen in the flowchart (Page X), an arrest can be made at any stage through other investigative techniques.

Consideration should be given to undertaking a validation-verification sub-project that incorporates a validation of the value of forensics within the investigative process. The project has generated a sub-sample of data from three metropolitan and one country sites. In total, data is available for 2,418 cases from the total of 8,179 provided for the project.

This sub-sample assembly was only considered after the data collection period had commenced and the project team agreed that any further validation should be undertaken as a stand-alone project due to the limits of methodology applied.

However, limited analysis has indicated that to charge an offender, there is a statistically significant higher success rate if CSI attend and statistically significant higher success rate if forensic evidence is collected.

Further analysis of each case is likely to lead to a far more comprehensive evaluation of the data. Further information involves collating the following:

- circumstances surrounding the arrest of the suspect.
- whether the forensic evidence led to the identification of the suspect arrested.
- whether the forensic identification was a significant component of the arrest brief.
- whether any subsequent arrests were made as a result of the initial arrest based on forensic evidence.

Recommendations

This report has provided an indicative evaluation of the current lead time and success rates in relation to the performance of burglary investigations in Australia. The data provided and the analysis conducted is by no means the complete picture, but is an indication of the possibilities that exist to improve service delivery with respect to forensic evidence.

The project team makes the following recommendations:

- Members of the project team attend each jurisdiction to:
  - present the findings across the five stages of the forensic process to all relevant personnel; and
  - discuss processes and procedures within each jurisdiction that may provide further explanation of trends in observed data and identify opportunities for national learning;
- Following the implementation of national learning, repeat the study to measure the effects of implemented changes;
- Continue to track the cases with stage 5 results through the judicial process;
- Analyse the results for the individual CSI and the effectiveness of their practices at collecting evidence for comparison against the key attributes identified by the Crime Scene Investigator Skills and Attributes Project; and
- Complete the validation-verification sub-project that incorporates a validation of the value of forensics within the investigative process.

Appendix 1: Glossary

Early on in the project, the project officer defined common terminology. A broad range of definitions and cross referencing was required due to the different practices employed at local level.

Burglary	Refers to a breaking or attempted breaking offence on a dwelling or business premises, also referred to at various jurisdictions as serious criminal trespass (SCT), unlawful entry or break and enter.
Case File	A case file is generated by the Crime Scene Investigator (CSI) at the crime scene. This may be created as an electronic document at the scene or converted to an electronic document on return to the office.
Crime Reported	The time and date the crime was reported to Police. This time varied between jurisdictions as sometimes it was the first contact by the victim to the Police and sometimes it was when the written report was taken. The project agreed to use the time recorded for corporate reporting at jurisdictional level.
Crime Scene	The study only relates to the initial scene attendance at a burglary offence and does not include secondary scenes, travel time for attendance at scenes where the victim is not home and therefore no access to the scene is available.
CSI	Crime Scene Investigator also referred to as a Scenes of Crime Officer (SOCO) or Crime Scene Examiner (CSE). It does not include the attendance of general duties personnel or investigators examining the scene and collecting evidence.
DNA	Refers to the collection of DNA samples in the form of trace/contact, blood or saliva either as a swab or as items submitted to the Laboratory for analysis.
Fingerprints	Refers to the collection of fingerprints from the scene in the form of lifts, photographs or items for chemical treatment.
Study Data Collection Period	The period identified for the collection of data, 1 May 2011 to 30 September 2011.
Unique Case Identification	Case number applied to each case by the project team on the master spread-sheet.
State	Refers to the State from which that participating site is located.
Metro/Country	Refers to whether the jurisdiction considers that participating site to be a metropolitan or country policing area.
Site No	Number given to a participating site during the pilot study data collection period.
Project Case ID	The unique case number applied by the project officer
Stage 1: Attendance	Includes the period from when the crime is reported to the police and the end of the scene examination.
Scene Exam Start	The time and date that the CSI commences examination of the crime scene.
Scene Exam End	The time and date that the CSI completes the examination of the crime scene.





Stage 1 Comments	A notation was made in this column where there was a negative duration due to the crime report being taken after the commencement of the scene examination or other factors that impacted on the ability to collect the data.
Stage 2: Evidence Submission	Includes whether fingerprints or DNA were collected at the crime scene and the date and time the fingerprints and DNA are received at the Fingerprint Bureau or Laboratory.
FP Located	When fingerprints are located and collected at the crime scene a 'Y' was recorded and when fingerprints were not located an 'N' was recorded.
DNA Located	When DNA is located and collected at the crime scene a 'Y' was recorded and when DNA was not located an 'N' was recorded.
FP@FPB	Time and date the fingerprint case file/evidence was received at the Fingerprint Bureau.
DNA@Lab	Time and date the DNA case file/evidence was received at the DNA Laboratory.
Stage 2 Comments	A notation was made in this column where there was a deviation from the project requirements, i.e. inability to collect the time or the evidence was not submitted or rejected for analysis.
Stage 3: Analysis of Evidence	Includes the date and time that analyses of the evidence was commenced and whether the evidence was suitable for upload on the databases.
FP Analysis Start	The time and date the fingerprint case file was removed from the waiting list and the analysis commenced.
DNA Analysis Start	The time and date the DNA case file was removed from the waiting list and the analysis commenced.
FP Suitable NAFIS	When the fingerprint was suitable for upload to NAFIS a 'Y' was recorded and when it was not suitable an 'N' was recorded.
DNA Suitable NCIDD	When the DNA was suitable for upload to NCIDD a 'Y' was recorded and when it was not suitable an 'N' was recorded.
NAFIS	National Automated Fingerprint Identification System is a finger and palm print database and matching system that assist Australian policing agencies and the Department of Immigration and Citizenship (DIAC) to manage fingerprint records, confirm identities of persons of interest and resolve crime.
NCIDD	National Criminal Investigation DNA Database is a tool for police and forensic scientists to match DNA profiles nationally. It is a powerful investigative tool and intelligence resource crossing all jurisdictional boundaries.
Stage 3 Comments	A notation was made in this column where there was a deviation from the project requirements, i.e. an inability to collect the time or where the evidence was not analysed.
Stage 4: Identification	Includes the time and date that an identification was made from the fingerprints or DNA and the time and date that the identification was promulgated to the investigating officer.
FP ID	Date and time when a fingerprint identification was achieved.
DNA ID	Date and time when a DNA identification was achieved.

FP ID to IO	Date and time when a fingerprint identification advice was sent to the investigating officer.
DNA ID to IO	Date and time when a DNA identification advice was sent to the investigating officer.
Stage 4 Comments	A notation was made in this column where no identification was made.
Stage 5: Investigation	Includes the time and date the investigating officer took action as a result of the forensic led identification and the type of action taken.
FP ID Action	Date and time action was taken by the Investigating Officer in response to the Fingerprint Identification.
FP ID Action (Type)	Action taken by the Investigating Officer in response to the Fingerprint Identification (charged, not charged, eliminated, no action).
DNA ID Action	Date and time action was taken by the Investigating Officer in response to the DNA Identification.
DNA ID Action (Type)	Action taken by the Investigating Officer in response to the DNA Identification (charged, not charged, eliminated, no action).
Stage 5 Comments	A notation was made in this column where a suspect was charged prior to the identification or where the identification led to a victim or otherwise elimination.
Validation	Validation studies were applied to a quarter of the cases to evaluate the effectiveness of forensic evidence and to validate the project. For these cases a notation was made in regard to whether a suspect was charged or not charged.
Validation comments	Where a suspect was made one of the following comments was made: Not Charged Charged – no forensic attendance Charged – nil forensic evidence Charged – negative forensic evidence Charged – forensic evidence

Appendix 2: Participating Jurisdictions

Tasmania

Burnie/Devonport

Population: 20,000
Key Industries: Heavy machinery manufacturing; forestry; farming
Burnie is located on the north-west coast of Tasmania and is Tasmania's largest general cargo port and Australia's fifth largest container port, located 35 kilometres north-west of Hobart. It is the nearest Tasmanian port to the Australian mainland. Burnie is connected to Devonport via the four lane Bass Highway and connected to the west coast of Tasmania by the Murchison Highway.
Policing Description: Burnie Police Station is the District Headquarters for the Western District of Tasmania Police. The Burnie Division contains six police stations and has a CIB contingent, the Forensic Services headquarters, Traffic Services and Marine policing, as well as support services for the District. The Burnie Division has one 24 hour station (Burnie) and the others are staffed day shift/afternoon shift/on call. There are 125 sworn police personnel in this Division.

Launceston

Population: 68,000
Key Industries: Launceston is Tasmania's second largest city and has redefined itself as a cultural hub with vibrant cafes, museums and open parkland. Launceston sits at the junction of the North and South Esk rivers. From here, the broad Tamar River Valley opens to Bass Strait 58 kilometres away. Launceston is 198 kilometres north of Hobart.
Policing Description: Launceston Police Station is the District Headquarters for the Northern District of Tasmania Police. The Launceston Division consists of seven police stations and has a CIB contingent, Drug Investigation, Forensic, Traffic and Prosecution Services, Marine policing, as well as support services for the District. The Launceston Division has one 24 hour station (Launceston) and the others are staffed day shift/afternoon shift/on call. There are 189 sworn police personnel in this Division.

Victoria

Ballarat

Population: 90,000
Key Industries: Manufacturing, agriculture, technology and retail
Ballarat is one of the largest inland cities in Australia. Located in the Central Highlands Region of Victoria, Ballarat is approximately 110 kilometres north-west of Melbourne. Access to other key regional centres is via four main State highways; the Western, the Midland, the Glenelg and the Sunraysia Highways. The urban settlement patterns offer a diversity of living

environments, including small villages and country towns, as well as the main cityscape of central Ballarat.

Policing Description: Ballarat is the Western Region Division 3 Headquarters and has two 24 hour Police Stations, the largest and busiest at Ballarat. There are eight 16 hour stations and nine one man stations scattered throughout the various small towns. In all there are 225 sworn positions to Police the Division. Out of that number there are two CIU stations, a Sex Offence Office, two Traffic units, one plain clothes unit and one Crime Scene Officer Unit.

Wyndham

Population: 158,000

Key Industries: Strong industrial area at Laverton North and technology districts and intensive vegetable growing

Spanning 542 square kilometres on a coastal plain in the outer south-western suburbs of Melbourne and between Melbourne and the regional city of Geelong the city is large and diverse, with principal areas of population being Werribee and Hoppers Crossing containing new housing estates and is one of the fastest growing residential areas in Victoria. The City of Wyndham's population has experienced a 5.9% or about 6,000 people increase per annum which equates to about five new families moving into the municipality each day.

Policing Description: There are two police stations being Werribee and Wyndham North. Werribee is the central police headquarters providing 24/7 services and Wyndham North has approximately 30 members.

South Australia

Murray Mallee

Population: 66,700

Key Industries: Agriculture and farming

The Murray Mallee Local Service Area (LSA) spans 54,000 square kilometres, the area stretches from the pastoral districts above Renmark in the north, the Victorian Border in the East, the Coorong in the South and the foot hills of the Flinders Rangers in the West. This is a strong wine and fruit growing region including the Murray River with a diverse multi-cultural component of 50 different nationalities. The Sturt Highway, Mallee Highway and Princes Highway are the main arterial roads.

Policing Description: Murray Mallee LSA has 17 police stations including nine multi member stations and eight single person police stations jointly staffed by 156 sworn personnel and 12 non-sworn personnel. The headquarters is Berri Township 2.5 hours from Adelaide CBD. Berri/Renmark and Murray Bridge Police provide 24/7 services to their communities and each Station has dedicated CIB, Crime Prevention, Criminal Justice, Intelligence and Training Officer Sections.

Holden Hill

Population: 187,000
Key Industries: Residential
Holden Hill Local Service Area (LSA) spans 495 square kilometres the area commences at the northern edge of the Adelaide CBD and continues to the north eastern foothills approximately 30 kms from the CBD. The area is a diverse community of mainly middle class origins.
Policing Description: Holden Hill LSA has two central police stations, being Holden Hill and Golden Grove with smaller stations being Pooraka, Modbury, Gumeracha and Tea Tree Gully. Holden Hill Police Station provides dedicated CIB, Crime Prevention, Criminal Justice, Intelligence and Training Officer Sections and provides 24/7 services.

Australian Capital Territory

Canberra

Population: 347,000
Key Industries: Home of Federal Government of Australia
Canberra is the nation's capital, and is a planned city being a city in a park surrounded by bushlands. Tourism highlights what it means to be Australian through its identity, culture, history, Indigenous heritage, politics, flora and fauna.
Policing Description: ACT Policing is a business unit of the AFP and was created for the purpose of providing policing services to the ACT. There are five police stations across the North and South District of the ACT. Police attached to these stations work together to respond to general and urgent requests for police assistance across the ACT. There are three police stations located in North District - Belconnen, City and Gungahlin. There are two police stations located in South District - Tuggeranong and Woden. South District also operates a two member Rural Patrol team from the Tuggeranong Police Station that services the ACT's rural population with the support of other ACT Policing teams as required. In addition to patrol response, all stations provide a 24-hour-a-day general enquiry and face-to-face reporting service.

New South Wales

Flemington, Campsie and Marrickville

Population: 80,000 for Auburn City Council
Key Industries: Residential and industrial
Flemington Local Area Command (LAC) is diverse culturally and in socio-economic terms and has the largest overseas population with the highest percentage of new arrivals from refugee backgrounds, per capita, than any other local government area in the state. Auburn is the centre of this area and is 17 kilometres from Sydney CBD and 6 kilometres from Parramatta. Heavily residential but includes Olympic Park at Homebush. Auburn City is bounded by the Parramatta River in the north, the City of Canada Bay and the Strathfield Council area in the east, Bankstown City in the south and Parramatta City in the west. The M44 is the main freeway in the area.
Policing Description: Flemington Local Area Command (LAC) is located within the South West Metropolitan Region of the New South Wales Police Force. Police stations within this

LAC include Auburn and Strathfield. Auburn is the only station open 24 hours. Also includes Campsie and Marrickville.

Griffith

Population: 23, 801 (Griffith Shire)
Key Industries: Agriculture and Murrumbidgee Irrigation
570 kilometres south-west of Sydney the Griffith Shire area is 1,605 square kilometres. Griffith was established as part of the NSW State Government Murrumbidgee Irrigation Area project to supply irrigation from the Murrumbidgee River in western NSW to be used for farming. Farming includes rice, citrus and other fruit and vegetables and is one of the most productive agricultural regions in Australia. This can be partly attributed to the high Italian population which has also aided in the growing and successful wine region. It can be accessed by road from Sydney and Canberra via the Hume Highway and the Burley Griffin Way and from Melbourne via the Newell Highway.
Policing Description: Griffith Local Area Command (LAC) is located within the Southern Region of the New South Wales Police Force. Police stations within this LAC include Barellan, Barmedman, Carrathool, Coleambally, Darlington Point, Goolgowi, Griffith, Grong Grong, Hillston, Leeton, Narrandera, Rankins Springs, Tallimba, Ungarie, Weethalle, West Wyalong, Whitton and Yenda. Griffith is the only station open 24 hours.

Western Australia

South Metropolitan District

Population: 230,000
Key Industries: Residential and port
The area is approx. 19 kilometres southwest of Perth CBD and covers a geographical area of 256 square kilometres. This South Metropolitan District is bordered by the Swan River to the north, the west with the Australian coastline and the south with the Murdoch district a rapidly developing residential, University and hospital area. Fremantle is the inner harbour of the Fremantle Port and is located at the mouth of the Swan River. Freemantle Port is a deep water facility for handling container trade, live exports, cruising ships and visiting naval vessels. Freemantle Port is also the closest of Australia's five major capital city ports to Singapore and is often the first and last port of call for shipping operating between Australia and overseas destinations. This area is a broad mixed-class of professionals.
Policing Description: This area is overseen by South Metro District Forensic Investigation office, based at Fremantle police station; 45 Henderson Street, Fremantle, tel: [redacted]
The district contains five Police Stations with the Fremantle station the only open 24 hours. This district includes police stations at Cockburn, Murdoch, Palmyra and Rottnest.

Great Southern District

Population: 33,000
Key Industries: Agriculture and farming

Albany is 409 kilometres South East of Perth on the South Coast of Western Australia. Great Southern geographical area amount to 100,289 square kilometres of which 4,310 square kilometres is Albany police area. Albany is located on Princess Royal Harbour and King George Sound. A profound and continuing connection with the Anzac legend as Albany was the place of assembly and departure for some 30,000 troops serving in the Great War and Gallipoli in 1914. Bounded by the Southern Ocean, the picturesque Stirling Range and the Great Southern hinterland, Albany embraces clean, green principles, from wind-generated energy to sustainable and organic agriculture, to ensure its continuing viability as a liveable, progressive centre.

Policing Description: To ensure the accurate collection of data I am narrowing the area to that specific to Albany District Forensic Investigation office (see below), Albany Police Station, [redacted] Tel: [redacted] This district contains 23 Police Stations. For ease of reference and data recording the defined service area being used for this project is specific to postcode 6330.

Northern Territory

Darwin

Population: 70,055
Key Industries: Mining, offshore gas production, pastoralism, tourism, tropical horticulture
Darwin is Australia's most northerly city, on the coast of the Timor Sea, at the 'Top End' and covers an area 112 square kilometres. As the capital of the Northern Territory, Darwin is the centre of government and the major administrative and commercial centre. The Port of Darwin is the main outlet for Australia's live cattle export trade into South East Asia. Darwin has an onshore $1.75 billion LNG gas plant, at the end of a 500km pipeline from the Timor Sea gas fields. Darwin has more than 60 nationalities and some 76 ethnic groups living in the city and about 28 percent of the Territory's population is Aboriginal.
Policing Description: There are three police stations within the city bounds. The Peter McAulay Centre at Berrimah contains the administrative and specialist areas including Forensic Services. Headquarters, Darwin Police Station is in the Central Business District and contains the watch house. The most common issues for police in the suburbs are juvenile crime and unlawful entries and in the city are associated with nightclubs, hotels and busy tourist trade.

Katherine

Population: Town 8,500 and region a further 18,000
Key Industries: Cattle, horticulture, mining and tourism
Katherine is located 310 kilometres south of Darwin on the Katherine River and covers an area of 22,500 square kilometres. Katherine is a regional centre for communities from the Western Australia border to the Gulf of Carpentaria on the Queensland border. The Jawoyn people are the traditional owners of the Katherine Gorge and joint management of Nitimiluk National Park provides work and training opportunities for Aboriginal people. Tindal RAAF Base, Australia's northern air defence command centre, is 15 kilometres south of the town.
Policing Description: Pine Creek, Lajamanu, Kalkaringi, Timber Creek, Mataranka, Maranboy and Ngukurr. The station includes a range of services including one Forensic Officer. Police will attend a diverse range of incidents in this district.

Queensland

Metropolitan District

Population: 250,000
Key Industries:
300,000 square kilometres
Policing Description:
5 Divisions

Regional District

Population: 80,000
Key Industries:
35,000 square kilometres
Policing Description:
12 Divisions



NIFS KEY PROJECT

End-to-End Forensic Identification Process Project

Appendix 3: Spread-Sheet Template

STAGE 1: SCENE ATTENDANCE					STAGE 2: EVIDENCE SUBMISSION				STAGE 3: ANALYSIS				STAGE 4: IDENTIFICATION				STAGE 5: INVESTIGATION			
Case ID	Reported (Date Time)	Offence Code (B&E)	Scene Exam Start (Date Time)	Scene Exam End (Date Time)	FP Located (Y/N)	DNA Located (Y/N)	FP @ FPB (Date Time)	DNA @ Lab (Date Time)	FP Analysis Start (Date Time)	DNA Analysis Start (Date Time)	FP Suitable NAFIS (Y/N)	DNA Suitable NCIDD (Y/N)	FP ID (Date Time)	DNA ID (Date Time)	FP ID to IO (Date Time)	DNA ID to IO (Date Time)	FP ID Action (Date Time)	DNA ID Action (Date Time)	FP ID Action (Type)	DNA ID Action (Type)





NIFS KEY PROJECT

End-to-End Forensic Identification Process Project

Letters

Dear ,

Re: **End-to-End Volume Crime Identification Process Project**

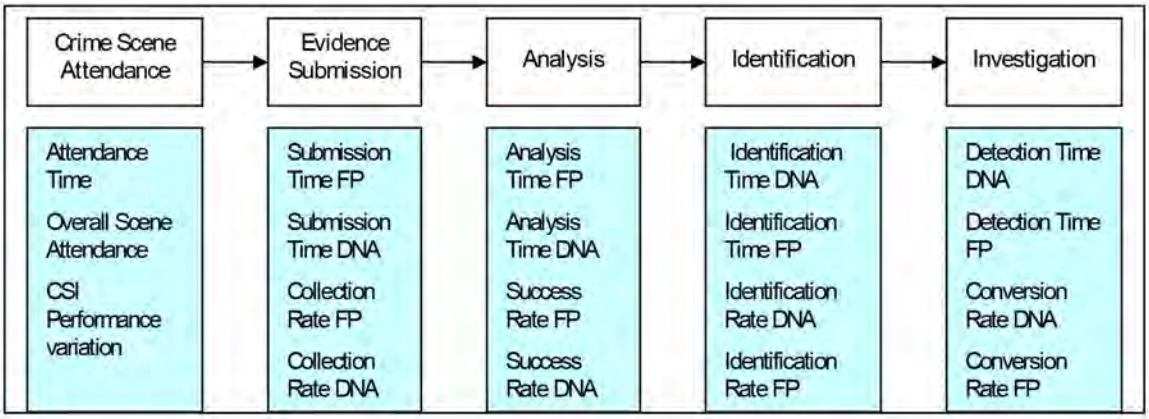
As you are aware, in response to the ANZPAA Strategic Priorities, NIFS has commenced a project to review end-to-end forensic processes and develop a national framework for efficient crime scene analysis.

The approach is fundamentally a systematic five-step process of analysis designed to measure the effectiveness of forensic processes. The project is based on the UK Scientific Work Improvement Model (SWIM Report). The project aims to evaluate forensic systems in Australia and make recommendations for improvements in much the same manner as occurred in the UK and is now occurring in New Zealand. The development of a framework for consistent reporting will lead to a situation where all jurisdictions will be in a position to learn from better performers both at an organisational and individual level.

The aim of the process ultimately is crime reduction by utilising rapid forensic processes to convert scientific evidence into arrests at an increased rate. A framework has been developed with a defined scope designed to be implemented as a pilot project for 6 months. In the first instance it is proposed that the pilot study will apply only to volume crime (burglary dwelling) and evidence types of fingerprints and DNA. The project team is seeking to implement the pilot study in only two service areas within each jurisdiction, one country and one metropolitan district.

NIFS and the project team will work together with the jurisdictions to provide advice and guidance on the relevant metrics and implementation of the pilot study. The project team proposes to provide a one day workshop with all relevant participants in each jurisdiction to ensure participants are fully conversant with the requirements of the pilot study. As can be seen the data collation for the entire end-to-end process involves coordination and communication between both law enforcement and forensic science facilities.

The schematic of the Framework for the pilot study is similar to that developed for the SWIM Report:



The measures are as follows:

Attendance

- ⇒ *Attendance time:* time lapse between victims' call and scene attendance by CSI
- ⇒ *Overall scene attendance:* the percentage of burglary dwelling crime scenes attended by CSI
- ⇒ *CSI performance variation:* average time spent at a burglary dwelling crime scene by CSI

Evidence Submission

- ⇒ *Submission time fingerprints:* time lapse between the time the item is collected at the scene and time it is received for analysis at the Fingerprint Bureau
- ⇒ *Submission time DNA:* time lapse between the time the item is collected at the scene and the time it is received for analysis at the Laboratory.
- ⇒ *Fingerprint collection rate:* the percentage of scenes attended from which fingerprints are collected and submitted for analysis.
- ⇒ *DNA collection rate:* the percentage of scenes attended from which items for DNA analysis are collected and submitted for analysis.

Analysis

- ⇒ *Analysis time fingerprints:* time lapse between the time the item is received for analysis and the time it was analysed.
- ⇒ *Analysis time DNA:* time lapse between the time the item is received for analysis and the time it was analysed.
- ⇒ *Fingerprint success rate:* the percentage of items received for analyses that were uploaded for comparison.
- ⇒ *DNA success rate:* the percentage of items received for analyses that were uploaded for comparison.

Identification

- ⇒ *Identification time fingerprints:* time lapse between the time an item was analysed and a notification of identification (result) is provided to the investigating officer.





NIFS KEY PROJECT

End-to-End Forensic Identification Process Project

- ⇒ *Identification time DNA:* time lapse between the time an item was analysed and a notification of identification (result) is provided to the investigating officer.
- ⇒ *Identification rate fingerprints:* the percentage of fingerprints uploaded for comparison that resulted in a database link (person to crime).
- ⇒ *Identification rate DNA:* the percentage of DNA items that were uploaded for comparison that resulted in a database link (person to crime).

Investigation

- ⇒ *Detection time fingerprints:* time lapse between the time that a notification of identification is provided to the investigating officer and the time taken to act on the information (i.e. charges laid).
- ⇒ *Detection time DNA:* time lapse between the time that a notification of identification is provided to the investigating officer and the time taken to act on the information (i.e. charges laid).
- ⇒ *Conversion rate fingerprints:* the percentage of fingerprint identifications that result in a crime clearance.
- ⇒ *Conversion rate DNA:* the percentage of DNA identifications that result in a crime clearance.

All data collated will be kept confidential and for the purposes of any report will be de-personalised. An evaluation of the data and recommendations will be available for all jurisdictions on completion of the pilot study.

As identified at the 2010 SMANZFL Meeting in Adelaide, to proceed with the project requires the commitment of the relevant organisations in this forensic process. Initial contact has been made with the police organisations to evaluate the ability to obtain data for the above measures. Some jurisdictions will require further advice and guidance in implementing data collection and this advice can be provided.

I am seeking a commitment from your organisation to participate in the pilot study and the nomination of a contact officer from within your organisation with whom I can liaise and coordinate the progress of the organisation in preparation for the pilot study.

The project team aims to provide the workshops in February 2011 with commencement of the pilot study shortly thereafter hence I seek the name of the contact officer by 1 January 2011.

If I can be of any further assistance please do not hesitate to contact me.

Thank you in anticipation.

Yours sincerely,

Cheryl Brown APM
ANZPAA NIFS Project Officer
Ph wk: [redacted]
[redacted]





NIFS KEY PROJECT

End-to-End Forensic Identification Process Project

Acknowledgements

ANZPAA would like to acknowledge the following personnel for their contribution to the project.

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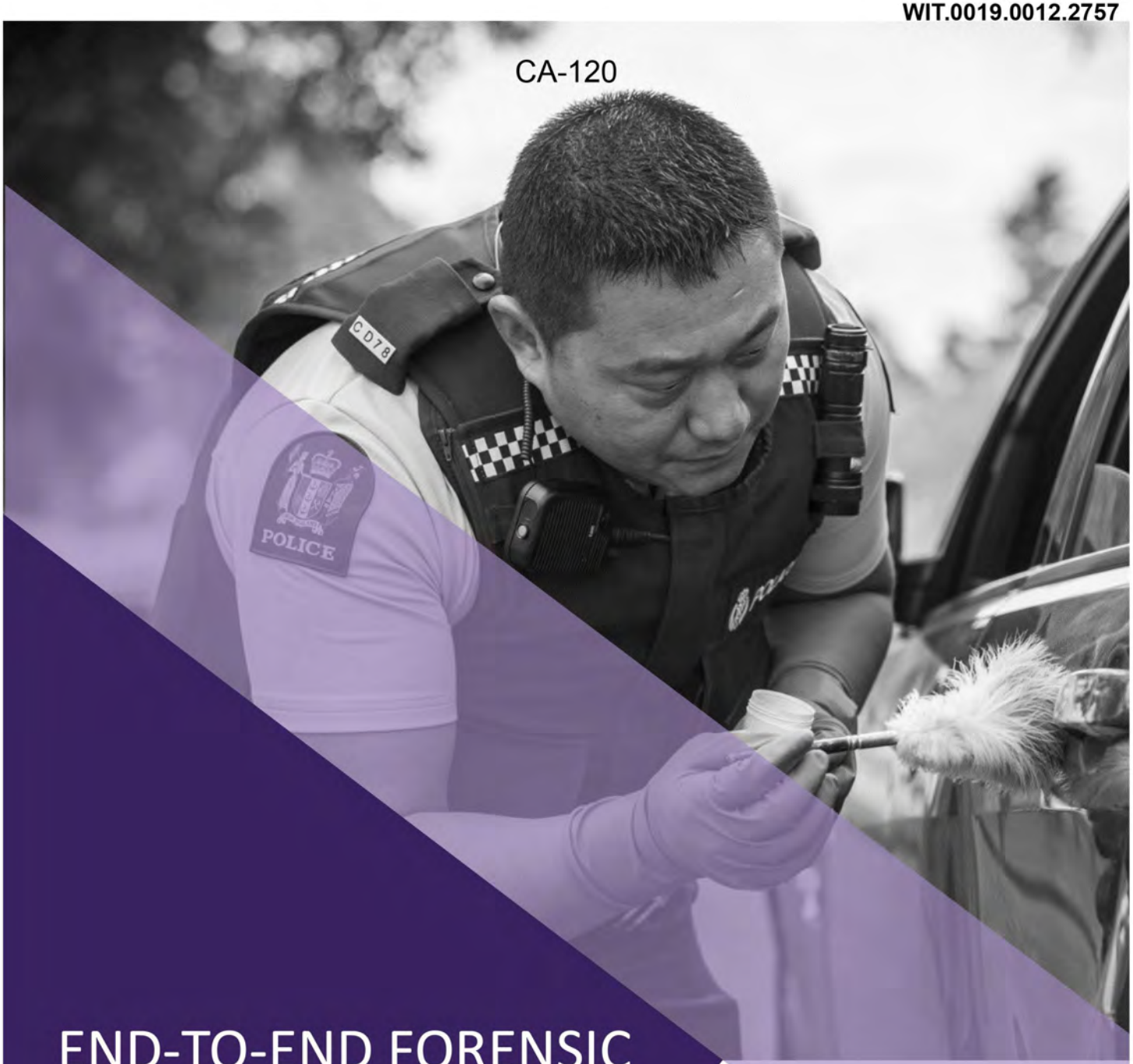

END-TO-END FORENSIC IDENTIFICATION PROCESS PROJECT

Phase 2 – Final Report

2016

ANZPAA
Australia New Zealand Policing Advisory Agency

NIFS
National Institute of Forensic Science Australia New Zealand

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FOREWORD

There are few studies like the End-to-End project, which aims to assess the effectiveness of forensic science as a function of the quality of the scientific analysis and the timeliness with which that analysis is provided. The End-to-End project is fundamentally different from more discrete studies that measure individual components or stages, in that it provides a whole-of-process assessment, mirroring the complex process of criminal investigations. The End-to-End project has provided a framework for assessing the impact of change on service delivery, be it organisational change or technical change. This report details the results of the second time the End-to-End project has been run. The repeat of the project enables jurisdictions to compare previous performance to current, as well as examine cross-jurisdictional performance, providing a real opportunity to learn from the best performers.

By applying consistent performance criteria across both projects, examination of the wealth of data that has resulted can reveal how different organisational approaches, technology impacts and the extent to which forensic science is integrated into investigations can impact service delivery. Not only does a study like End-to-End help improve effectiveness by identifying efficient processes or repetitive effort, it also identifies future risks and opportunities. The more fingerprint and DNA databases continue to grow, the more effective a tool they become in assisting law enforcement's ability to solve cases, further validating the use of forensic evidence to build databasing capabilities.

The End-to-End projects, while limited in scope to fingerprint and DNA evidence from non-aggravated burglaries, provide a series of snapshots of forensic performance, highlight the responsiveness of the participating agencies in adopting the recommendations for improved use of resources, and givesome direction to future endeavours to ultimately improve the efficiency and effectiveness of forensic science.

[redacted]

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Director National Institute of Forensic Science
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EXECUTIVE SUMMARY

This report presents the findings from a repeat of the original End-to-End (E2E1) project run in 2011. This repeat project has been termed End-to-End Phase 2 (E2E2). E2E2 was conducted in 2015 in the same eight Australian jurisdictions, with the same data collection period (May – Sept) as E2E1, and under the same conditions.

One of the main challenges in re-running the End-to-End project was identifying jurisdictional changes occurring since 2011, whether legal, technological or organisational, and to what extent recommendations from the original End-to-End project had been implemented. A core benefit of repeating the project was enabling agencies to compare their own data from the previous phase and establish whether such changes have had any significant impact on efficiency or effectiveness. To this end, individual jurisdictional results from E2E2 were made available to each relevant jurisdiction and responses were sought from each of the Australian forensic agencies to identify what changes have occurred since E2E1 and to provide possible explanations for any variations between the two projects.

This report makes available the findings from the analysis of the 2015 data, provides a comparison with 2011 data, and offers future recommendations.

RESULTS OVERVIEW

Based on data collected from 17 sites across Australia for more than 7,500 burglaries reported over a five month period, this study has established that:

- There is wide variation between state jurisdictions across each stage of the forensic process, both in terms of success (except for analysis success) and lead times (including the analysis stage).
- 76% of burglaries reported to police were attended by CSI with a median response time of 3.5 hours and a median time spent at the scene of 44 minutes.
- In 2011 regional areas had higher attendance rates and longer scene examination times than metropolitan areas. However, in 2015, metro had higher attendance rates and the scene examination times were essentially equivalent.
- Again there was more fingerprint evidence collected compared with DNA (32% versus 14%). And again there was a (this time slightly) higher arrest rate based on DNA identification than fingerprint identifications (42% versus 41%).
- Identification rates were the same for both fingerprints and DNA (32%), up from 23% in 2011, reflecting the improved collection of value evidence and generally more mature databases.
- At each stage in the End-to-End process, national median lead times were shorter for fingerprint evidence than DNA evidence and the 2015 data showed a median overall End-to-End process time of 16 (previously 19) days for arrests based on fingerprint identifications compared with 49 days (same) for arrests based on DNA identifications only. Overall when fingerprint and DNA evidence is considered together, forensic evidence achieves a median End-to-End process time of 28 (previously 29) days.
- In 2011, the last stage dominated the overall time in almost all jurisdictions. The majority of jurisdictions have since reduced their overall lead times significantly and the 2015 data shows the National average is down by almost 50%.
- The overall arrest rate after forensic identification is 4.7 per 100 crimes reported, nearly double that of 2.4 per 100 from 2011 data.

On a stage by stage basis, again from the 2015 data, there was no consistent evidence to suggest that strong performance at one stage of the process correlated with strong performance for another stage or that there was a link between stages. There remained significant variation in performance across the jurisdictions, indicating a potential scope for further improvement across the many stages of the forensic process. Again, understanding that each police agency operates under different legislation and internal practices, it is anticipated that each jurisdiction may need to tailor their strategy in order to further improve performance in processing burglary cases.

Table 1: Success rates and lead times across the five stages of the forensic process aggregated from 7,598 reported burglary cases in 17 sites across Australia, 2015.

Stage	Success rate		Lead time (median)	
	Fingerprint	DNA	Fingerprint	DNA
Attendance	76%		3.5 hrs (and 44 minutes at the scene)	
Submission	32%	14%	Same day	6 days
Analysis	100%	100%	One day	3 days
Identification	32%	32%	One day	20 days
Arrest	41%	42%	6 days	11 days
End-to-end	3%	1.5%	16 days	49 days

CRIME SCENE ATTENDANCE

- 76% of burglaries reported were attended by CSI, with statistical variation between the jurisdictions (54% to 100%) and by location (Regional 73% to Metro 78%).
- While the attendance median lead time nationally is 3.5 hours (down from four hours), there is statistical variation between jurisdictions (one hour to eight hours) but no variation by location.

EVIDENCE SUBMISSION

- In 32% of scenes attended, fingerprint evidence is collected, with statistical variation between the jurisdictions (17% to 54%) and in 14% DNA evidence is collected, again with statistical variation between the jurisdictions (4% to 42%).
- Submission of fingerprint evidence is largely electronic for Australian police agencies and as such, fingerprints are submitted within 24 hours on a consistent basis, a fact that is supported by the fingerprint submission lead time data of 'same day' for this study.
- Statistical variation still existed between the jurisdictions for submission of fingerprint evidence (0 to 1 day).
- The submission of DNA evidence across the sites surveyed is a manual process requiring physical transportation to the laboratory. In 2015 the national median lead time for submission of DNA evidence is six days with statistical variation between jurisdictions (four to 12 days).

ANALYSIS OF EVIDENCE

- In 100% of cases, fingerprint evidence and DNA evidence submitted for analysis was analysed.

- Overall, the percentage of cases with a profile suitable for upload to the National Automated Fingerprint Identification System (NAFIS) database is nearly double that of the percentage of cases with a profile suitable for upload to the National Criminal Investigation DNA Database (NCIDD). 91% of fingerprint evidence analysed resulted in a print suitable for upload to NAFIS (up from 87% in 2011), compared to 47% of DNA evidence being found suitable for upload to NCIDD, up from 42% in 2011.

IDENTIFICATION

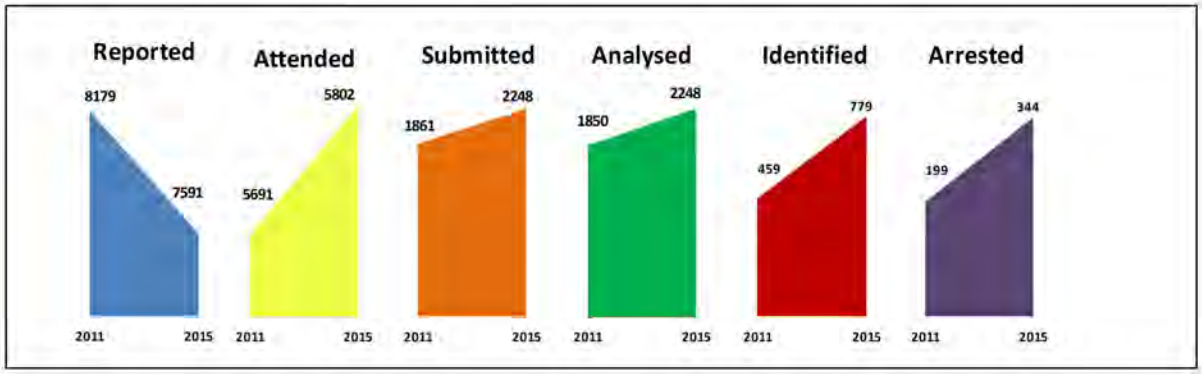
- The overall identification rate for fingerprints and DNA was 32% for each. There was variation observed between the jurisdictions (fingerprints 17% to 83% and DNA 17% to 69%).
- There are higher identification rates in DNA by location at regional sites (37%) as opposed to metropolitan sites (31%), but not much difference for fingerprints by location (31% versus 32%).
- There are longer median lead times for DNA identification than for fingerprints. The increase in the number of DNA markers examined and new methods of interpreting DNA mixtures (i.e. introduction of STRmix) was anticipated to increase the time it takes to analyse and interpret DNA profiles (however, it appears to have had a greater effect in some jurisdictions).

INVESTIGATION

- For cases in which the identification of an offender was made from fingerprint evidence, 41% resulted in the arrest of the offender. Comparatively, for cases in which the identification was made from DNA evidence, 42% resulted in an arrest. In 2011 these percentages were 37% and 50% respectively.
- In 2015 there are still longer lead times for DNA based arrests than for fingerprint based arrests.
- The national lead time for investigation (i.e. the time from identification to arrest) has reduced significantly in 2015, where as in 2011 it was longer than the lead time for all other stages put together.
- The overall arrest rate after forensic identification is 4.7 per 100 crimes reported (rounded to total 4.5 in Table 1 above), with a range across the jurisdictions of 2 to 10 arrests per 100 crimes reported.

COMPARISON OF THE RESULTS BETWEEN E2E1 AND E2E2

Figure 1: Attrition of Cases across Stages of the Forensic Process



Note: The unit of observation for this study was a case, not an offender. Two or more arrests based on forensic evidence from one burglary scene were only counted as one successful unit or case as the focus was only on the success of the case, not the number of arrests.

KEY POINTS:

- There is attrition at all stages of the process.
- 39% of cases for which a CSI attended the scene have forensic evidence collected (up slightly for 2011 data at 33%).
- Almost 35% of forensic evidence analysed results in an identification (up from 25%). This result possibly reflects the overall better collection of value evidence and more mature databases since 2011. Databases have increased in size since 2011. This may reflect a continuing upward trend.
- 4.7 arrests are linked to forensic evidence out of 100 reported burglary cases (up from 2.4 in 2011).
- 6.1 (previous 3.5) arrests are linked to forensic evidence out of 100 attended burglary cases.

Table 2: Success rate and lead time comparison between 2011 and 2015

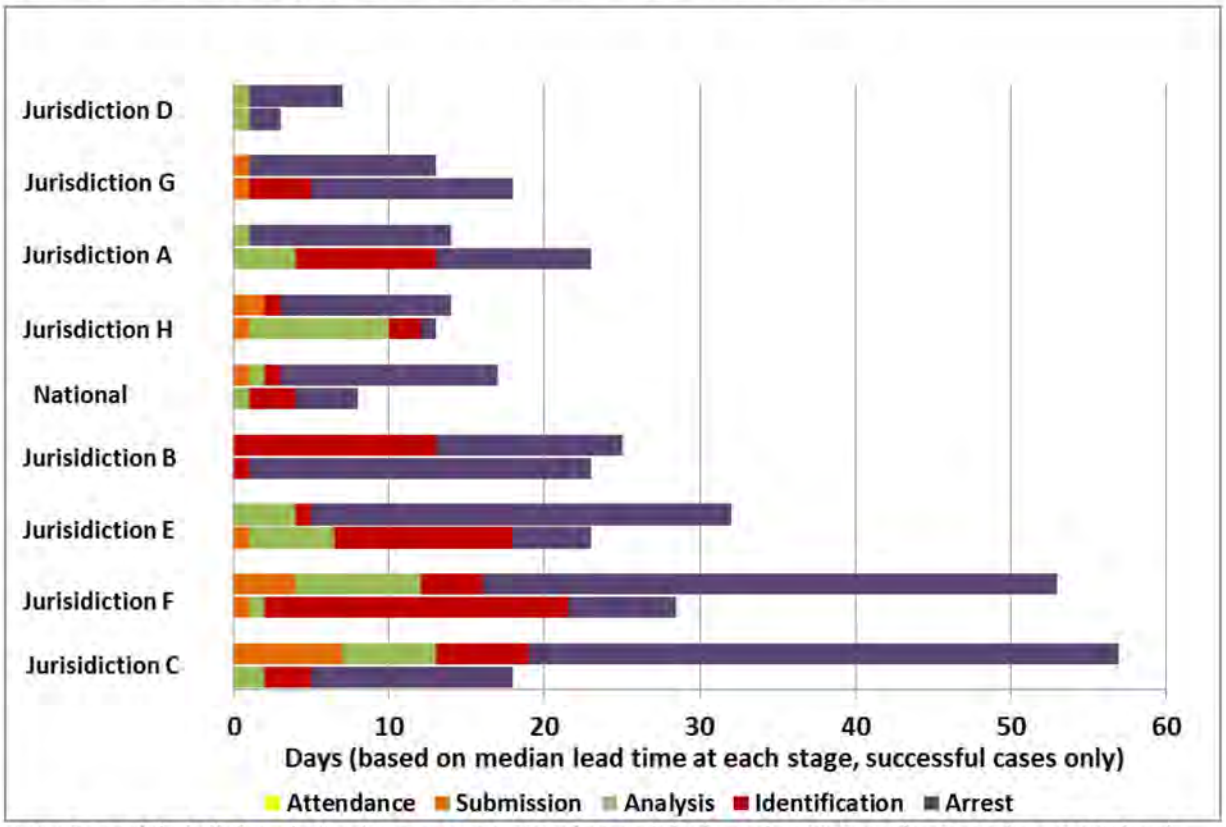
Stage	Success rate		Lead time (median)	
	Fingerprint	DNA	Fingerprint	DNA
Attendance	76% Vs 70%		3.5 hrs (and 44 minutes at the scene) Vs 4 hrs (and 30 min at the scene)	
Submission	32% Vs 28%	14% Vs 10%	Same day Vs Same day	6 days Vs 5 days
Analysis	100% Vs 100%	100% Vs 98%	One day Vs One day	3 days Vs 3 days
Identification	32% Vs 23%	32% Vs 23%	One day Vs Same day	20 days Vs 15 days
Arrest	41% Vs 37%	42% Vs 50%	6 days Vs 11 days	11 days Vs 20 days
End-to-end	3% Vs 2%	1.5% Vs 1%	16 days Vs 19 days	49 days Vs 49 days

Note: Attendance is measured in hrs, and minutes, not days. Success refers to progression to the next stage. Upper number 2015 data vs lower number 2011 data. Green: improvement, Red: decline, Black: status quo.

KEY POINTS:

- Again, as in 2011, the 2015 results showed there was more fingerprint evidence collected compared to DNA (32% versus 14%). However, the arrest rate based on DNA identification compared to fingerprint identifications was similar (42% versus 41% respectively).
- Identification rates were the same for both fingerprints and DNA (32%), up from 23% in 2011, reflecting both an improved collection of value evidence and generally more mature databases.
- At each stage of the End-to-End process, national median lead times were shorter for fingerprint evidence than DNA evidence.

Figure 2: Lead times (Median): By Jurisdiction (Forensic Evidence) – 2011 vs 2015 results

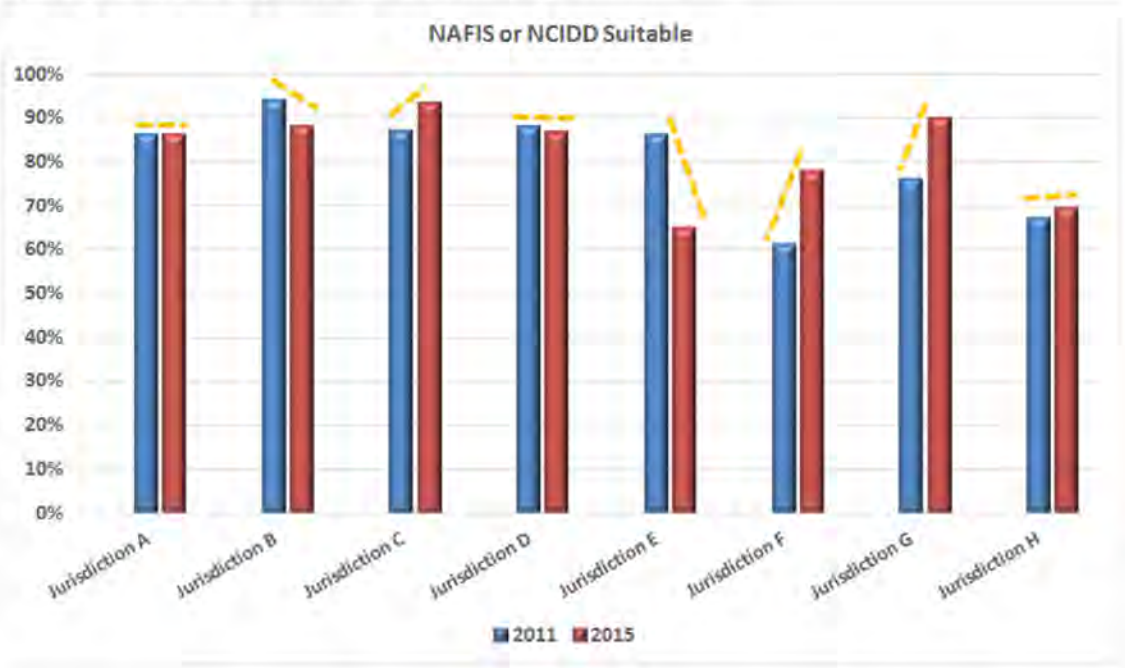


Note: For each jurisdiction, the top bar represents 2011 data and the lower bar 2015 results. Same day = 0. National = aggregate across all 17 sites. Forensic evidence = combining fingerprint and DNA information, where available for the same case. Attrition of cases may impact the median lead times calculated at each stage and how these values can be compared.

KEY POINTS:

- This figure illustrates the relative length of each stage in contributing to the End-to-End lead time.
- In 2011 the last stage dominated in almost all jurisdictions. The majority of jurisdictions have since reduced their lead times significantly.
- By comparison the 2015 data shows the national median lead time is down by almost 50.

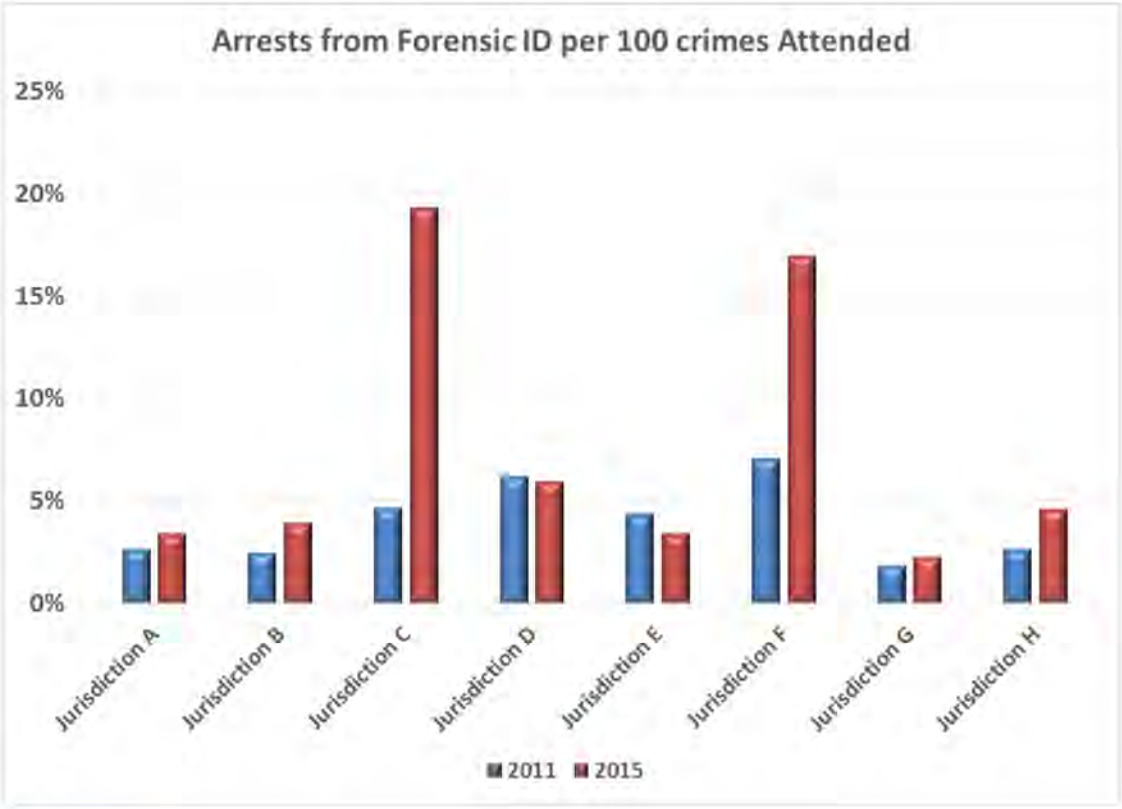
Figure 3: Results percentage NAFIS or NCIDD suitable: By Jurisdiction



KEY POINTS:

- Improved collection of value evidence for some jurisdictions is linked to training and organisation change. For example, feedback from Jurisdiction G indicates the number of value fingerprint lifts by CSI's has improved, due in part to enhanced training of CSI's. This finding is supported in E2E2 data where the percentage of NAFIS suitable fingerprints for Jurisdiction G increased in 2015, and its effect is shown here contributing to the overall gain in suitable fingerprint and DNA evidence. Similarly, feedback from Jurisdiction F also indicated that they have implemented an improved collection strategy for forensic evidence and also improved training for CSI's for taking DNA swabs.
- Other jurisdictions remained much the same or showed a decrease in 2015. For example, 2015 data illustrates that of all jurisdictions, Jurisdiction E had the lowest number of cases where DNA was located. This may reflect a training opportunity for those jurisdictions that have shown a reduction since 2011.

Figure 4: Arrests from Forensic Evidence per 100 Crimes Attended: By Jurisdiction

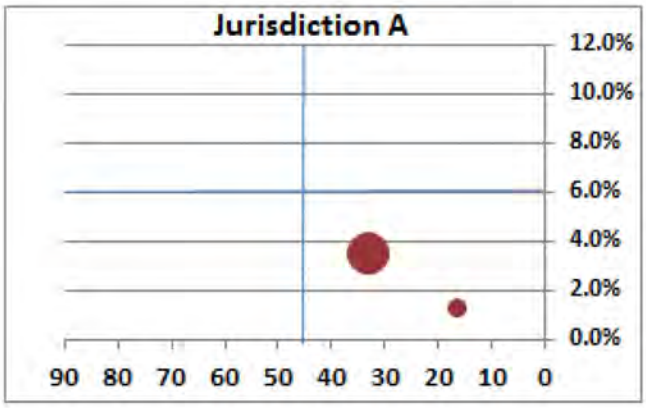


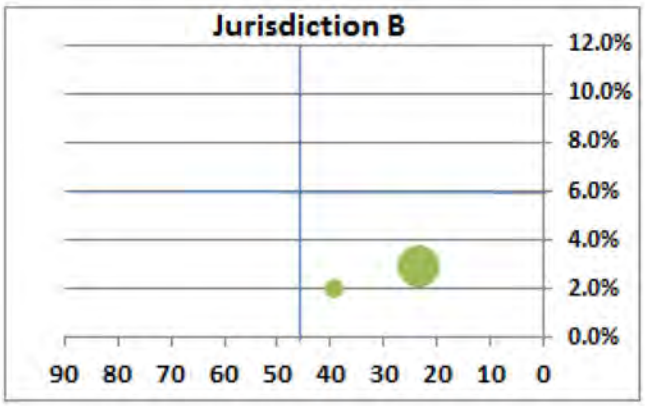
KEY POINTS:

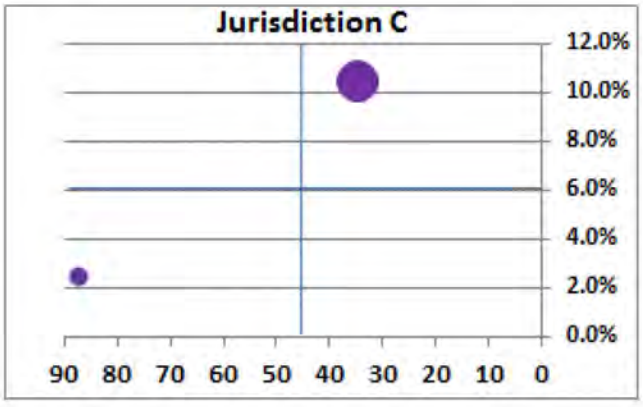
- The large increase for Jurisdiction C can be attributed to the relevant police agency in this jurisdiction creating a group to specifically target property crime between 2011 and 2015. Also, between 2011 and 2015 Jurisdiction F reduced the number of DNA samples accepted by the laboratory and engaged in training around the type of high value samples to collect.

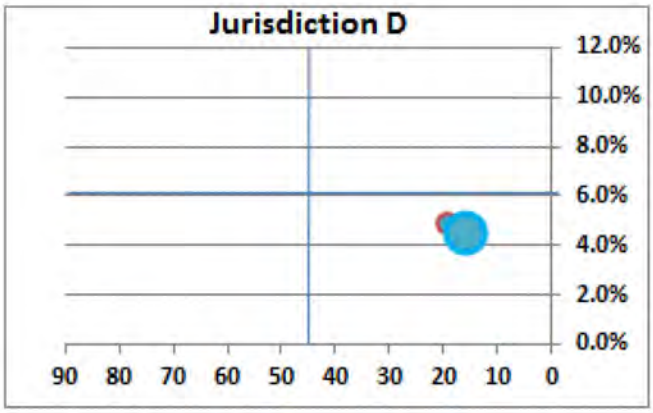
Figure 5: Success vs. Time (Median) per 100 Crimes Reported: By Jurisdiction -

Arrests after forensic ID per 100 crimes reported v. Speed, days (based on median of end-to-end time)





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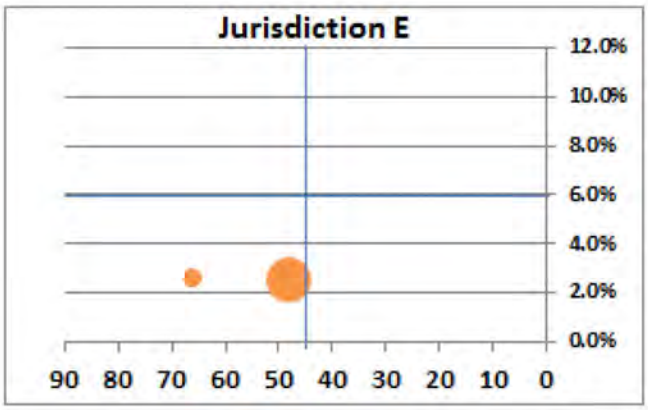
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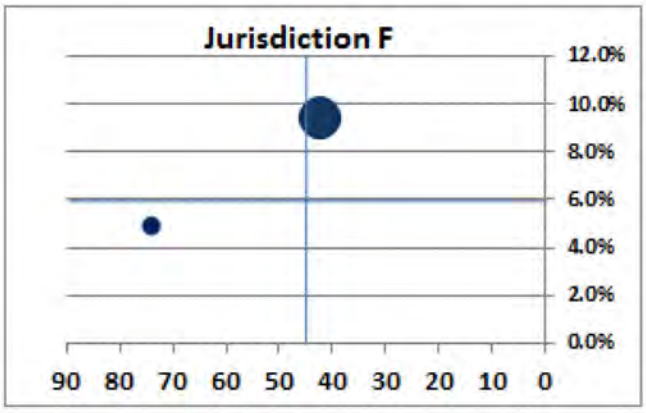
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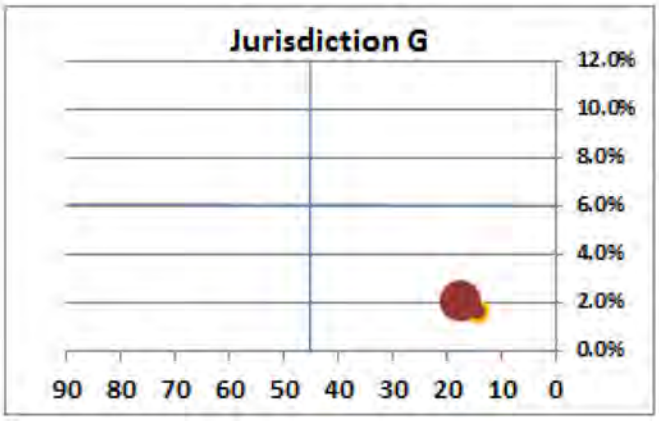
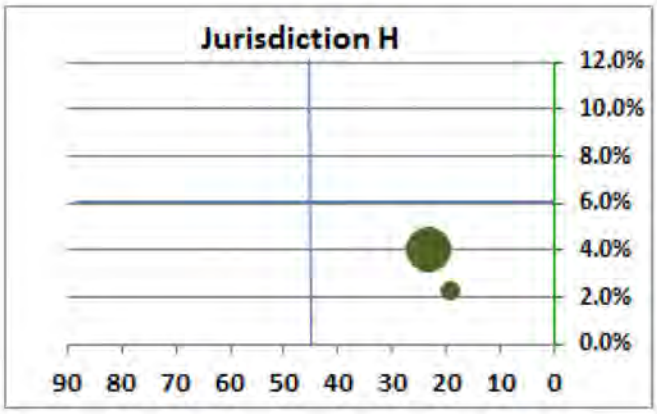




Note: Small circles represents 2011 data and large circles represents 2015 data. Due to the attrition of cases across the stages, these jurisdictional End-to-End graphs (i.e. of success vs time) represent the analysis of relatively small datasets.

KEY POINTS:

- This graph provides an overall performance summary plotting end-to-end effectiveness (arrest rates) against end-to-end efficiency (lead time). The scale is adjusted so that the top right area (quadrant) of the graph indicates best performance in both dimensions.
- The overall arrest rate is 4.7 per 100 crimes reported (range two to ten), with a median lead time of 28 days (previously 29 days), almost double that of 2.4 per 100 from 2011 data.
- There is significant variation in the arrest rates and lead times across jurisdictions.
- However, there is no consistent correlation between these two measures. The jurisdictions with the fastest lead times are not necessarily the ones with the highest arrests.
- Almost all jurisdictions have vacated the lowest performing quarter (bottom left quadrant).
- Jurisdiction F and C achieved significant improvements in both lead times and arrest rates.
- From an overall forensic performance perspective, the top performer remains Jurisdiction D.

RECOMMENDATION

That the 2015 comparative data be used to identify further learnings which when implemented result in improved service delivery.

INTRODUCTION

The original 'End-to-End Forensic Identification Process Project' (E2E1) was designed to measure performance by jurisdiction and nationally for the crime type of burglary and evidence types of fingerprints and DNA. The End-to-End process was defined as the time from the report of a crime through to the arrest of an offender. The performance of police agencies and DNA laboratories was examined in relation to both the overall end-to-end processing of volume crime and also broken down into five further distinct stages of attendance, submission, analysis, identification and investigation to draw out key insights within the End-to-End process. This approach provided a framework to capture and compare data and put in place a national model that could highlight efficiency and effectiveness throughout the end-to end process.

After the initial running of the E2E1 project and data capture in 2011, the findings from E2E1 were presented to the ANZPAA Board in June 2012 and briefings for staff in each jurisdiction were also held. Support was given for the project to be repeated three years later in order to measure any improvements and lessons learned from E2E1. In January 2015 the ANZPAA Board approved the repeat of the project, with data collection to again be conducted between May and September 2015 in the same 17 sites as E2E1. All jurisdictions that participated in E2E1 again committed to participate in the End-to-End project repeat (E2E2). Feedback was sought from participating agencies in relation to any reasons for differences in the results between the data collected from the two projects.

Reference codes have been applied to each jurisdiction and these codes (shown on the graphs etc.) were assigned by the original project team and have been used consistently between the E2E reports. A guide to relevant terminology used within the project can be found in **Appendix 1**. Performance measures at each stage are described in **Appendix 2**. Data collection and analysis methodology is described in **Appendix 3**. A full account of the background and methodology adopted in E2E2 can be found in the original End-to-End project report [1]

FINDINGS

The findings are a summary of actual data from cases that have occurred within Australia and provide an opportunity for agencies to compare and contrast performance in the processing of fingerprint and DNA evidence in volume crime cases across all stages of the forensic process.

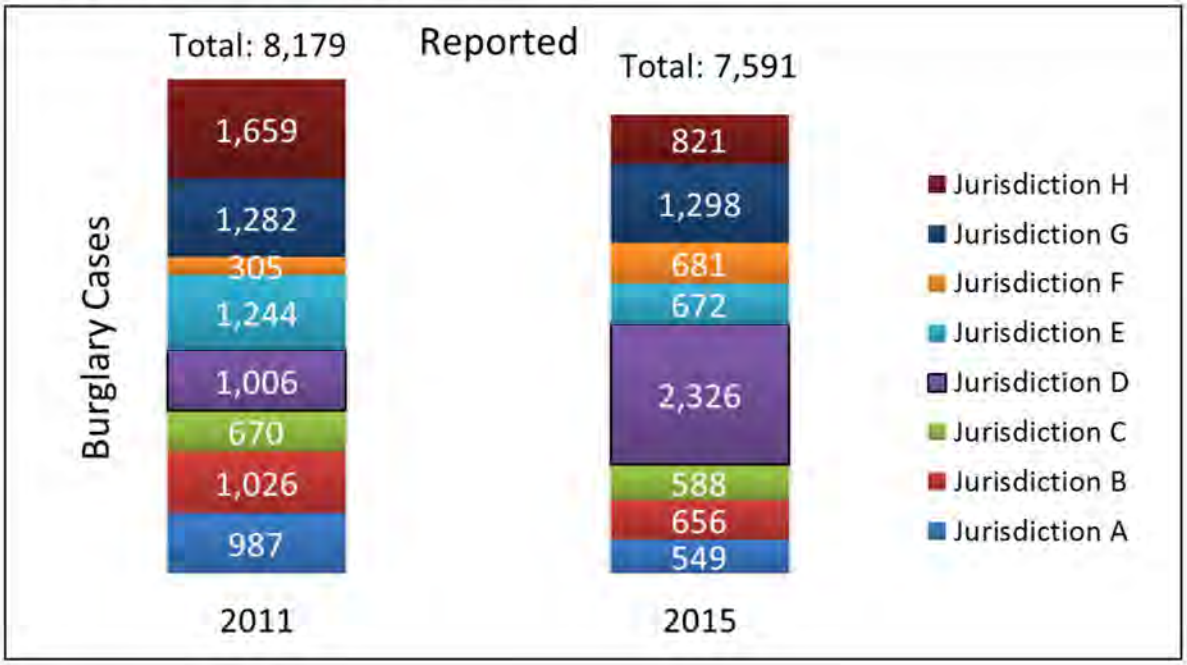
For consistency, the findings have been produced covering the following categories:

- 2015 Data Overview Nationally
- Results by Stages
- Overall Forensic Performance; with reference to the two main measures being the lead time and success measures.

Analysis is provided on the national performance, jurisdictional performance, metropolitan and regional areas, and DNA and fingerprint data individually and combined as 'forensic evidence'. The Figures and Tables used to present the findings are followed by key summary points and interpretation.

DATA OVERVIEW NATIONALLY

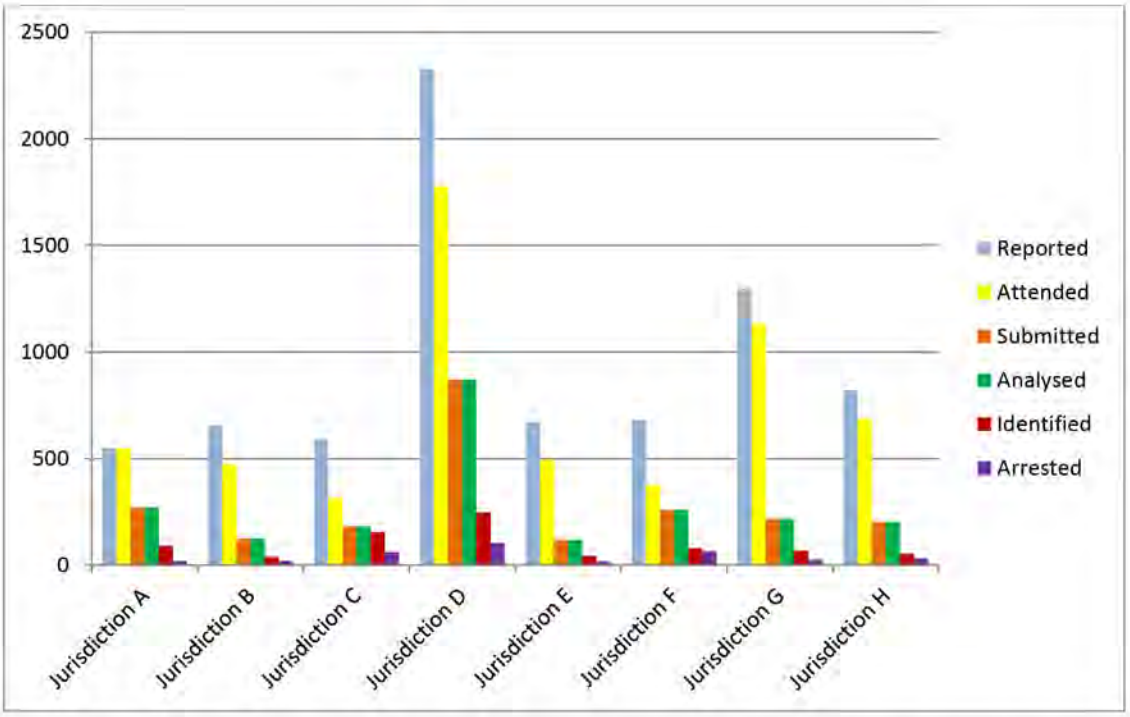
Figure 6: Distribution of Data Nationally



KEY POINTS:

- 7,591 burglary cases were reported in the five month period in 2015.
- The same 17 sites (10 metro, seven regional) were used as in 2011.
- Each State/Territory is represented.
- The majority of cases are in metropolitan locations (75%).
- Since 2011, the number of cases reported has doubled for D and F, halved (or close to) for A, B, E and H, decreased for C and remained mostly the same for G. Explanations for changes vary from a change in the boundaries of sites within jurisdictions to change in the level of criminality. For example, a regional boundary within Jurisdiction D changed substantially between 2011 and 2015 (i.e. the site area was redrawn and grew to be about twice the size, resulting in double the number of cases). Whereas the increase in cases for Jurisdiction F reflects actual case volumes, with the sites involved in data collection experiencing consistent spikes in the rate of burglaries during the data collection period (spikes were attributed to a high number of known recidivist offenders being out of custody at the time, particularly in one population centre).

Figure 7: 2015 results showing attrition of cases across Stages of the Forensic Process: By Jurisdiction



Note: This figure represents 2015 jurisdictional data on attrition across stages for combined forensic evidence (i.e. combining FP & DNA evidence together, where available).

Figure 8: Attrition of Fingerprint Cases across Stages: By Jurisdiction

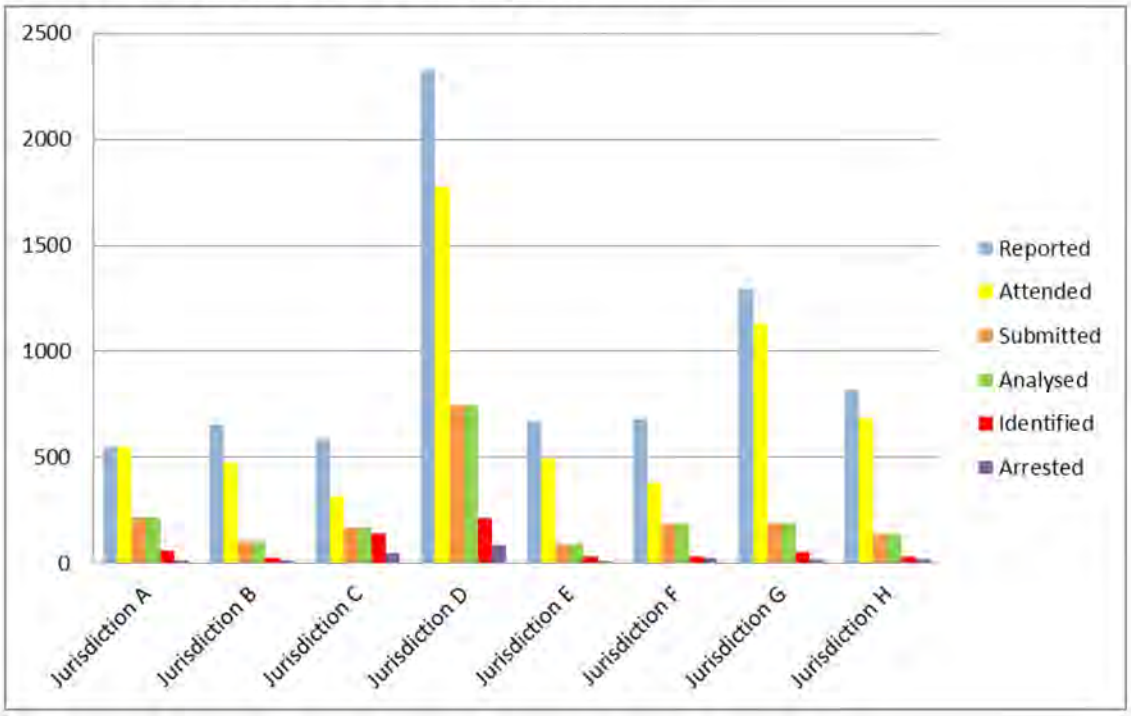
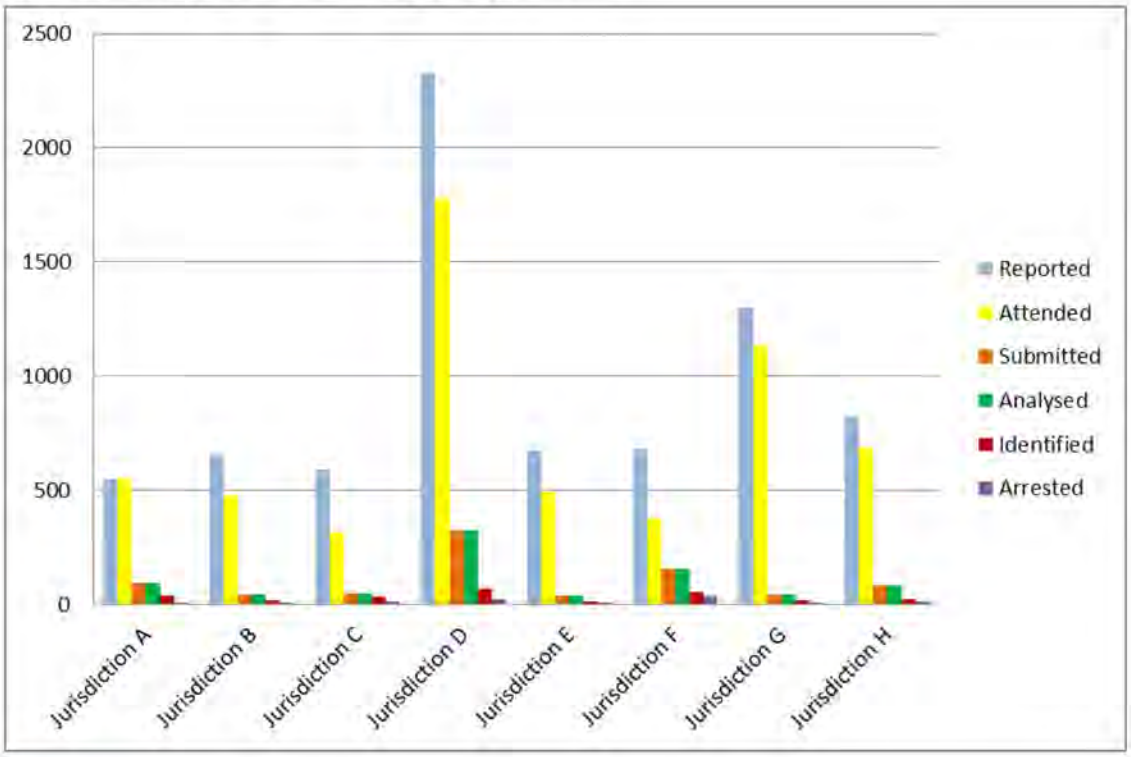


Figure 9: Attrition of DNA Cases across Stages: By Jurisdiction



KEY POINTS:

- There is attrition at all stages, except between Submitted and Analysed, as 100% of fingerprint and DNA evidence submitted was analysed in 2015.
- While attrition occurs at different rates across jurisdictions for the different types of evidence, generally, for each evidence type, most jurisdictions showed a similar pattern of attrition across the different stages.
- With the exception of Jurisdiction A, there is a move to 100% scene assessment rather than 100% scene attendance. For intelligence purposes indications are that attendance rates should be as high as possible. However, most labs have vetting processes in place for forensic evidence that are designed to prioritise high probative value evidence, so it is anticipated that not all forensic evidence is submitted. Further attrition occurs between Identified and Arrested, as not all identifications made will be relevant to an offence (i.e. there may be legitimate reasons to account for the evidence).
- In 2015, 14% of DNA evidence and 32% of Fingerprint evidence is submitted for analysis. So again in 2015 the overall DNA collection rate is lower than for fingerprints.

RESULTS BY STAGE

Table 3: 2015 results by Stages

2015 Results	Stage 1 Attendance		Stage 2 Evidence Submission		Stage 3 Analysis		Stage 4 Identification		Stage 5 Investigation	
Success Rate			FP	DNA	FP	DNA	FP	DNA	FP	DNA
Description	Attended / Reported		Submitted to Lab / Attended		Analysed / Submitted to Lab		Identification / Analysed		Arrest / ID	
Cases	5802/7591		1846/5802	833/5802	1846/1846	832/832	586/1846	267/832	243/586	111/267
National mean	76%		32%	14%	100%	100%	32%	32%	41%	42%
95% CI	75%-77%		31%-33%	13%-15%	100%-100%	100%-100%	30%-34%	29%-35%	37%-45%	36%-47%
Lowest, highest	54%, 100%		17%, 54%	4%, 42%	100%, 100%	100%, 100%	17%, 83%	17%, 69%	21%, 97%	15%, 71%
Metro, Regional	78%, 73%		31%, 35%	15%, 13%	100%, 100%	100%, 99%	32%, 31%	31%, 37%	41%, 50%	40%, 44%
Lead Time										
Description	Attendance lead time	At scene	Days from attendance to submission to lab		Days from receipt to analysis		Days from analysis to ID		Days from ID to arrest	
Units	hrs	min	days	days	days	days	days	days	days	days
National mean	13	47	1	8	6	5	6	27	17	18
Lowest, highest	5, 22	37, 59	0, 2	4, 17	0, 29	0, 39	1, 13	7, 50	6, 28	4, 42
Metro, Regional	12,13	45, 44	1, 0	8, 8	6, 4	4, 9	6, 7	26, 29	15, 21	17, 24
National median	3.5	44	0	6	1	3	1	20	6	11
Lowest, highest	1, 8	25, 50	0, 0	4, 12	0, 15	0, 53	0, 6	5, 40	2, 18	1, 31
Metro, Regional	3, 3	40, 45	0, 0	5, 6	1, 1	3, 5	1, 1	20, 21	4, 12	10, 13
Cases	5698	5802	1846	833	1846	832	586	267	231	107

Note: The national mean is the overall mean across all sites in the study. Lowest, highest: are the lowest and highest aggregated means across each of the 8 jurisdictions.

KEY POINTS:

- This table provides success rate and lead times across each stage of the forensic process. It also shows the variation in the measures across jurisdictions and across locations.
- Metropolitan and regional results generally show little differences across the stages.
- These results will be discussed in more detail in subsequent sections.

Figure 10: Success rate by Stages for Fingerprint evidence with 95% Confidence Intervals

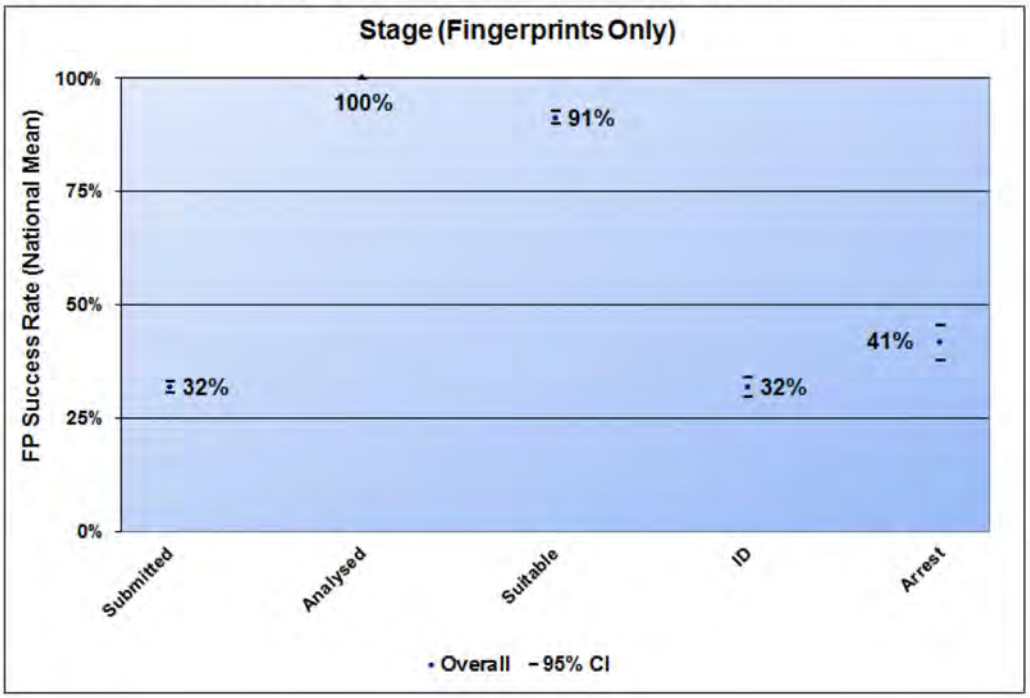
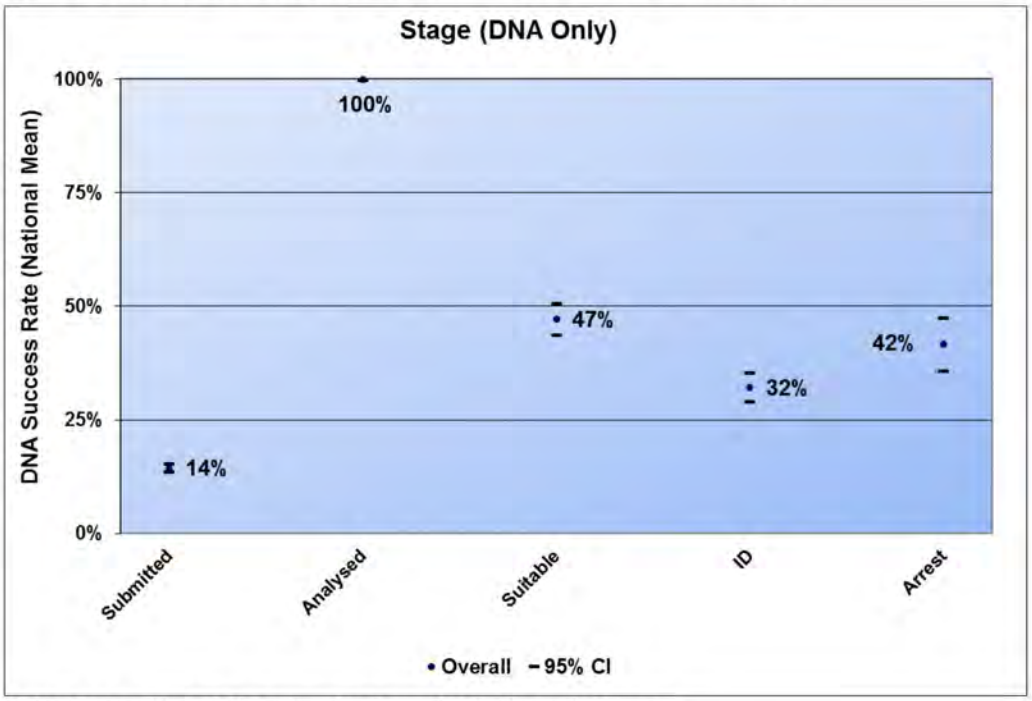
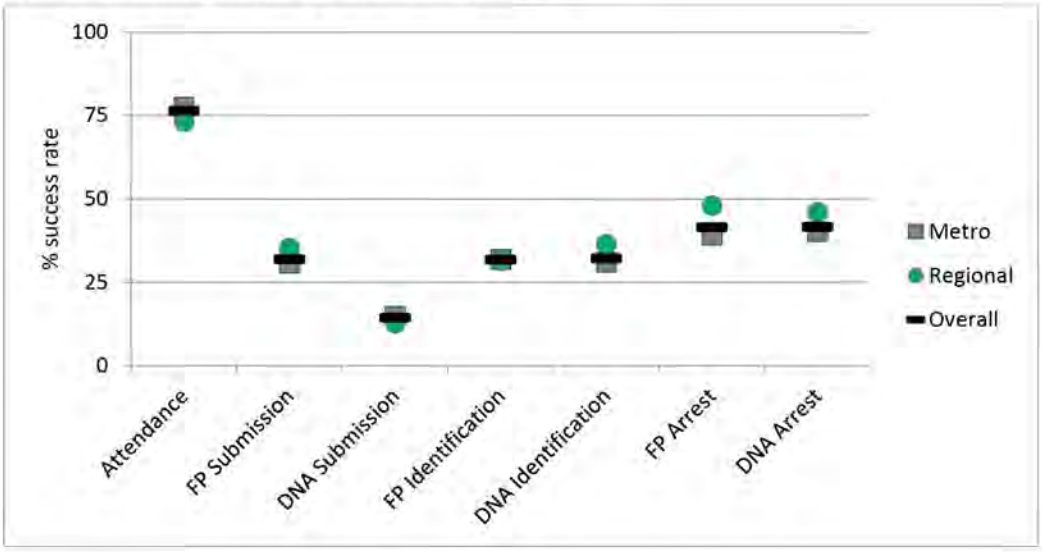


Figure 11: Success rate by Stages for DNA evidence with 95% Confidence Intervals



Note: the precision of the estimates is greater in the earlier stages.

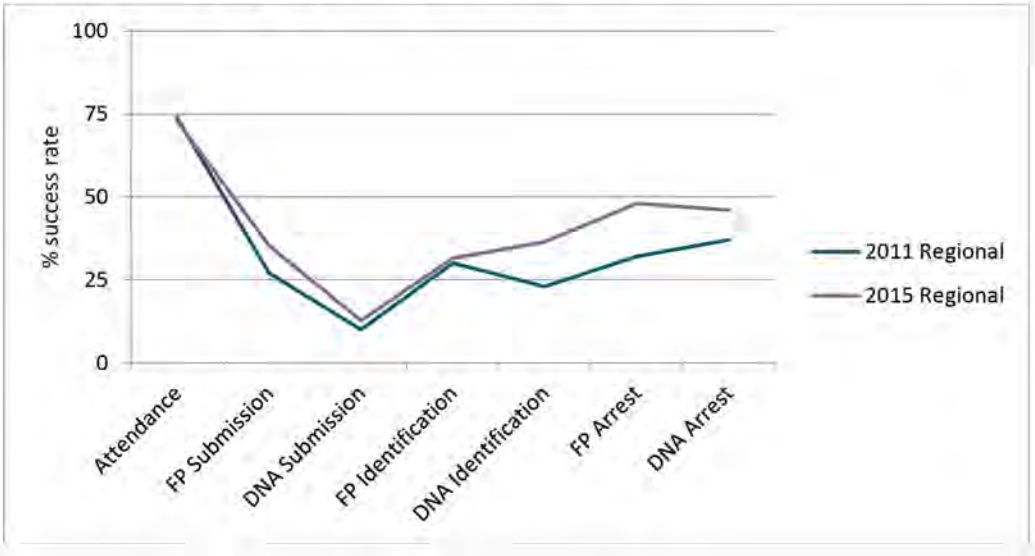
Figure 12: Success by Stage: By Location – 2015 results



KEY POINTS:

- The results by location are similar across the stages.

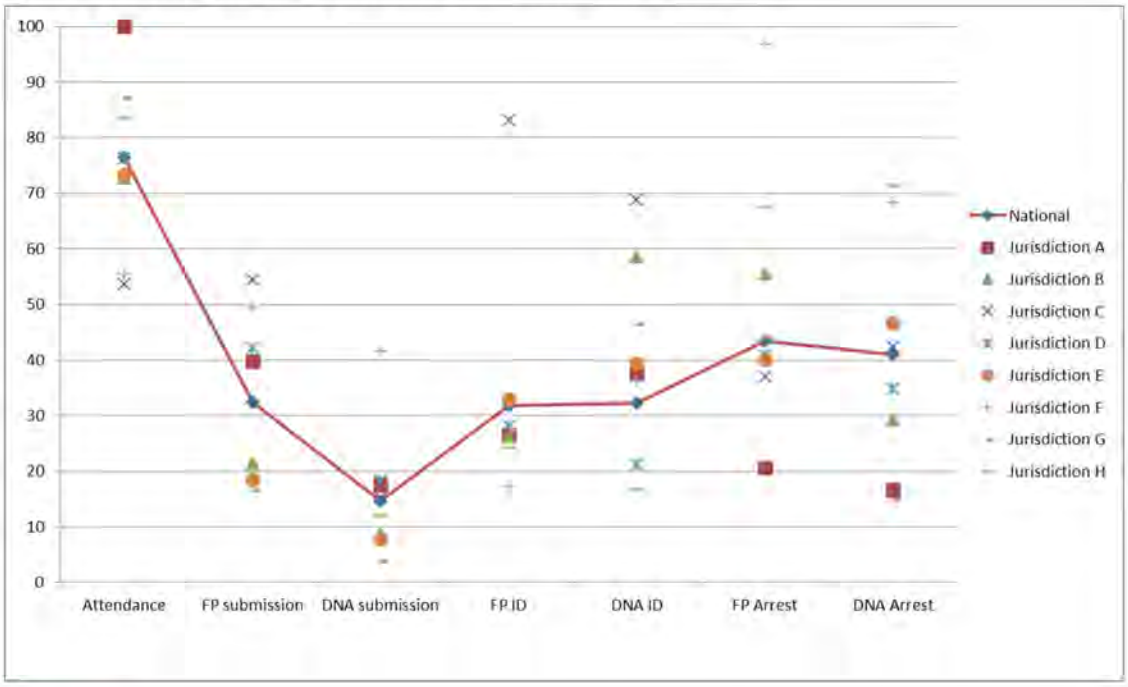
Figure 13: Success by Stage: By Location – 2011 vs 2015 results



KEY POINTS:

- Previously in 2011 when metro and regional data were compared, regional areas had higher identification rates through fingerprints. In 2015, for fingerprint evidence, metro and regional areas are now similar and for regional areas, DNA identifications have now closed the gap.

Figure 14: Success by Stage: By Jurisdiction with National – 2015 results



KEY POINTS:

- Note the accuracy of the jurisdictional estimates in the later stages is less than the earlier stages.
- The jurisdictions with the highest attendance rate did not necessarily have the highest fingerprint submission rate or highest DNA submission rate.
- The submission rate was lower for DNA than for fingerprints with a variation across the jurisdictions, but jurisdictional outliers from 2011 have moved closer to the mean.
- Nationally fingerprint and DNA identifications, and fingerprint arrests, have increased since 2011 however there is still a wide range in success rates across jurisdictions.

Table 4: Stage 1 (Attendance)

2015	Stage 1 Attendance	
Success Rate		
Description	Attended / Reported	
Cases	5812/7598	
National mean	76%	
95% CI	75%-77%	
Lowest, highest	54%, 100%	
Metro, Regional	78%, 73%	
Lead Time		
Description	Attendance lead time	At scene
Units	hrs	min
National mean	13	47
Lowest, highest	5, 22	37, 59
Metro, Regional	12,13	45, 44
National median	3.5	44
Lowest, highest	1, 8	25, 50
Metro, Regional	3, 3	40, 45
Cases	5698	5812

KEY POINTS:

- Overall 76% of burglary cases reported are attended by CSI, up from 70% in 2011.
- The mean lead time is 13 hours but the median lead time of 3.5 hours better reflects the performance, and is a half hour less than in 2011.
- There is a wide range in the response times between jurisdictions, but not by locations.
- There is a median of 44 minutes for time spent at the scene, up 14 minutes from 2011. With a range of 25 to 50 minutes across the Jurisdictions.

Table 5: Stage 2 (Submission)

2015	Stage 2 Evidence Submission	
Success Rate	FP	DNA
Description	Submitted to Lab / Attended	
Cases	1848/5812	832/5812
National mean	32%	14%
95% CI	31%-33%	13%-15%
Lowest, highest	17%, 54%	4%, 42%
Metro, Regional	31%, 35%	15%, 13%
Lead Time		
Description	Days from attendance to submission to Lab	
Units	Days	Days
National mean	1	8
Lowest, highest	0, 2	4, 17
Metro, Regional	1, 0	8, 8
National median	0	6
Lowest, highest	0, 0	4, 12
Metro, Regional	0, 0	5, 6
Cases	1848	832

Note: zero lead time indicates submission on same day as attended.

KEY POINTS:

- Fingerprint evidence was submitted in 32% of cases where CSI attended and DNA evidence submitted in 14% of such cases.
- Fingerprints have a substantially shorter submission lead time than DNA.
- There is little difference in the submission rate by location.

Table 6: Stage 3 (Analysis)

2015	Stage 3 Analysis		Stage 3 Analysis (FP & DNA Suitability)	
Success rate	FP	DNA	FP	DNA
Description	Analysed / Submitted to Lab		Suitable for upload to NAFIS database / Submitted to Lab	Suitable for upload to NCIDD database / Submitted to Lab
Cases	1848/1848	831/832	1682 / 1848	392/ 832
National mean	100%	100%	91%	47%
95% CI	100-100%	100-100%	90%, 93%	44%, 51%
Low est, highest	100%,100%	100%, 100%	85%, 97%	33%, 86%
Metro, Regional	100%, 100%	100%, 99%	91%, 99%	47%, 47%
Lead Time				
Description	Days from receipt to analysis		As per left column	
Units	Days	Days		
National mean	6	5		
Low est, highest	0, 29	0, 39		
Metro, Regional	6, 4	4, 9		
National median	1	3		
Low est, highest	0, 15	0, 53		
Metro, Regional	1, 1	3, 5		
Cases	1848	831		

KEY POINTS:

- Virtually all fingerprint and DNA evidence is analysed.
- Fingerprints have a shorter analysis lead time than DNA (median one versus three days).
- There is variation across jurisdictions in lead time for both fingerprints and DNA.
- The suitability for upload to NAFIS is 91% for fingerprint evidence (national mean, up slightly from 87% in 2011) and for DNA cases it is 47% (also up slightly from 42% in 2011).

Table 7: Stage 4 (Identification)

2015	Stage 4 Identification	
Success rate	FP	DNA
Description	Identification / Analysed	
Cases	587/1848	268/831
National mean	32%	32%
95% CI	30%-34%	29%-35%
Lowest, highest	17%, 83%	17%, 69%
Metro, Regional	32%, 31%	31%, 37%
Lead Time		
Description	Days from analysis to ID	
Units	Days	Days
National mean	6	27
Lowest, highest	1, 13	7, 50
Metro, Regional	6, 7	26, 29
National median	1	20
Lowest, highest	0, 6	5, 40
Metro, Regional	1, 1	20, 21
Cases	587	268

KEY POINTS:

- Overall identification rate for both fingerprints and DNA is up 9% from 23% in 2011 to 32% in 2015.
- This increase may be a reflection of both an improvement in the collection of value evidence and also generally more mature databases.
- The DNA data available is from a smaller sample than for fingerprints.

Table 8: Stage 5 (Investigation)

2015	Stage 5 Investigation	
Success rate	FP	DNA
Description	Arrest / ID	
Cases	243/587	110/268
National mean	41%	42%
95% CI	37%-45%	37%-47%
Low est, highest	21%, 97%	15%, 71%
Metro, Regional	41%, 50%	40%, 44%
Lead Time		
Description	Days from ID to arrest	
Units	Days	Days
National mean	17	18
Low est, highest	6, 28	4, 42
Metro, Regional	15, 21	17, 24
National median	6	11
Low est, highest	2, 18	1, 31
Metro, Regional	4, 12	10, 13
Cases	231	107

KEY POINTS:

- The overall arrest rate after fingerprint identification is 41%, representing a rise in fingerprint identifications from 2011 data, and 42% after DNA identification.
- Variation is observed by jurisdiction but there is more variation for DNA identification than fingerprints.
- Only small differences were observed between locations.
- Note that the DNA data available is a smaller sample than for fingerprints.

OVERALL FORENSIC PERFORMANCE

Table 9: 2015 Overall Forensic performance for stages 1 to 5

2015	Stage 1 - Stage 5 Investigation			Stage 1 - Stage 5 Investigation		
Success rate	FP	DNA	FP and/or DNA	FP	DNA	FP and/or DNA
Description	Arrest/Reported			Arrest/Attended		
Cases	243/7591	110/7591	353/7591	243/5802	110/5802	353/5802
National mean	3.20%	1.45%	4.65%	4.20%	1.90%	6.10%
95% CI	2.8-3.6%	1.2-1.7%	4.1-5.0	3.7-4.7%	1.6-2.3%	5.3-6.5%
Low est, highest	1.6-6.3%	0.3-4.4%	1.4-9.4%	1.4-11.8%	1.3-8.1%	1.3-17.9%
Metro, Regional	3,3.9%	1.4,1.5%	4.3,5.2%	3.8,5.3%	1.8,2.1%	5.5,7.2%
Lead Time						
Description	Days from report to arrest			As per left column		
Units	Days	Days	Days			
National mean	28	55	36			
Low est, highest	18,49	37,136	28,44			
Metro, Regional	27,31	55,55	36,37			
National median	16	49	28			
Low est, highest	11,51	37,136	16,48			
Metro, Regional	15,18	47,50	31,24			
Cases	231	107	328			

KEY POINTS:

- When the arrests are related back to the number of crimes reported, the overall success rates are 3.2% (previously 1.7 per 100 crimes reported) for fingerprints and 1.45% (previously 0.8%) for DNA.
- There are significant differences across jurisdictions but not by location.

Figure 15: Overall End-to-End Lead times: By Jurisdiction (fingerprints)

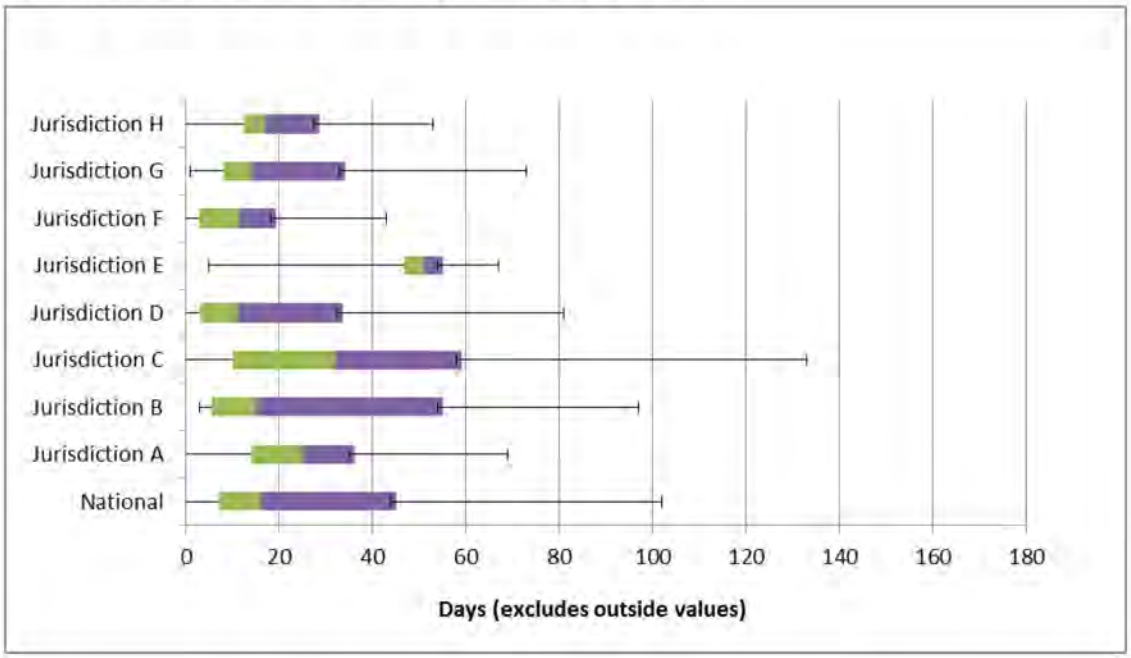


Figure 16: Overall End-to-End Lead times: By Jurisdiction (DNA)

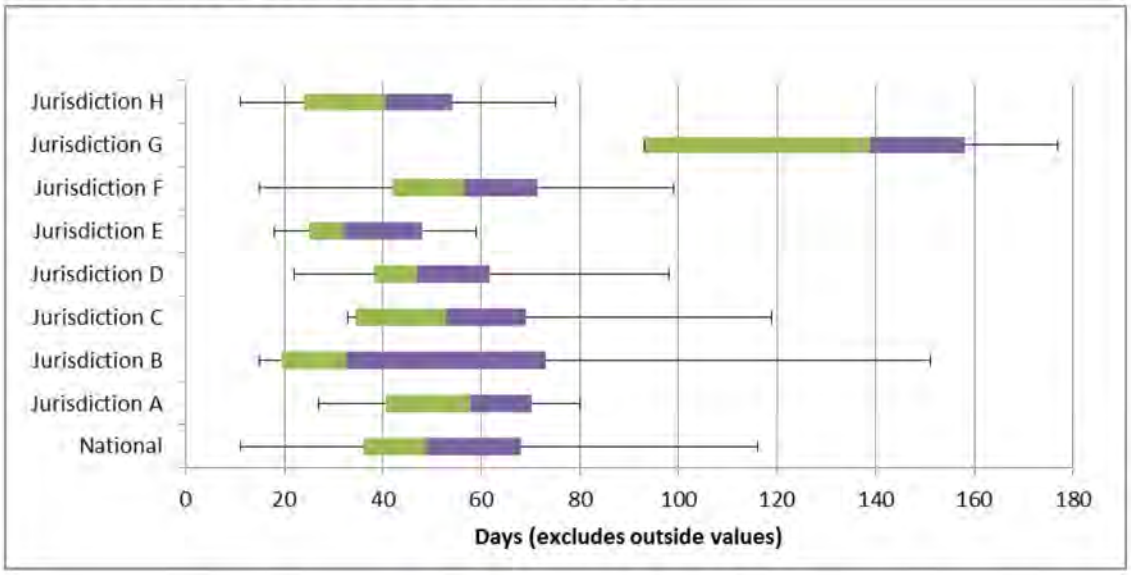
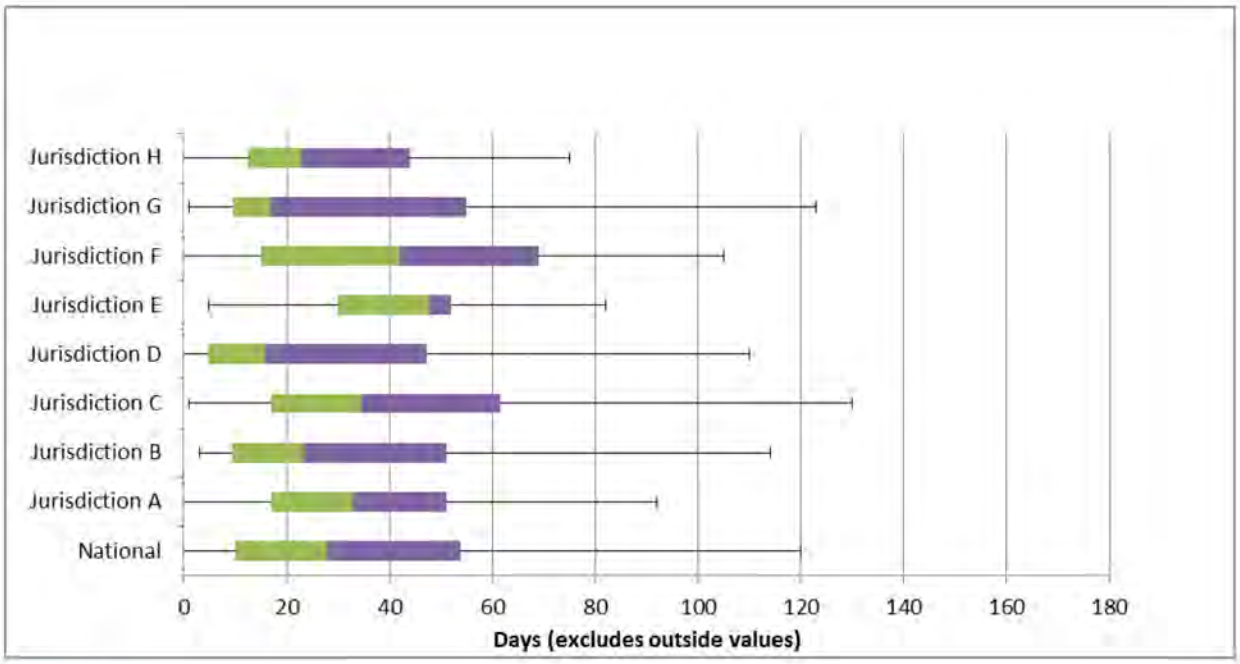


Figure 17: Overall End-to-End Lead times: By Jurisdiction (Forensic Evidence)



KEY POINTS:

- Overall median lead times across all sites, from report to arrest, were 16 days for fingerprints and 49 days for DNA evidence.
- The median lead time for the cases with an arrest, from the report to arrest, regardless of evidence type is 28 days.

Figure 18: Lead times (Median): By Jurisdiction (Fingerprint)

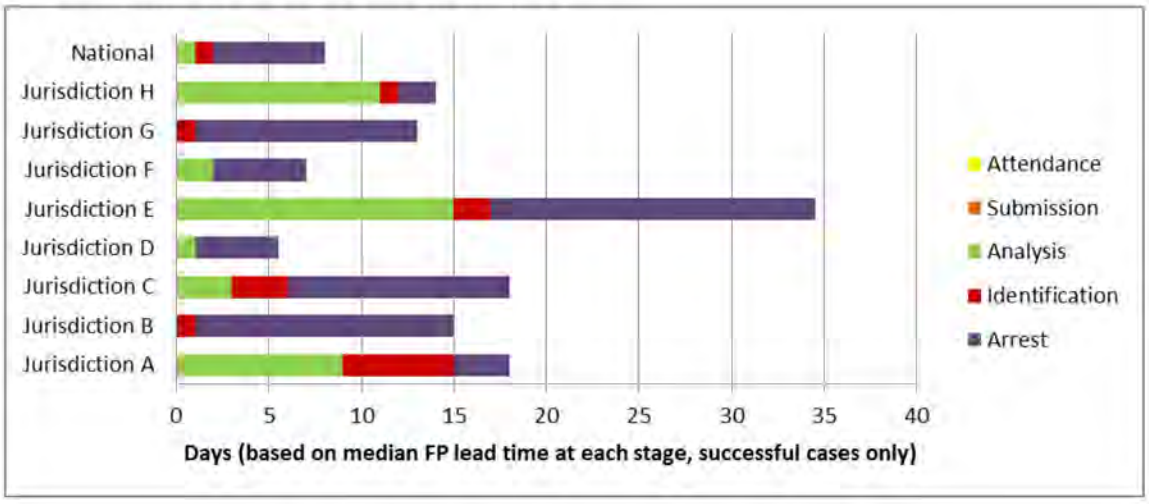
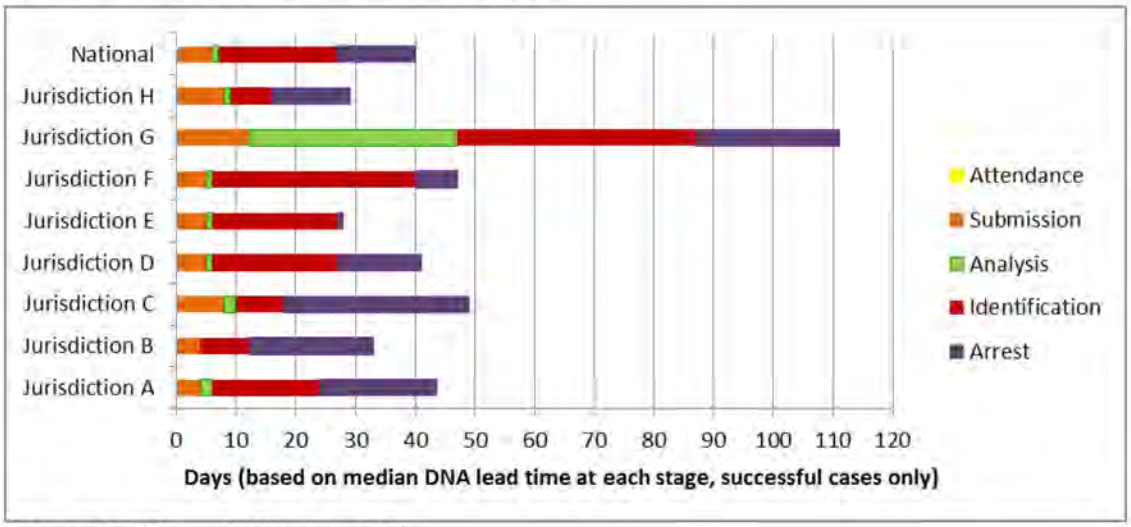


Figure 19: Lead times (Median): By Jurisdiction (DNA)



Note: scale difference between two plots.

KEY POINTS:

- Longer submission and identification lead times for DNA contribute to the longer overall lead times for DNA compared with fingerprints.

DISCUSSION

Processing and analysing volume crime samples is a difficult area to make improvements in as gains from changes in any of the stages can be offset by critical weaknesses at another. The vetting of evidence to maximise the value of return for effort leads to attrition of cases, which impacts on success rates where success is measured as progression to the next stage. Similarly, the performance measurement of lead time does not always reflect the complexity of value-adding to the forensic evidence process by implementing changes that may extend the lead time of a stage but gain an increase in the quality of evidence (e.g. testing of samples using the expanded DNA marker set and analysis using STRmix).

The repeat of the End-to-End project (E2E2) has helped consolidate learnings from the original project and measured the impact of advances in technology such as the conversion to digital imaging and the subsequent transmission of fingerprint evidence electronically, which has resulted in significant gains with respect to lead times. Other technology improvements, such as the introduction of robot ready sub-sampling and robotic analytical workflows have also had an impact, and further technology advances are expected to continue to do so (e.g. lights out latents, rapid DNA). Also having an impact is a cultural shift toward greater emphasis on service delivery models and organisational reviews that incorporate LEAN thinking and focus on efficiency gains, especially in relation to fit-for-purpose Integrated IT systems that support item and information management. From end-to-end, extended hours of coverage for CSIs, at scene data entry and triage, and relocation of resources to target property crime, are a few examples of the kind of changes that have been implemented and which are improving efficiency.

The Impact of E2E2 is possibly best described in terms of the response by jurisdictions to the performance measurements originally made in E2E1. Feedback from agencies indicates many jurisdictions implemented the recommendations arising from E2E1, though with varying degrees of success in terms of approaches, but with consideration of the learnings from top performers. An emphasis on training for CSI's, with regard to collection of value evidence and importance of collecting relevant reference and crime scene DNA samples, has been shown to have a positive impact on service delivery. As jurisdictional databases grow, the

identification rate for DNA profiles and fingerprints obtained at crime scenes is on the increase. Also encouragingly, since 2011, police organisations have been able to apply strategies to develop means to improve communication and outcomes at the investigation stage, allowing the benefits gained at earlier stages of the process to be realised at the arrest stage and in the overall lead times.

The End-to-End project has helped develop and refine a national model for end-to-end forensic processing of volume crime samples, providing a useful tool to enable agencies to capture and compare data, which in turn provides valuable information on efficiency and effectiveness of the forensic processes which support investigations.

RECOMMENDATION

Based on the findings from the repeat of the End-to-End project, the following recommendations are made:

- The data be used to identify further learnings that when implemented result in improved service delivery.
- ANZPAA NIFS to provide workshops based upon request from individual jurisdictions.

ACKNOWLEDGEMENTS

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- Dr Linzi Wilson-Wilde, Director, ANZPAA NIFS
- Eva Bruenisholz, End-to-End Phase 2 - Project Officer, ANZPAA NIFS
- Nicholas Vandenberg, End-to-End Phase 2 - Project Officer, ANZPAA NIFS
- Cheryl Brown, End-to-End Project Phase 1 - Project Officer, South Australia Police

APPENDIX 1: GLOSSARY

E2E1 defined common terminology. A broad range of definitions and cross referencing was required due to the different practices employed at the local level.

Burglary	Refers to a breaking or attempted breaking offence on a dwelling or business premises, also referred to at various jurisdictions as serious criminal trespass (SCT), unlawful entry or break and enter.
Case File	A case file is generated by the Crime Scene Investigator (CSI) at the crime scene. This may be created as an electronic document at the scene or converted to an electronic document on return to the office.
Crime Reported	The time and date the crime was reported to Police. This time varied between jurisdictions, as sometimes it was the first contact by the victim to the Police and sometimes it was when the written report was taken. The project agreed to use the time recorded for corporate reporting at jurisdictional level.
Crime Scene	The study only relates to the initial scene attendance at a burglary offence and does not include secondary scenes, travel time for attendance at scenes where the victim is not home and therefore no access to the scene is available.
CSI	Crime Scene Investigator also referred to as a Scenes of Crime Officer (SOCO) or Crime Scene Examiner/Officer (CSE/CSO). It does not include the attendance of general duties personnel or investigators examining the scene and collecting evidence.
DNA	Refers to the collection of DNA samples in the form of trace/contact, blood or saliva either as a swab or as items submitted to the Laboratory for analysis.
Fingerprints	Refers to the collection of fingerprints from the scene in the form of lifts, photographs or items for chemical treatment.
Study Data Collection Period	The period identified for the collection of data, 1 May 2011 to 30 September 2011 for E2E1 and 1 May 2015 to 30 September 2015 for E2E2.
Unique Case Identification	Case number applied to each case by the project team on the master spread-sheet.
State	Refers to the State from which that participating site is located.
Metro/Country	Refers to whether the jurisdiction considers that participating site to be a metropolitan or country policing area.
Site No	Number given to a participating site during the pilot study data collection period.
Project Case ID	The unique case number applied by the project officer
Stage 1: Attendance	Includes the period from when the crime is reported to the police and the end of the scene examination.
Scene Exam Start	The time and date that the CSI commences examination of the crime scene.

Scene Exam End	The time and date that the CSI completes the examination of the crime scene.
Stage 2: Evidence Submission	Includes whether fingerprints or DNA were collected at the crime scene and the date and time the fingerprints and DNA are received at the Fingerprint Bureau or Laboratory.
FP Located	When fingerprints are located and collected at the crime scene a 'Y' was recorded and when fingerprints were not located an 'N' was recorded.
DNA Located	When DNA is located and collected at the crime scene a 'Y' was recorded and when DNA was not located an 'N' was recorded.
FP@FPB	Time and date the fingerprint case file/evidence was received at the Fingerprint Bureau.
DNA@Lab	Time and date the DNA case file/evidence was received at the DNA Laboratory.
Stage 3: Analysis of Evidence	Includes the date and time that analyses of the evidence was commenced and whether the evidence was suitable for upload on the databases.
FP Analysis Start	The time and date the fingerprint case file was removed from the waiting list and the analysis commenced.
DNA Analysis Start	The time and date the DNA case file was removed from the waiting list and the analysis commenced.
FP Suitable NAFIS	When the fingerprint was suitable for upload to NAFIS a 'Y' was recorded and when it was not suitable an 'N' was recorded.
DNA Suitable NCIDD	When the DNA was suitable for upload to NCIDD a 'Y' was recorded and when it was not suitable an 'N' was recorded.
NAFIS	National Automated Fingerprint Identification System is a finger and palm print database and matching system that assists Australian policing agencies and the Department of Immigration and Citizenship (DIAC) to manage fingerprint records, confirm identities of persons of interest and resolve crime.
NCIDD	National Criminal Investigation DNA Database is a tool for police and forensic scientists to match DNA profiles nationally. It is a powerful investigative tool and intelligence resource crossing all jurisdictional boundaries.
Stage 4: Identification	Includes the time and date that an identification was made from the fingerprints or DNA and the time and date that the identification was promulgated to the investigating officer.
FP ID	Date and time when a fingerprint identification was achieved.
DNA ID	Date and time when a DNA identification was achieved.
FP ID to IO	Date and time when a fingerprint identification advice was sent to the investigating officer.
DNA ID to IO	Date and time when a DNA identification advice was sent to the investigating officer.

Stage 5: Investigation	Includes the time and date the Investigating Officer took action as a result of the forensic led identification and the type of action taken.
FP ID Action	Date and time action was taken by the Investigating Officer in response to the Fingerprint Identification.
FP ID Action (Type)	Action taken by the Investigating Officer in response to the Fingerprint Identification (charged, not charged, eliminated, no action).
DNA ID Action	Date and time action was taken by the Investigating Officer in response to the DNA Identification.
DNA ID Action (Type)	Action taken by the Investigating Officer in response to the DNA Identification (charged, not charged, eliminated, no action).

APPENDIX 2: PERFORMANCE MEASURES AT EACH STAGE

The repeat of the End-to-End project followed the performance measures and stages designed for the original End-to-End project, so that a direct comparison of the results between the 2011 and 2015 data could be conducted. Definitions of lead times and success rates across the different stages that appear in this Appendix are consistent with/taken directly from the original End-to-End report.

LEAD TIME (DURATION)

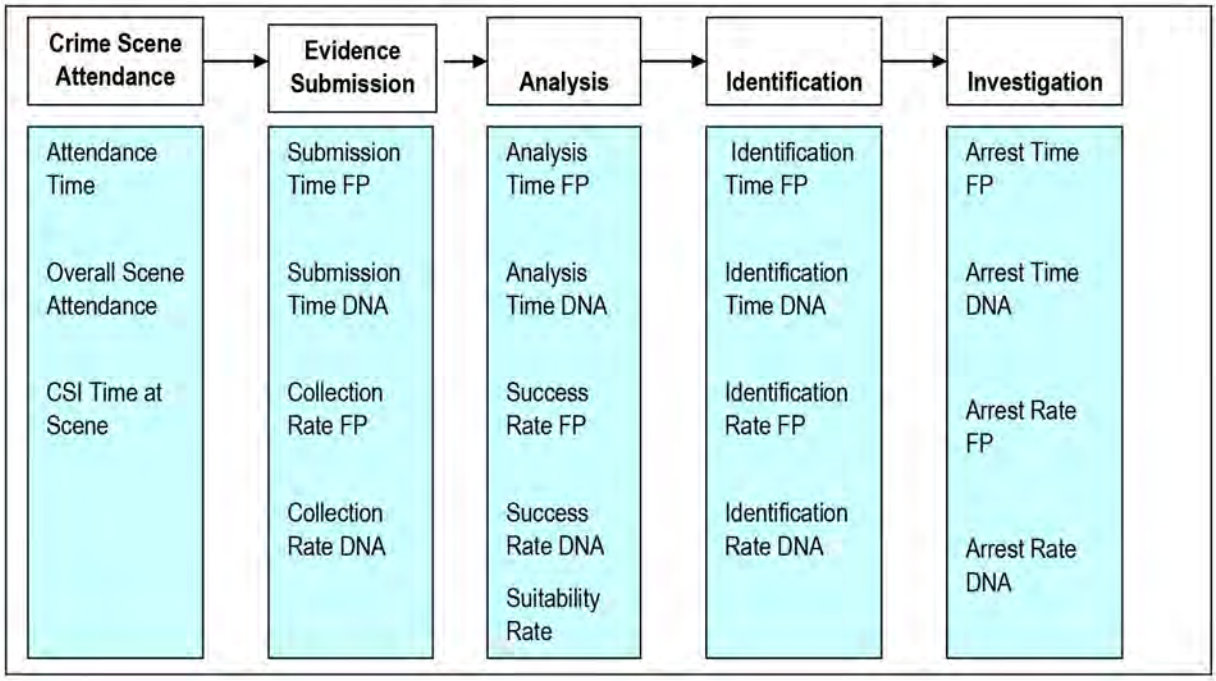
Lead time refers to the time interval between each stage. This was determined through the collection of date and time entries at key points within the defined stages. The project could then measure the time taken for a case to move from one stage to another and eventually the total time taken to move from the beginning of stage 1 to the end of stage 5.

SUCCESS RATE (PROPORTION)

The success rate measures the progress of a case to the next stage. This was determined by the recording of the date and time entry for the next stage.

Success rate is based on the case, not the number of offenders or arrests. For example, two or more arrests based on forensic evidence from one burglary scene are only counted as one successful case.

STAGES



STAGE 1: CRIME SCENE ATTENDANCE

This stage relates to the response by police personnel to the crime scene.

Stage 1 data relates to the time when a crime was reported, the crime scene examination start time and the crime scene examination end time. From this data the following three measures were determined.

ATTENDANCE TIME

The time lapse between the report of the crime and scene attendance by CSI.

The purpose of this measure is to determine the typical lag time between the victim reporting the crime to the police and CSI attending.

OVERALL SCENE ATTENDANCE

The proportion of scenes attended by CSI.

Police jurisdictions have differing policy in regard to responding to volume crime. It is not always deemed practical or feasible to attend all scenes, however the goal of 100% scene assessment is desirable and was a recommendation arising from the E2E1 report for improved use of resources.

CSI TIME AT THE SCENE

The time spent at a scene by CSI.

This measure determines the time required at a crime scene for the most efficient and effective collection of evidence that maximises success rates through all stages of the process. Good quality evidence collection is required to ensure successful analysis, identification and investigation.

STAGE 2: EVIDENCE SUBMISSION

From stage 2 onwards, the data is separated into fingerprint evidence and DNA evidence. This stage contains data identifying the collection of DNA and/or fingerprints and the date/time entry for submission to the DNA laboratory or fingerprint bureau.

SUBMISSION LEAD TIME

The time lapse between the fingerprint and DNA evidence being collected at the scene and the time it is submitted to the DNA laboratory or fingerprint bureau.

The date/time entry relates to the time the laboratory or bureau records the case as having been received, as opposed to the time when the CSI may send the evidence. There may be a lag time in relation to the submission, but this lag time is not calculated separately as it is included in the time that the CSI has control of the evidence.

COLLECTION RATE

The proportion of scenes attended from which fingerprints or DNA are collected and subsequently submitted for analysis.

STAGE 3: ANALYSIS OF EVIDENCE

Stage 3 includes the date and time that analysis of the evidence was commenced and whether the evidence was suitable for upload on the NAFIS or NCIDD.

Both databases have a national standard for upload, which provides the project with a perspective on the suitability of the evidence for analysis. However, each jurisdiction can analyse and conduct comparisons with internal databases or records, outside of the requirements for NAFIS and NCIDD. Therefore identification may still occur even if the evidence is not suitable for upload according to the national standard.

ANALYSIS LEAD TIME

The time lapse between the time the case file was received for analysis and the time the analysis was commenced.

In some jurisdictions the time the case file was received for analysis, is also considered the time the analysis was commenced.

ANALYSIS RATE

The proportion of cases containing evidence that was analysed.

SUITABILITY RATE

The proportion of cases containing evidence of a standard suitable for upload to a national database.

STAGE 4: IDENTIFICATION

Stage 4 relates to the identification of a suspect from the evidence analysed. The identification might occur as a result of a search on the national database, or it may result from a direct comparison between the evidence and a suspect.

Stage 4 contains two date/time entries: one referring to the date/time when the identification was made; and the second referring to date/time when the identification was forwarded to the investigating officer (IO). The purpose of the two entries was to allow for an evaluation of the time lapse between the achievement of identification and the transmission of that information for investigation.

IDENTIFICATION LEAD TIME

The time lapse between the analysis commencing and the time identification is achieved.

IDENTIFICATION RATE

The proportion of cases that were analysed and resulted in at least one identification.

STAGE 5: INVESTIGATION

Stage 5 relates to the investigation of a case file pertinent to the identification of a suspect through the forensic process. It is acknowledged that a suspect may be arrested prior to the commencement or completion of the forensic analysis as a result of normal investigative procedures, or as a result of witness involvement. Furthermore, unlike the other stages, an investigator has to physically locate the suspect to take action that is recorded in this stage.

A large range of actions could be taken against a person identified through the forensic process. In some cases a person identified through the forensic process can ultimately be eliminated from the investigation as they may be the victim or complainant with legitimate reasons for their fingerprints or DNA being at the scene. Only data indicating the arrest of a suspect subsequent to the identification was included in this analysis.

ARREST LEAD TIME

Time lapse between the time the identification was achieved and the time the nominated suspect was arrested or charged.

ARREST RATE

The proportion of cases where identification is achieved and the nominated suspect was arrested or charged.

STAGE 1 – STAGE 5: END-TO-END PERFORMANCE

Analysis has also been carried out on the overall performance from the report of the crime to the arrest of the suspect as opposed to the stage-by-stage analysis. This is represented in the overall forensic performance section of the Findings.

APPENDIX 3: DATA COLLECTION, QUALITY & DESCRIPTIVE STATISTICS

DATA COLLECTION

Date collection and analysis was consistent with the approach adopted in the original End-to-End project.

Cases were recorded across an Excel spread-sheet requiring date/time entries (dd/mm/yyyy h:min) and information on the success or otherwise of the progress of the case regarding fingerprint and DNA evidence.

The data collection period for E2E phase 2 was between May and 30 September 2015.

Each case was identified through a unique case identifier applied by each jurisdiction. This was later converted to a Project Case ID for the purposes of ensuring the anonymity of each case. Jurisdictional performance is de-identified (e.g. A, B, C etc)

The data collection in some jurisdictions was still manually intensive with little alignment between police and forensic data management systems. The organisations that were better able to manage the data collection primarily utilised a forensic case management system networked to a police management system.

DATA QUALITY

There are limitations around the data collected and the methodology applied. For example, the data collected is only across a five month window and from sites nominated by jurisdictions as opposed to being selected by the project team.

For some jurisdictions the data collection window fell outside of timeframes for organisational review/service delivery enhancement changes which means that for some agencies this data may be outdated where as for other jurisdictions it still reflects current practice.

The category of 'forensic evidence' reflects combining fingerprint and DNA information where available for the same case. This may be less than the individual totals for fingerprint or DNA information on their own.

Where necessary, comments were added to each stage to explain any anomalies or deviations from the project requirements and to identify at which stage the case was finalised.

DESCRIPTIVE STATISTICS

Success rates at each stage and lead times between stages were summarised for each:

- site
- jurisdiction (aggregating across forensic sites for that State or Territory)
- location (aggregating across all regional sites and across all metropolitan sites)
- overall/national (aggregating across all 17 sites).

The precision in the estimates of success rates was measured by 95% confidence intervals for proportions. Due to the attrition of fingerprint and DNA cases across the different stages, the precision of the estimates is greater in the earlier stages than in the later stages where the sample size decreases.

The lead time data follow skewed distributions and are therefore summarised using medians (50th percentile) rather than means. Lead times are illustrated with box and whisker plots (**Appendix 4**). The boxes show the 25th, 50th and 75th percentiles and the whiskers show the range (excluding outliers).

APPENDIX 4: HORIZONTAL BOX PLOTS FOR LEAD TIMES

Figure 20: Lead times from Report to Attendance: By Jurisdiction with National (Median)

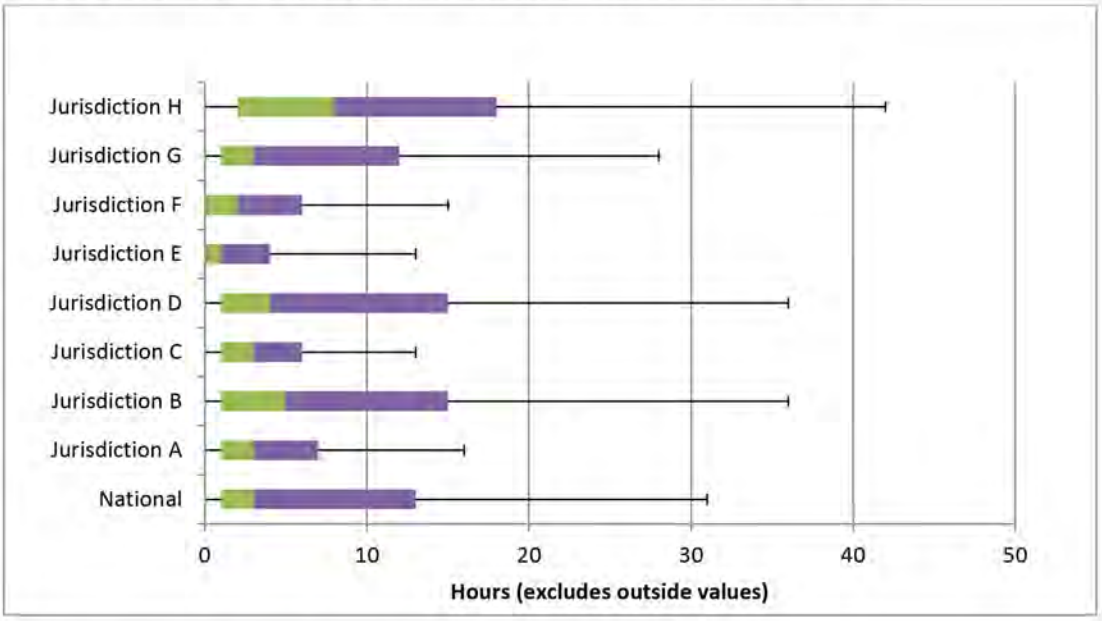


Figure 21: Time at the Scene: By Jurisdiction

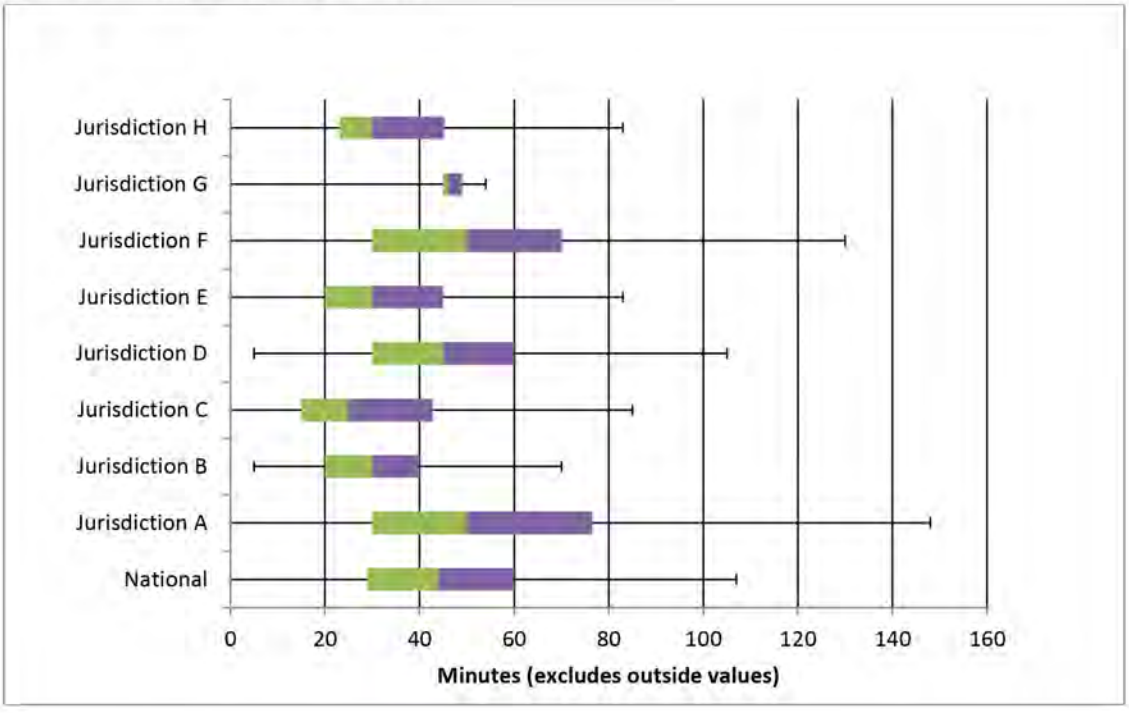


Figure 22: Time at the Scene: By Location

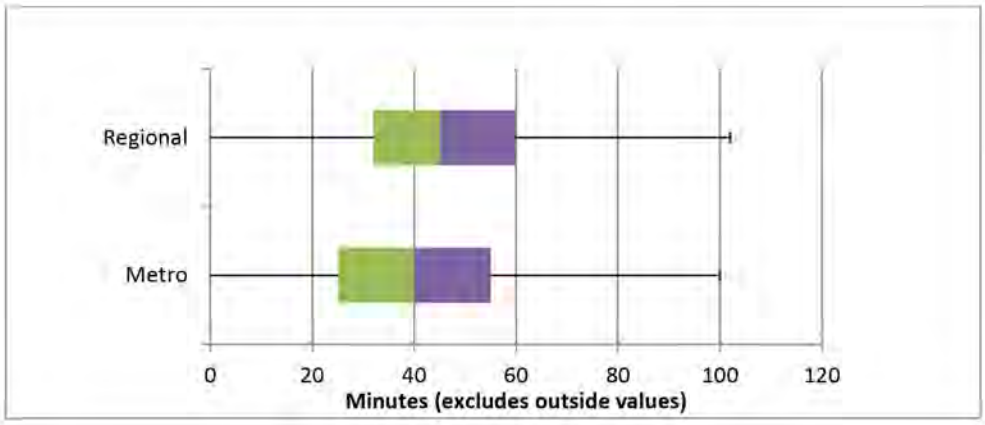


Figure 23: DNA Submission Lead time: By Jurisdiction

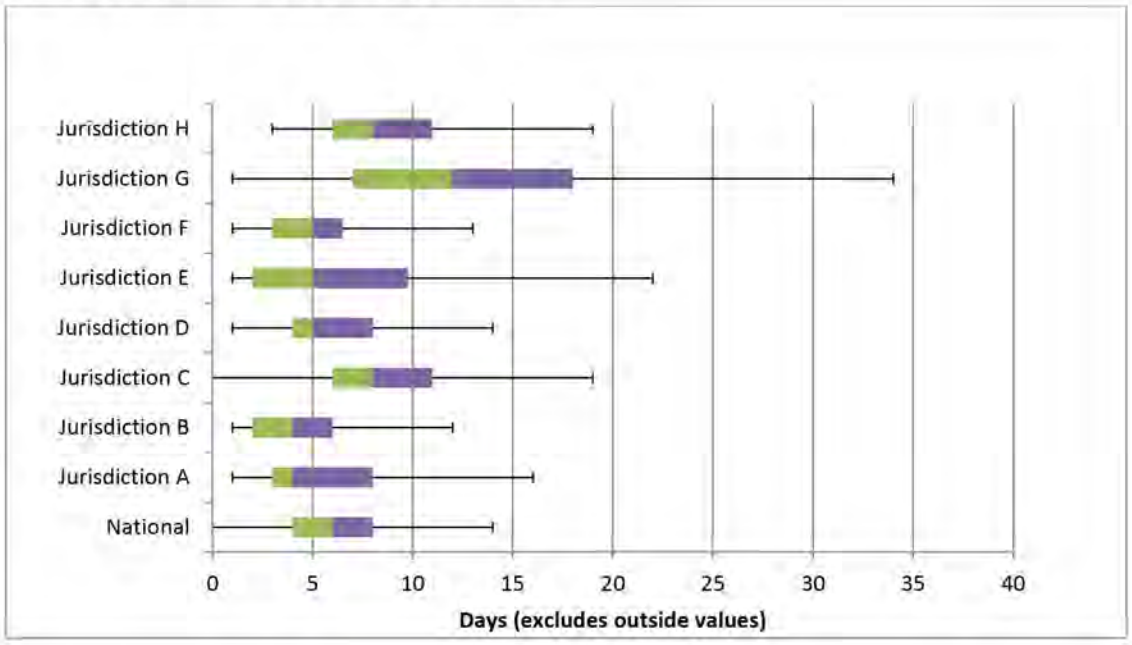


Figure 24: DNA Submission Lead time: By Location

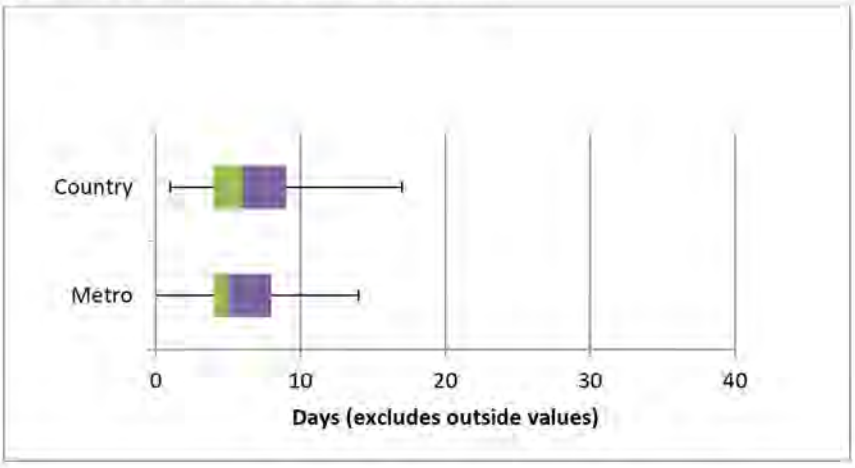


Figure 25: Fingerprint Analysis Lead time: By Jurisdiction with National (Median)

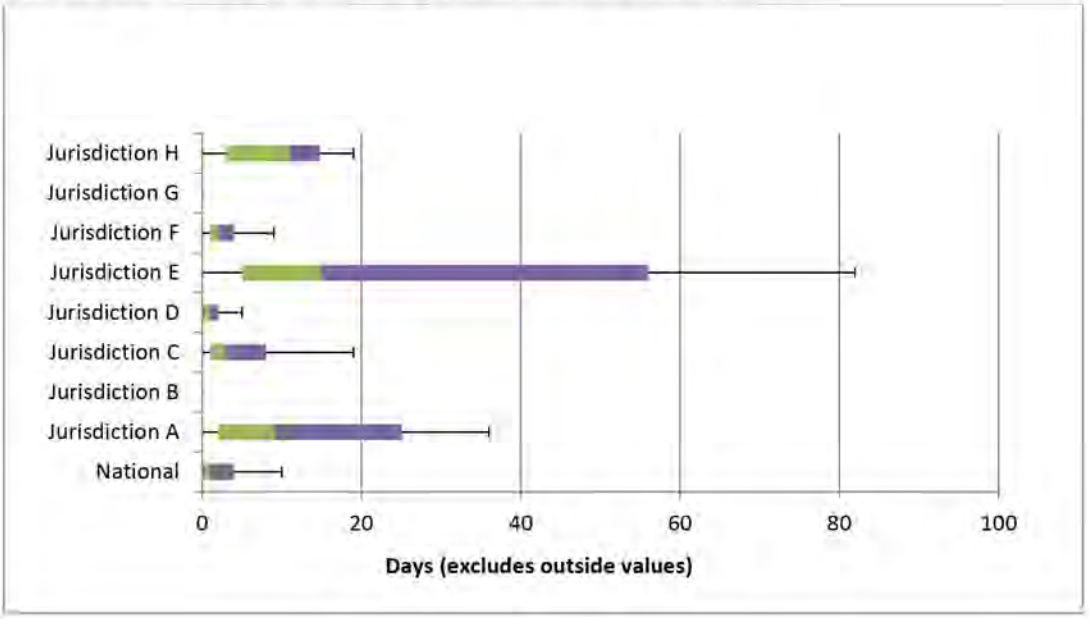


Figure 26: DNA Analysis Lead time: By Jurisdiction with National (Median)

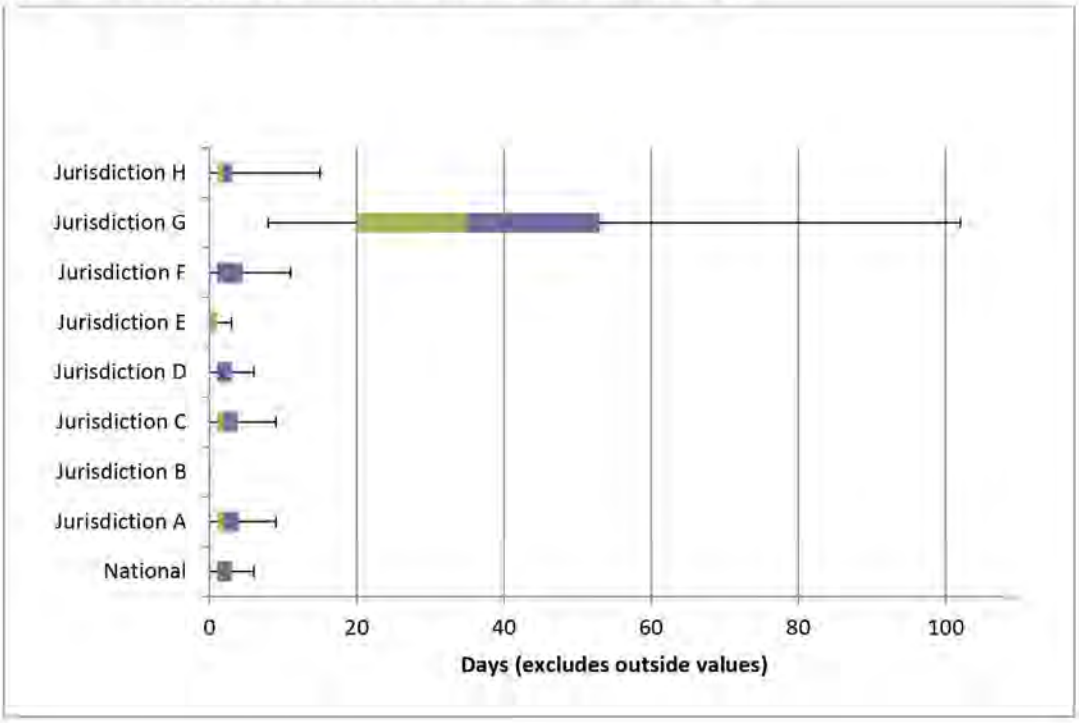


Figure 27: Fingerprint Analysis Lead time: By Location

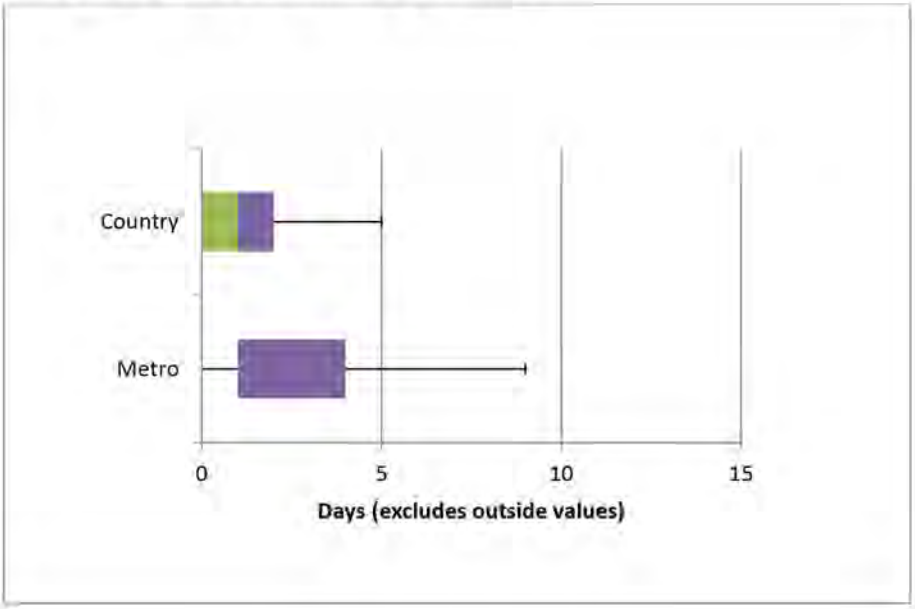


Figure 28: DNA Analysis Lead time: By Location

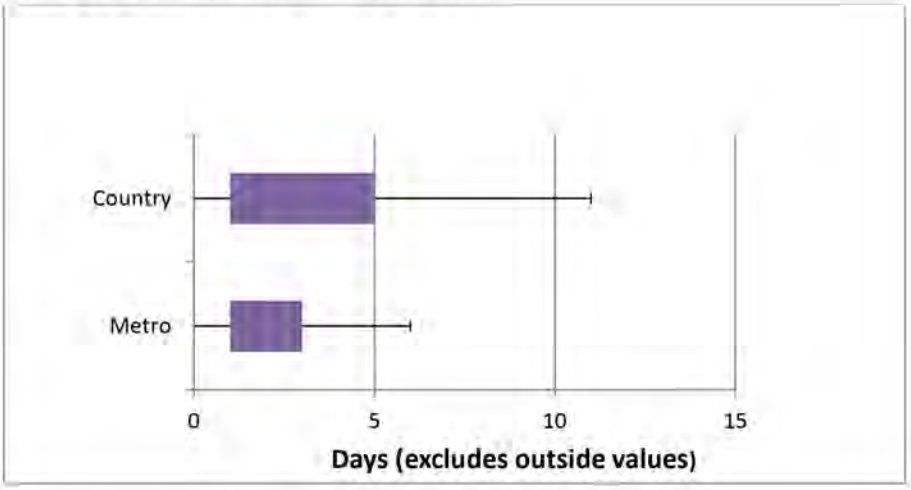


Figure 29: Fingerprint Identification Lead time: By Jurisdiction with National (Median)

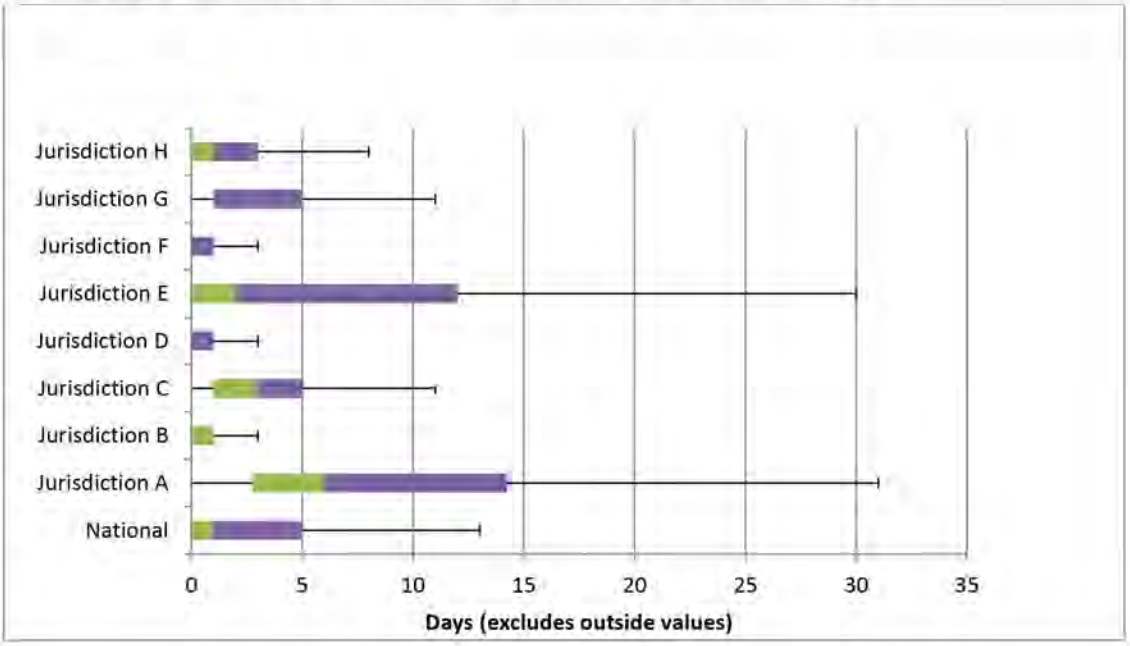
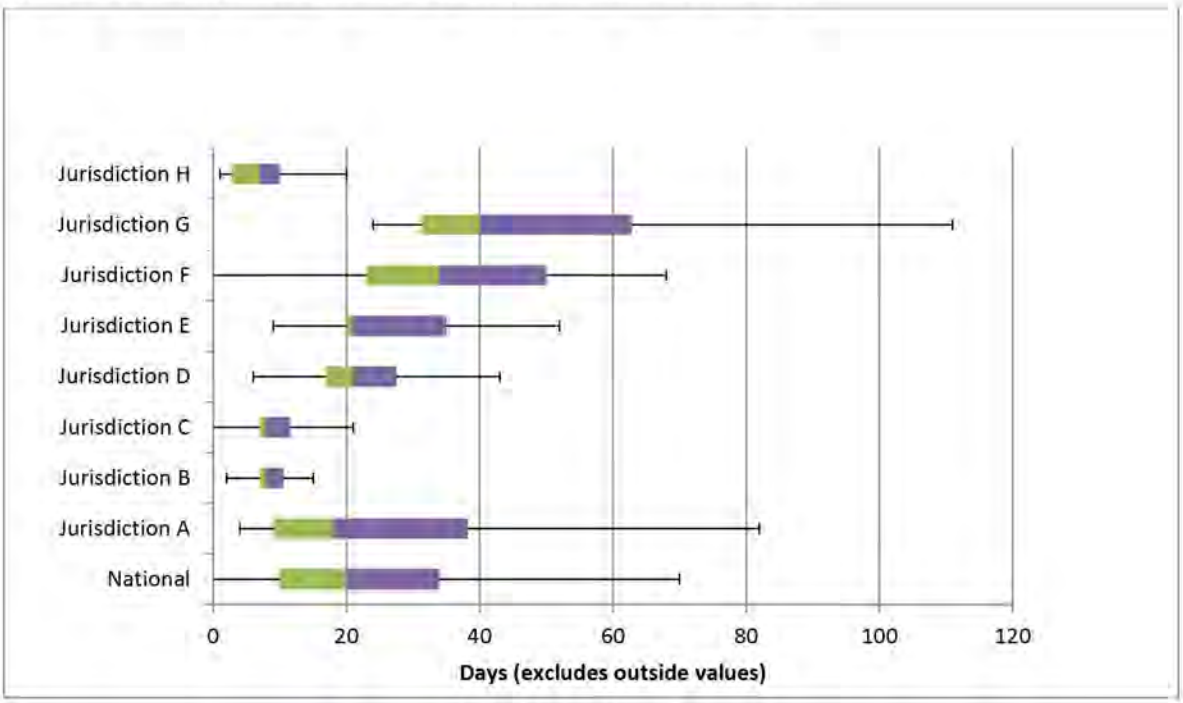


Figure 30: DNA Identification Lead time: By Jurisdiction with National (Median)



Note: scale difference between the two plots

Figure 31: Fingerprint Identification Lead time: By Location

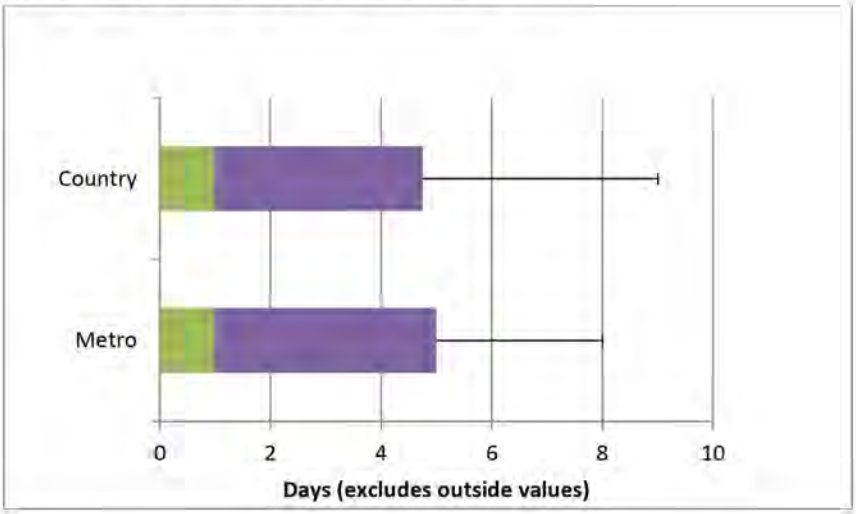
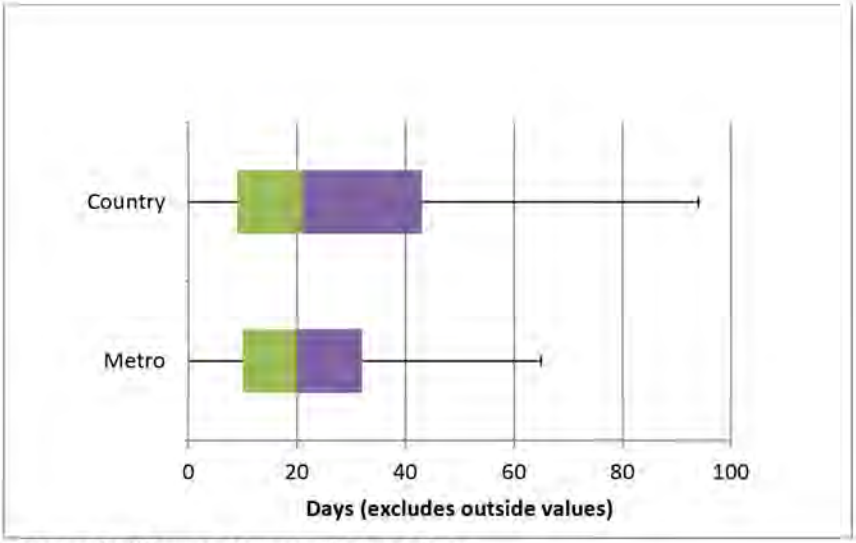


Figure 32: DNA Identification Lead time: By Location



Note: scale difference between the two plots

Figure 33: Fingerprint Arrest Lead time: By Jurisdiction with National (Median)

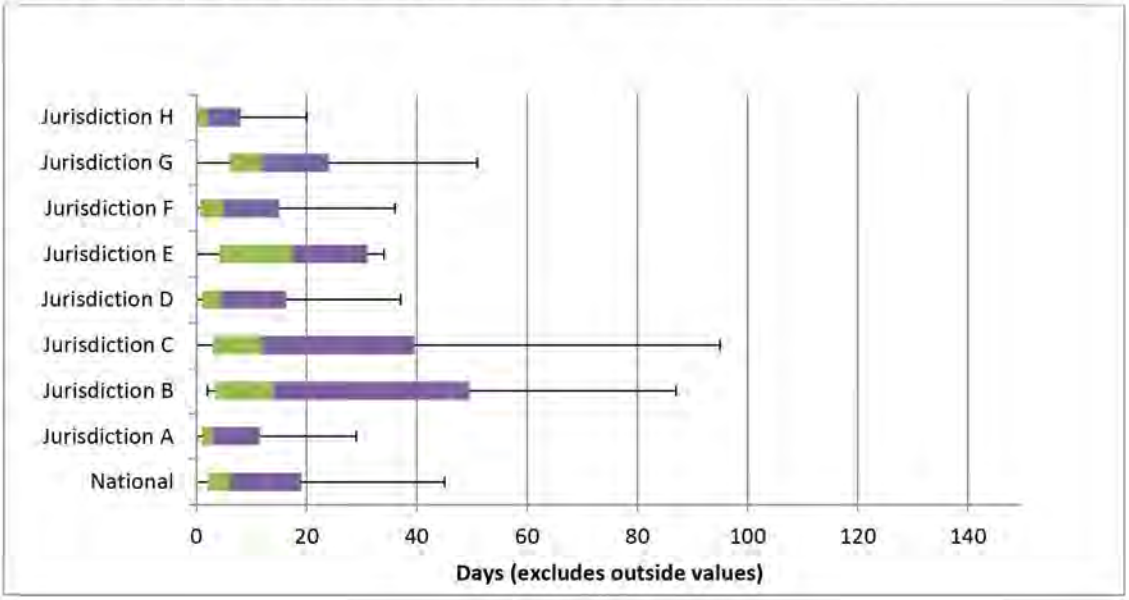


Figure 34: DNA Arrest Lead time: By Jurisdiction with National (Median)

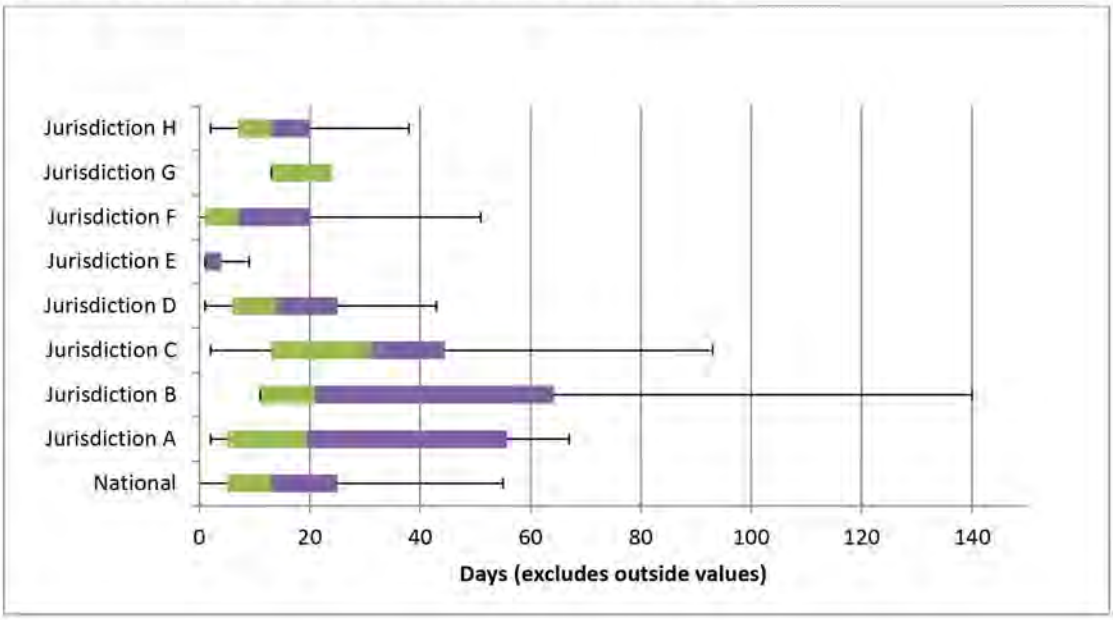


Figure 35: Fingerprint Arrest Lead time: By Location

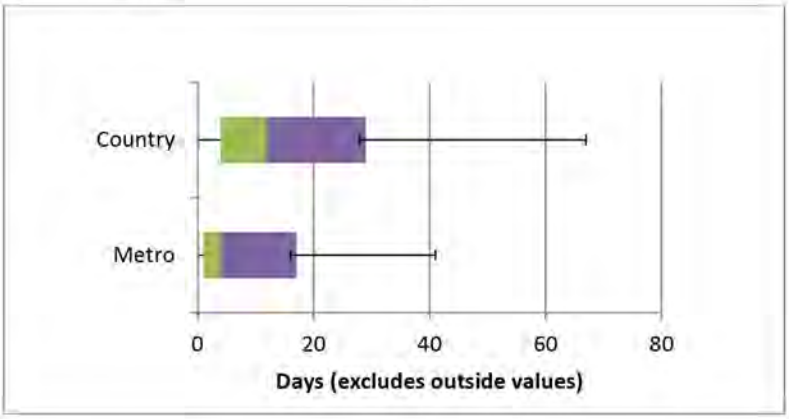
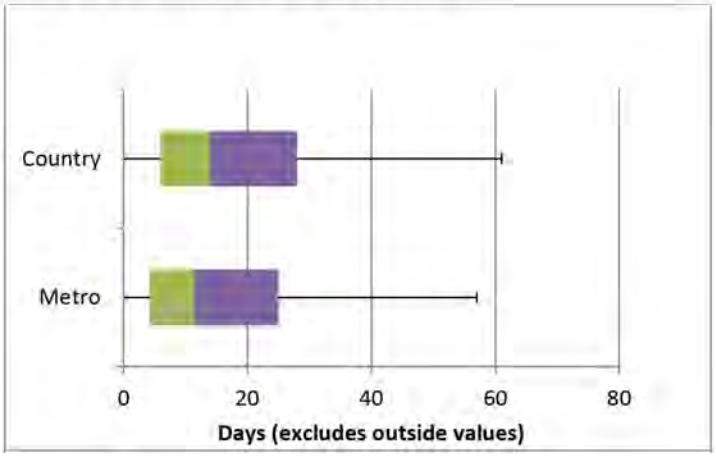


Figure 36: DNA Arrest Lead time: By Location



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1. End-to-end Forensic Identification Process Project, Volume Crime Report, May 2012, ANZPAA NIFS. DOI: http://www.anzpaa.org.au/forensic-science/our-work/products/publications





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CA-121

MONTH	CTS Proficiency Testing Schedule 2022 CTS Proficiency Tests 57x require sample screening CTS Proficiency Tests 58x are sample specific and pre-screened. No screening techniques are required and therefore this set of proficiencies should **NOT** be used for sampling scientists.										
	CTS type	**Participant Number (Web Code)**	**Lab Number(s)**	**FR Number**	**Staff**	**Role**	**Received Date**	**Due Date**	**Date Submitted**	**Follow-up completed**	**Feedback presented**
January	FB5701 Forensic Biology	[redacted]	[redacted]	[redacted]	Luke Ryan	Reporter	18/01/2022	7/03/2022	10/02/2022	14/04/2022	13/05/2022
					Allison Lloyd	Reviewer					
					Valerie Caldwell	Sampler					
					Kevin Avdic	Reference sampler					
	FB5801 DNA-Mixture				Kerry-Anne Lancaster	Reporter	18/01/2022	7/03/2022	1/03/2022	14/04/2022	13/05/2022
					Deborah Nicoletti (Rogers)	Reviewer					
					Helen Williams	Sampler					
					Mike Hart	Reference sampler					
February	FB5840 (A) DNA Database - Saliva				Helen Williams	Reporter	10/02/2022	4/04/2022	29/03/2022	13/05/2022	13/05/2022
					Pierre Acedo	Reviewer					
					Janine Seymour-Murray	Sampler					
					Kim Estreich	Reference sampler					
	FB5840 (B) DNA Database - Saliva				Biljana Micic	Reporter	10/02/2022	4/04/2022	9/03/2022	13/05/2022	13/05/2022
					Kirsten Scott	Reviewer					
					Kristina Morton	Sampler					
					Madison Gulliver	Reference sampler					
	FB5840 (C) DNA Database - Saliva				Tara Prowse	Reporter	10/02/2022	4/04/2022	6/03/2022	13/05/2022	13/05/2022
					Abbie Ryan	Reviewer					
					Amy Morgan	Sampler					
					Madison Gulliver	Reference sampler					
	FB5870 (A) DNA Parentage				Alicia Quartermain	Reporter	24/02/2022	18/04/2022	12/04/2022	13/05/2022	13/05/2022
					Angelina Keller	Reviewer					
					Cindy Chang	Sampler					
					Mike Hart	Reference sampler					
	FB5870 (B) DNA Parentage				Adrian Pippia	Reporter	24/02/2022	18/04/2022	24/03/2022	13/05/2022	13/05/2022
					Rhys Parry	Reviewer					
					Michelle Margetts	Sampler					
					Mike Hart	Reference sampler					
	FB5702 Forensic Biology				Justin Howes	Reporter	10/03/2022	2/05/2022	13/04/2022	27/05/2022	13/07/2022
					Josie Entwistle	Reviewer					
					Valerie Caldwell	Sampler					
					Kevin Avdic	Reference sampler					
					Sharon Johnstone	Reporter					

MONTH	CTS Proficiency Testing Schedule 2022 CTS Proficiency Tests 57x require sample screening CTS Proficiency Tests 58x are sample specific and pre-screened. No screening techniques are required and therefore this set of proficiencies should **NOT** be used for sampling scientists.											
	CTS type	**Participant Number (Web Code)**	**Lab Number(s)**	**FR Number**	**Staff**	**Role**	**Received Date**	**Due Date**	**Date Submitted**	**Follow-up completed**	**Feedback presented**
March	FB5802 DNA - Semen	[redacted]	[redacted]	[redacted]	Thomas Nurthen	Reviewer	10/03/2022	2/05/2022	26/04/2022	24/05/2022	13/07/2022
					Helen Williams	Sampler					
					Kevin Avdic	Reference sampler					
	FB5781 Body Fluid Identification				Abbie Ryan	Reporter	11/04/2022	23/05/2022	20/05/2022	15/06/2022	13/07/2022
					Allison Lloyd	Reviewer					
					Kristina Morton	Sampler Item 1					
					Helen Williams	Sampler Item 2					
					Cindy Chang	Sampler Item 3					
					Michelle Margetts	Sampler Item 4					
					Valerie Caldwell	Sampler Item 5					
					Amy Morgan	Sampler Item 6					
April	FB5703 Forensic Biology				Angelina Keller	Reporter	9/05/2022	21/06/2022	8/06/2022	Awaiting summary report	
					Emma Caunt	Reviewer					
					Michelle Margetts	Sampler					
					Kevin Avdic	Reference sampler					
	FB5803 DNA - Blood				Alicia Quartermain	Reporter	9/05/2022	21/06/2022	7/06/2022	13/07/2022	
					Adrian Pippia	Reviewer					
					Cindy Chang	Sampler					
					Kevin Avdic	Reference sampler					
May	FB5871 (A) DNA Parentage				Penelope Taylor	Reporter	14/06/2022	1/08/2022	5/07/2022		
					Thomas Nurthen	Reviewer					
					Abigail Ryan	Sampler					
					Kevin Avdic	Reference sampler					
	FB5871 (B) DNA Parentage				Sharon Johnstone	Reporter	14/06/2022	1/08/2022	19/07/2022		
					Justin Howes	Reviewer					
					Janine Seymour-Murray	Sampler					
					Mike Hart	Reference sampler					
	FB5871 (C) DNA Parentage				Josie Entwistle	Reporter	14/06/2022	1/08/2022	8/07/2022		
					Jacqui Wilson	Reviewer					
					Amy Morgan	Sampler					
					Kevin Avdic	Reference sampler					
	FB5704 Forensic				Allan McNevin	Reporter	[illegible]	[illegible]			
					Penelope Taylor	Reviewer					

MONTH	CTS Proficiency Testing Schedule 2022 CTS Proficiency Tests 57x require sample screening CTS Proficiency Tests 58x are sample specific and pre-screened. No screening techniques are required and therefore this set of proficiencies should **NOT** be used for sampling scientists.										
	CTS type	**Participant Number (Web Code)**	**Lab Number(s)**	**FR Number**	**Staff**	**Role**	**Received Date**	**Due Date**	**Date Submitted**	**Follow-up completed**	**Feedback presented**
July	Biology	[redacted]	[redacted]	[redacted]	Valerie Caldwell	Sampler					
						Reference sampler					
	FB5804 DNA-Semen				Kylie Rika	Reporter	18/07/2022	6/09/2022			
					Ingrid Moeller	Reviewer					
					Kristina Morton	Sampler					
						Reference sampler					
	FB5843 (a) DNA Database - Saliva					Reporter					
						Reviewer					
						Sampler					
						Reference sampler					
	FB5843 (b) DNA Database - Saliva					Reporter					
						Reviewer					
						Sampler					
						Reference sampler					
	FB5843 (c) DNA Database - Saliva					Reporter					
						Reviewer					
						Sampler					
						Reference sampler					
August	FB5872 DNA Parentage					Reporter					
						Reviewer					
						Sampler					
						Reference sampler					
	FB5872 DNA Parentage					Reporter					
						Reviewer					
						Sampler					
						Reference sampler					
	FB5705 Forensic Biology					Reporter					
						Reviewer					
						Sampler					
						Reference sampler					
	FB5805 DNA-Blood					Reporter					
						Reviewer					
						Sampler					

MONTH	CTS Proficiency Testing Schedule 2022											
	CTS Proficiency Tests 57x require sample screening											
	CTS Proficiency Tests 58x are sample specific and pre-screened. No screening techniques are required and therefore this set of proficiencies should **NOT** be used for sampling scientists.											
	CTS type	**Participant Number (Web Code)**	**Lab Number(s)**	**FR Number**	**Staff**	**Role**	**Received Date**	**Due Date**	**Date Submitted**	**Follow-up completed**	**Feedback presented**
September						Reference sampler					
	FB5782 Body Fluid Identification					Reporter					
						Reviewer					
						Sampler Item 1					
						Sampler Item 2					
						Sampler Item 3					
						Sampler Item 4					
						Sampler Item 5					
						Sampler Item 6					
October	**FBS5706 Forensic Biology**					Reporter					
						Reviewer					
						Sampler					
						Reference sampler					
	FB5806 DNA-Mixture					Reporter					
						Reviewer					
						Sampler					
						Reference sampler					
TBA (NEW TESTS)	**5905 Probabilistic Genotyping (FTA)**					Reporter					
						Reviewer					
						Sampler					
						Reference sampler					
	5905 Probabilistic Genotyping (FTA)					Reporter					
						Reviewer					
						Sampler					
						Reference sampler					

CA-122

HealthSupport Queensland

SSLU DNA Assistance

1 Purpose

To ensure the Liaison staff are all using the same procedure when working on cases submitted through the Forensic Register.

2 Scope

The procedure will apply to all Liaison officers working within Scientific Services Liaison Unit (SSLU) and dealing with DNA cases within the Forensic Register.

3 Definitions

CM	Case Management
FR	Forensic Register
IO	Investigating Officer
QH	Queensland Health
QPS	Queensland Police Service
QWIC	Queensland Wide Interlinked Court system
SMU	Sample Management Unit
SSLU	Scientific Service Liaison Unit

4 Actions

1. Statement Request

The requests/tasks will originate from a QPS officer or from the Office of the Department of Public Prosecutions.
A Liaison officer will copy all the relevant information from the QPS original statement request/task and then create a new Request/task. Once the new Request/task is completed, enter into the original request from SMU and remove the case officer number and tick request completed. When verbal statement requests are received from DPP a Liaison officer will create the statement request on behalf of DPP adding the names of the defendant and complainant along with the name, address and email of the DPP person requesting.

1. Click on the Case management tab.
2. Press the plus button
3. Tick the request/task button
4. Tick the Statement button in the request Type
5. Tick the Forensic DNA button
6. Paste the copied contents into the Comments field.
7. Check QWIC and add the court date, court type, proceedings and location.
8. Add a four week 'bring up' date (this date will depend on court, complexity & allocation)
9. The required date field is to be left blank unless a case officers number is listed, then negotiate a date required with the nominated Reporting Scientist.
10. Save
11. Add an exhibit barcode to the exhibit field and save.
12. Add a note marked High if required, if a time frame has been given or there are extenuating circumstances within the request.

If a scientist's registered number has not been added to the Case Officers field this case will populate a list in DNA, (Unallocated Statement) The Team leaders in the Reporting Team will allocate to a scientist.

If the case is already allocated to a scientist, add their number to the Case Officers field and this will drop onto their work list.

If a statement request has been received from DPP, create a statement request page as above. If a statement request is later received from the Investigating officer for the same case and the previous request has been allocated to a scientist, then close the request for this second statement request. Add the relevant information for the investigating officer to the previous statement request.

SSLU are to notify SMU of all Statement requests from DPP.

Once a statement is finalised, emailed and posted, SSLU to enter release details under the statement report page. Remove the bring up date from the statement request page.

2. Court List

This list enables the Liaison staff to follow and add information to the FR for scientists that are required to either attend court in person, give phone or video evidence.. This information may be received multiple ways. (Subpoena, email or phone).

1. Click onto the Case File Tab
2. Click in Search Field, enter the QP number or the Forensic Register number
3. Click on to the plus button to create a request/task
4. Add a request type – Court
5. Click on the Forensic DNA button in the Job/Request type
6. Add the court information (date type proceeding and location
7. Add a 'bring up' date. (This should be at least 2 days prior to court)
8. Add the information into the comments
9. Add the date required
10. Add the Scientist's FR number in the Case Officers field.
11. Add an exhibit barcode to the exhibit field and save
12. Press Save

Once a case officer's name is added to the Case officer field it will automatically populate their work list.
If there is no scientist or the nominated scientist has left the organisation, contact the Senior Reporting scientists via email for the name of person who will be available to give the evidence. Contact the investigating officer and DPP advising them of the change of name.

A new court page is to be created with each new court notice.

If there is a subpoena or email this needs to be saved to the file as a PDF file. Once saved as a PDF on your desktop.

1. Select the edit button
2. Go to "choose file" and click
3. Add the saved file then press save.

Court Testimony Monitoring & Evaluation forms:

It is a requirement that all scientists in DNA analysis who give evidence in the court obtain a court evaluation form once every twelve months, these forms aid in the court training of each scientist.

The scientist will request SSLU to have this form completed by the Prosecutor of the case. SSLU to enter into QIS to download the appropriate form (17047)
Enter name of scientist in – Name of Witness
Enter name of Defendant – Matter of Defendant
Enter date – day evidence given
Enter court type – eg. Trial
Enter Lab Reference No: - QP number of the case
Enter Location – Place of court, eg. Cairns
Liaison officer will email the form to the prosecutor
Follow up with the Prosecutor within three days if no response from the previous request.

4. Task requests

Task requests can come from SMU or DNA scientist. These requests will vary from
QPS – Time Frames, Final result requests, PM samples and Statement requests.
DNA scientist – Requesting information from IO's or courts, PM samples
Scientist requesting information for testing or item description

SSLU will also create task request to SMU and to Scientists for various reasons

1. Type in the QP number in the search field
2. Select the plus button
3. Select the CM button
4. Select DNA
5. Add notes to the comment field
6. Add a bring up date

When sending a task to DNA, send to either of the two senior scientists in the Reporting Team.

If the information required by a scientist is in relation to an item discrepancy or an ownership query, the task needs to go to SMU to obtain the correct information. Add the Registration number of one of the SMU staff members requesting the required information.
Close the task once completed by selecting Request complete.

5. Completing cases

Once a case has been finished, SSLU need to complete the case by doing the following.

1. Type in the QP number
2. Select edit
3. Select Request Complete
4. Remove the Bring up date
5. Select save

This will then remove the case from any list unless you have it pinned to your Personal work list.

6. Pinning cases to worklist

This allows you to keep a case on your personal worklist to follow.

1. Open the case required
2. Enter into Case Management
3. Enter into the note you wish to pin.
4. Click on the pin located in the top right-hand side
5. When the pin faces downwards this indicates the case is on your personal list only.

To unpin a case, repeat the above process.

Avoid using your personal worklist as a follow up list as cases can be followed by adding a bring up date.

7. Coronial Cases

PM samples are required to be sort from various agencies to ensure a case can be completed. These cases may vary from identification, murders or an order from the Coroner. Requests may come from the Coronial meetings, SMU, IO or the scientist. Reference samples are sometimes required to be obtained from family members to aid the Identification of the deceased.
Refer to QIS Document number 25685

1. View the Form 3 in Auslab, scanned under the CA number for the deceased in order to see what PM samples have been taken at autopsy. Send a task to SMU for confirmation that these samples require testing and the type of testing required; list each sample as SMU do not have visibility of the samples.
2. If required, send an email to the Mortuary requesting samples taken to be transferred to DNA analysis via property point. Copy Property Point in the email request. North Queensland Pathologists often hand QPS the PM samples, if this is the case –request SMU to follow up with the Investigating officer.
3. If a PDNA sample is available, SSLU must email SMU asking authority to use this sample for the comparison and reporting of the Identification of the deceased.
4. All information emails are to be recorded in FR. (save email and response as PDF and attach to FR. **Do not transcribe email**, copy and paste if required.
5. Add a 'bring up' date to ensure we receive the response required.

8. Timeframe Requests

SSLU are usually notified of timeframe requests from QPS, DPP and Prosecutions.

1. Enter into FR, type the required QP number in the search field
2. Click on Case Management tab
3. Click on the plus (+) sign
4. Click Request/Task
5. Click on DNA
6. Click on CM
7. Add notes to the comment field
8. For case officer field add one of the Senior Scientists in the Reporting Teams.

9. Miscellaneous

Correction tasks received from QPS in relation to FR do not require action by SSLU

10. References

Nil

11. Amendment History

12. Associated Documentation
25685

Revision	Date	Author/s	Amendments
1	10.8.17	Andrea Norton	First Issue
2	19.05.2020	Polly Williams	Removed and added relevant termiology

CA-123

Report for QIS OQI as of 26/07/2022 10:26:45 AM

Report for QIS OQI -

34043 Positive Extraction Controls with low DNA yields

OQI Details

Status	Closed Approved
Subject	A number of positive extraction controls were found to have much lower DNA quantification values than what is typically observed
Source of OQI	Internal Problem
Date Identified	22/03/2013

OQI Creator Contact Details

Creator	Allan MCNEVIN
Organisational Unit/s	Analytical
Service/s	Forensic and Scientific Service
Site Location/s	Coopers Plains

Investigator/Actioner Contact Details

Actioner	Allan MCNEVIN
Organisational Unit/s	Analytical
Service/s	Forensic and Scientific Service
Site Location/s	Coopers Plains

Investigation Details

Investigation Completed 06/05/2013 **Root Cause Type** | Procedure/Method/Process

Investigation Details

During the processing of quantification batch [redacted] it was noted that all samples on the batch contained very low quantification values. Typically reference samples yield high quantification values following extraction. The batch was repeated for quantification and the same results were obtained. In the process it was noted that the positive extraction controls on that batch contained much lower quantification values than what is typically observed.

Further investigations showed a number of positive extraction controls had yielded quantification values lower than typically observed. The quantification values observed were in the range of 0.01 - 0.1 ng/uL, whereas typically the positive extraction control yields values in the range of 1 - 3 ng/uL. Further investigation into the reagents used showed that the batches that had positive extraction controls with low quantification values had used a specific in-house lot of Proteinase K (a reagent integral to the extraction process that aids in the destruction of cell membranes and other proteins within the sample), whereas the unaffected batches had used alternative in-house lots of Proteinase K.

A test extraction using multiple positive extraction controls was then setup whereby all samples contained the same reagents with the

exception of Proteinase K (different in-house lots of Proteinase K were used for different positive controls). The results from this testing confirmed that a specific lot of Proteinase K was resulting in greatly reduced DNA yields compared with other lots.

Proteinase K is received by the laboratory as a lyophilized powder. Multiple discrete bottles of the same manufacturer lot number may be received. Specific quantities of nanopure water is added to the powder to form a solution of the desired Proteinase K concentration. As more volume of Proteinase K solution is required for some extraction procedures compared with others, and some extraction procedures require differing concentrations of Proteinase K, various volumes and / or concentrations are aliquot at different times. Each single bottle of Proteinase K is prepared at a specific volume and concentration. Each preparation is designated an internal (in-house) lot number. Therefore, multiple in-house lot numbers or aliquots of Proteinase K may be in use within the laboratory at any given time and more than one in-house lot number may have been produced from the same manufacturer lot number.

When it was identified that a specific in-house lot of Proteinase K was affected, all of the available in-house lot numbers were pH tested using Macherey-Nagel pH strips. The affected Proteinase K was shown to have a pH of 14, compared to other in-house lots with pH in the 7-8 range. For the DNA IQ extraction procedures, 180 uL of 10 mg/mL Proteinase K is added to 6200 uL of TNE buffer. When this mixture was made with the affected Proteinase K, the resulting pH was in the range of pH 11-12. This would then radically affect the ability of any free DNA to bind to the paramagnetic particles in the DNA IQ extraction.

At the same time as the investigation into the affected Proteinase K was being conducted, it was noted that the industrial dishwasher used to clean laboratory glassware was not operating to full specification. A caustic detergent is used in this cleaning process. It is proposed that a measuring cylinder used for the preparation of the affected lot of Proteinase K may have contained residue of the caustic detergent due to the malfunctioning dishwasher, thereby resulting in an in-house lot of Proteinase K with a drastically high pH.

Once it was discovered that a specific in-house lot of Proteinase K had been affected, this lot had been set aside and staff notified that this lot was the cause of the low positive control yields identified. Unfortunately, due to human error, as the investigation was nearing completion, the affected lot was used for some subsequent extraction procedures resulting in additional samples being affected.

Preformed By Allan MCNEVIN

Action Details

Action Complete 06/05/2013 **Action Fix Type** Changed ProcessCorrective Actions

Title

Action Description Appropriate AUSLAB audit entries & notes have been made for all affected samples / batches.

Two letters were sent to the client (QPS) notifying them of all samples that were affected. A copy of each of these letters are retained by the Quality Team within the Intell Letters folder.

All affected samples, where substrate remained following the initial extraction, were re-extracted. Whilst the initial DNA extraction performed sub-optimally (low DNA yields) any DNA profiles obtained from either the original extraction or the re-extraction (or any pooled samples) are reportable.

A change to some laboratory procedures has been instituted as a result of this OQI. All in-house lots of Proteinase K & DTT will be pH tested and processed through a test extraction prior to release for routine use. This procedure will be placed into the QIS document "19994 Procedure for testing DNA Quantification Standards, DNA Quantification and Amplification kits & Reagents and Quality Control Samples", the title of the document will also be adjusted accordingly. A process of checking quantification values for positive extraction controls at the time of testing has been introduced. Additionally, a change to the process for quarantining kits or reagents under investigation has also been introduced (refer Analytical team minutes dated 15-04-2013.

Repair of the malfunctioning industrial dishwasher is also underway.

Task Details

No Tasks found

Follow-up And Approval

Follow-up Status	Accepted
Follow-up Status Comment	6/05/2013 4:38:25 PM Allan MCNEVIN: OK
Approver	Paula BRISOTTO
Approval/Rejection Date	16/09/2013
Approval/Rejection Comment	16/09/2013 1:43:51 PM Paula BRISOTTO: Approve the investigation performed and the actions taken to resolve the incident, plus the introduction of testing going forward. The industrial dishwasher is still under repair; an acceptable temporary alternative process for washing and rinsing glassware has been implemented until the dishwasher repair is complete.

Associations

No Associations found

Records

No Records found

34043 Positive Extraction Controls with low DNA yields

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CA-124

Report for QIS OQI as of 26/07/2022 10:29:37 AM

Report for QIS OQI -

[redacted] Incorrect conditions used for Capillary Electrophoresis

OQI Details

Status	Closed Approved
Subject	It was identified that Genetic Analyzer 3130xl B was set with incorrect run module settings for the capillary electrophoresis of samples amplified using the PowerPlex 21 amplification kit
Source of OQI	Internal Problem
Date Identified	08/07/2013

OQI Creator Contact Details

Creator	Allan MCNEVIN
Organisational Unit/s	Analytical
Service/s	Forensic and Scientific Service
Site Location/s	Coopers Plains

Investigator/Actioner Contact Details

Actioner	Allan MCNEVIN
Organisational Unit/s	Analytical
Service/s	Forensic and Scientific Service
Site Location/s	Coopers Plains

Investigation Details

Investigation Completed 06/08/2013 **Root Cause Type** | Unintended Human Error

Investigation Details

Information was received from the manufacturer recommending a change to the run modules used for the 3130xl Genetic Analyzer instruments (used for Capillary Electrophoresis - CE). The new run modules contain an additional wash station and other minor changes designed to reduce potential instances of CE carry-over. When installing the updated run modules, it was noted that the run module used on 3130xl B for the analysis of samples amplified with the PowerPlex 21 (P21) amplification kit contained an injection time setting of 3 seconds. The 3130xl A instrument was set to 5 seconds. On consultation with the PP21 user guide, it was observed that 5 seconds is the default setting for 3130xl instruments, however a range of 3 - 22 seconds may be utilised. It is standard practice within the laboratory to use a single consistent injection time setting across both instruments for the same amplification kit.

Adjustment of the injection time affects the amount of amplified product that is potentially injected into the capillary at the start of the electrophoresis process. As such, depending on the amount of available product, it would be expected that a longer injection time will result in more product, resulting in more signal. Ultimately this theoretically

leads to increased peak heights for samples. Concomitantly, it would be expected that the background florescence (baseline) would be raised as well.

Once the discrepancy was noted, a test run was conducted. This involved taking a randomly selected batch of casework samples and injecting a single folder (consisting of 14 casework samples, 1 negative extraction control and one allelic ladder) with the previously used run module (3 second injection time), and the new run module provided by the manufacturer (set to 5 second injection time) concurrently. The data was then analysed and the following was found:
- There were no instances observed where the 3 second injection time yielded a higher peak height than the corresponding peak in the 5 second injection time run. Additionally, there were no instances of a peak present in the 3 second injection time run that was not present in the 5 second inection time run. There were however, instances where the 5 second injection time run showed additional peaks that were above the limit of reporting (LOD = 50 RFU) that were not above the LOD in the 3 second injection time run.
- On average, where peaks were observed in both runs, the peak heights in the 5 second injection time run were 1.75 times the height of those observed in the 3 second injection time run (maximum 2.48 times higher, minimum 1.3 times higher)
- The results for each peak from each run were paired and ordered according to the 3 second injection time peak height and graphed. A linear trend line showed an R-squared value of 0.968 and equation y = 1.65x + 22.63 (peak height range was 40 RFU to 2354 RFU for the 3 second results). This indicates a strongly linear relationship between the injection time and the peak height for the experiment conducted.

Additionally, it was found that these injection time settings (3130xl B - 3 seconds; 3130xl A - 5 seconds) had been applied since the start of investigations into the PP21 amplification kit, including kit validation. A review of all validation data showed that the majority of validation testing had been performed on 3130xl A, however there were some experiments that had been run on both instruments and both data was utilised. Refer to actions regarding the outcomes associated with this.

Preformed By Allan MCNEVIN

Action Details

Action Complete 30/08/2013 **Action Fix Type** Expenditure of Resources

Title Corrective Actions

Action Description Once the problem noted in this OQI was noted, a number of corrective actions were instituted.

All affected samples and batches were identified, and appropriate AUSLAB batch audit entries and specimen notes were made.

After analysis of the validation data, the DNA Analysis management team held a meeting and the following outcomes were decided on:

- where concordance or population data was run using a 3 second injection time, this data would not be repeated at 5 seconds, as increasing the injection time does not change the designation of any alleles called when run using a 3 second injection time.

- baseline & variance data for 3130xl B was re-checked using the original validation samples after re-running using a 5-second injection time. Data obtained did not differ from the values obtained from the validation using 3130xl A.

- stutter data was obtained from data obtained from both 3 and 5 second injection times. As the proportion of peak heights does not change with increased injection time, it was agreed that the stutter data was not significantly affected. Additionally, as the stutter files for STRmix software are based on national data, there is no effective change.

- drop-out rates were calculated using both injection times. This data was split and will be included as separate data in an undated PP21 validation report.

- as some additional data was obtained (but not utlised for the validation report), the PP21 validation report will be re-issued with some data split into 3 second and 5 second injection time data, and some additional data obtained from 3 second injection times included. This will also include data to show that half-volume reactions run using a 3 second injection time are reportable, however this method is not recommended due to the potential loss of information when peak heights are low.

For all samples that were amplified with a full-volume (25uL) PCR reaction with the PP21 amplification kit, all samples were sent for repeat CE. The results obtained from 3 second injection time were then compared with the result obtained from repeat CE with 5 second injection time. Results were updated and reported where a change to the reported result was found.

For all samples that were amplified with a half-volume (12.5uL) PCR reaction with the PP21 amplification kit, all samples were assessed. Where it was considered that repeat CE with a longer injection time may provide additional information (e.g the presence of possible peaks below reporting threshold), these samples were re-amplified with a full -volume amplification. Where it was considered that repeat CE would not change the result, the result was reported as obtained.

Task Details

No Tasks found

Follow-up And Approval

Follow-up Status	Accepted
Follow-up Status Comment	26/09/2013 3:47:12 PM Allan MCNEVIN: OK
Approver	Paula BRISOTTO
Approval/Rejection Date	01/11/2013
Approval/Rejection Comment	1/11/2013 3:04:57 PM Paula BRISOTTO: Appropriate investigation/actions taken. To clarify the action with respect to casework samples (full volume), all 3 sec results were rejected as 'do not use' due to the incorrect injection time parameter applied (these results were considered non-reportable due to a 'quality failure' in that an incorrect analysis parameter was applied). Given the large number of samples/results involved a decision was taken by the Reporting Team to not include the non-reportable or 'do not use' electropherograms in casefiles - only reportable/acceptable electropherograms will be included. Any affected samples will be able to be identified via specimen notes, and affected casefiles will be

identifiable via the inclusion of this OQI.

OQI approved by Amanda Reeves Acting Team Leader on behalf of Paula Brisotto.

Associations

No Associations found

Records

No Records found

[redacted] Incorrect conditions used for Capillary Electrophoresis

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CA-125

Queensland Government

Forensic and Scientific Services
HSSA | Health Services Support Agency

Intelligence Report

TO: Insp Tony Carstensen
DNA Management Section
Forensic Services Branch
Queensland Police Service
Brisbane QLD 4001

Client Reference : [redacted]

I am writing to advise that during the initial processing of 213 samples (186 casework samples and 26 reference samples), a suboptimal reagent was used resulting in below than expected DNA yields. Due to the samples being processed on the automated platforms or small automated instruments, the event has affected the entire batch of samples. The barcodes of the casework samples affected are listed below.

An attempt was made to obtain any DNA which may have remained in the original substrates, and these were subsequently processed as per normal operating procedures. It is expected that the majority of the DNA, if present, was contained within the original samples, that were subjected to the suboptimal reagent. Re-processing of the original substrates would not be expected to yield optimal results; however an attempt was made. Where possible, the extract DNA from the original substrates and the subsequent re-extraction will be combined.

The results for these samples have been reported electronically; however please note that the results obtained may not be a true representation of the DNA that may have been in the original sample, but the best we are able to obtain given the circumstances.

If any additional samples for these cases are submitted, they will be processed accordingly.

Reference samples have been reprocessed to obtain a DNA profile and have not been included in the table below. Additional steps have been added to ensure this type of event does not occur again.

[redacted]

NATA Accredited Laboratory 41
Accredited for compliance with ISO/IEC 17025

Cathie Allen, Managing Scientist: [redacted] Date: 05.04.13

The results relate solely to the item(s) and/or sample(s) as received.

[redacted]

Phone [redacted]
Fax
Email

Intelligence Report

Client Reference: [redacted]

[redacted]

[redacted]

Cathie Allen, Managing Scientist
DNA Analysis Unit
05 April 2013

[redacted]

Peer Reviewed by
Justin Howes, Team Leader
DNA Analysis Unit
05 April 2013

NATA Accredited
Laboratory 41
Accredited for compliance
with ISO/IEC 17025

The results relate solely to the item(s) and/or sample(s) as received.

39 Kessels Road
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AUSTRALIA

PO Box 594
Archerfield QLD 4108
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[redacted]

Queensland Government

Forensic and Scientific Services
HSSA | Health Services Support Agency

Intelligence Report

TO: Insp Tony Carstensen
DNA Management Section
Forensic Services Branch
Queensland Police Service
Brisbane QLD 4001

Client Reference : [redacted]

I am writing to advise of an additional 77 samples affected by a suboptimal reagent. Use of this reagent resulted in below than expected DNA yields. Due to the samples being processed on the automated platforms or small automated instruments, the event has affected the entire batch of samples. The barcodes of the casework samples affected are listed below.

An attempt was made to obtain any DNA which may have remained in the original substrates, and these were subsequently processed as per normal operating procedures. It is expected that the majority of the DNA, if present, was contained within the original samples, which were subjected to the suboptimal reagent. Re-processing of the original substrates would not be expected to yield optimal results; however an attempt was made. Where possible, the extract DNA from the original substrates and the subsequent re-extraction will be combined.

The results for these samples have been reported electronically; however please note that the results obtained may not be a true representation of the DNA that may have been in the original sample, but the best we are able to obtain given the circumstances.

If any additional samples for these cases are submitted, they will be processed accordingly. Additional steps have been added to ensure this type of event does not occur again.

[redacted]

[redacted]
Cathie Allen, Managing Scientist
DNA Analysis Unit
09 April 2013

Peer Reviewed by
Justin Howes, Team Leader
DNA Analysis Unit
09 April 2013

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025

Cathie Allen, Managing Scientist: [redacted] Date: 09.04.13

The results relate solely to the item(s) and/or sample(s) as received.

[redacted]

Phone [redacted]
Fax
Email

CA-126



HSSA | Health Services Support Agency

PowerPlex®21 – Amplification of Extracted DNA Validation

Megan Mathieson, Thomas Nurthen & Cathie Allen

DNA Analysis, Forensic & Scientific Services

December 2012

Document details

Contact for enquiries and proposed changes

If you have any questions regarding this document or if you have a suggestion for improvements, please contact:

Contact officer: Thomas Nurthen
Title: Senior Scientist Quality & Projects
Phone: [redacted]
Email: [redacted]

Version history

Version	Date	Changed by	Description
1.0	06/12/2012		1st Issue

Document sign off

This document has been **approved** by:

Name	Position	Signature	Date
Cathie Allen	Managing scientist		

This document has been **endorsed** by:

Name	Position	Signature	Date
Justin Howes	Team Leader FRIT		

Name	Position	Signature	Date
Paula Brisotto	Team Leader ER&Q		

Name	Position	Signature	Date
Sharon Johstone	Senior Scientist Intell Team		

Name	Position	Signature	Date
Amanda Reeves	Senior Scientist Reporting 1		

Name	Position	Signature	Date
Emma Caunt	A/Senior Scientist Reporting 2		

Name	Position	Signature	Date
Adrian Pippia	A/Senior Scientist ER		

Name	Position	Signature	Date
Allan McNevin	Senior Scientist Analytical		

Name	Position	Signature	Date
Thomas Nurthen	Senior Scientist Q & P		

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1 Abstract

To meet Queensland legislative requirements and core business needs, DNA Analysis has validated the PowerPlex® 21 system DNA profiling Kit. All Australian jurisdictions are expected to implement a new DNA profiling kit by the end of 2012. This project came about through the Australian and New Zealand Policing Advisory Agency (ANZPAA).

The loci within the AmpF*l*STR® Profiler Plus® and AmpF*l*STR® COfiler® kits, which are currently used in DNA Analysis, are represented within the PowerPlex® 21 system loci. This allows concordance of the kit for direct comparison and matching against existing AmpF*l*STR® Profiler Plus® crime scene and reference DNA profiles.

This validation has demonstrated the PowerPlex® 21 system kit is fit for purpose for the amplification of extracted DNA samples processed in the DNA Analysis Unit. A limit of reporting threshold of 40RFU will be adopted for analysis of extracted DNA samples amplified at either, 25µL and 12.5µL total PCR volumes.

The sensitivity of this next generation STR kits has greatly increased, however the increased sensitivity does not necessarily result in increased information. The results of the validation detailed here indicate that Promega's PowerPlex® 21 system is a very sensitive STR amplification kit, but to reduce the risk of type 2 errors (calling a heterozygous locus homozygous[1]) consideration needs to be given to restricting the range of DNA template added. Single source samples with DNA templates of greater than 0.5ng overload the PowerPlex® 21 system resulting in DNA profiles being unable to be interpreted. Generally samples with lower templates (reaching the often termed 'low copy number' level of 100-150pg) tend to exhibit enhanced stochastic effects as one would expect. Therefore, it should be considered whether samples around this input template level should be amplified given that interpretation of the results could be unwieldy. It would be possible to increase the template levels of samples that fall into this category by post extraction concentration or increase the total PCR volume.

At a total DNA input template of 0.5ng, for 25µL and 12.5µL total PCR volumes, all alleles were detected for the mixtures with ratios of 1:1, 2:1 and 5:1.

The results from this validation support that the Promega PowerPlex®21 System is suitable for analysis of short tandem repeats (STR).

2 Introduction

To meet Queensland legislative requirements and core business needs, DNA Analysis has validated the PowerPlex® 21 system DNA profiling Kit. All Australian jurisdictions are expected to implement a new DNA profiling kit by the end of 2012. This expectation has been directed by ANZPAA, which comprises a Police Commissioner from each jurisdiction.

The initial plan endorsed by the members of the Biological Specialist Advisory Group (BSAG) involved a series of experiments designed to enable each jurisdiction to choose an appropriate STR amplification kit but using the same methodology (national approach to STR kit validation)[2].

This plan included:

1. Sensitivity and amplification volume determination
2. Population studies
3. Concordance
4. Mixture studies
5. Baseline determinations, peak balance, stutter thresholds, minimum reporting threshold and probability of drop in. This last series of experiments were devised by the Statistics Scientific Working Group (StatSWG)[3].

The plans created by BSAG and StatSWG are a significant development with respect to STR validation and interpretation within Australia. In line with current research, these plans involve the move away from a binary approach to DNA profile interpretation to a continuous model. To achieve this, a new DNA profile interpretation software (STRmix™) has been developed by forensic DNA experts & statisticians from Australia and New Zealand forensic laboratories. The validation of the STRmix™ software will be covered in the STRmix™ validation document to be issued subsequent to this report.

The PowerPlex® 21 system[4] is a new short tandem repeat (STR) kit made available to the Australian forensic laboratories in early 2012. The kit has all of the nine loci amplified in AmpF*l*STR® Profiler Plus®[5] and the six loci amplified in AmpF*l*STR® COfiler®[6] and an additional seven loci. See Table 1 for kit loci.

Table 1 - Comparison of loci in three different kits

(dye colour indicated by colour text)

PowerPlex® 21 System	AmpFℓSTR® Profiler Plus®	AmpFℓSTR® COfiler®
AMEL	AMEL	AMEL
D3S1358	D3S1358	D3S1358
D1S1656		
D6S1043		
D13S317	D13S317	
Penta E		
D16S539		D16S539
D18S51	D18S51	
D2S1338		
CSF1PO		CSF1PO
Penta D		
TH01		TH01
vWA	vWA	
D21S11	D21S11	
D7S820	D7S820	D7S820
D5S818	D5S818	
TPOX		TPOX
D8S1179	D8S1179	
D12S391		
D19S433		
FGA	FGA	

The scope of this validation is to determine for the PowerPlex® 21 system, the limit of detection (LOD), limit of reporting (LOR), the optimal total PCR amplification volume, the range of DNA template, ensure concordance of the PowerPlex® 21 system against the AmpFℓSTR® Profiler Plus® and COfiler® kits, observe the performance of mixed DNA samples and create population datasets required for statistical calculations. Secondary to this, this validation provides the data necessary for STRmix™ validation.

3 Materials

The following materials were used within this validation:

- BSD Duet 600 Series II (BSD Robotics, Brisbane, QLD,AU)
- STORstar instrument (Process Analysis & Automation, Hampshire, GB)
- MultiPROBE II PLUS HT EX with Gripper Integration Platform (PerkinElmer, Downers Grove, IL, US)
- Sterile conductive filtered Roborack 25µL disposable tips (PerkinElmer, Downers Grove, IL, USA)
- 5804 centrifuge (Eppendorf AG, Hamburg, DE)
- 5424 centrifuge (Eppendorf AG, Hamburg, DE)
- Thermomixer (Eppendorf AG, Hamburg, DE)
- MixMate (Eppendorf AG, Hamburg, DE)

- Vortex (Ratek Instruments Pty Ltd, Melbourne, VIC, AU)
- Micro centrifuge (Tomy, Tokyo, JP)
- 1.5mL screw-cap tubes (Axygen Inc. Union City, CA, US)
- Pipettes (Eppendorf, Hamburg, DE and Thermo Fisher Scientific(Finnpipette), Waltham, MA, US)
- Pipette tips (VWR International LLC Radnor, PA, US and Molecular Bioproducts Inc., San Diego, CA, US)
- 96-well PCR plates(Axygen Inc. Union City, CA, US)
- 2.0mL sterile screw-cap tubes (Axygen Inc. Union City, CA, US)
- Plate septas (Axygen Inc. Union City, CA, US)
- Adhesive film (QIAGEN, Hilden, DE)
- FTA™ collection kits (Whatman™ GE Healthcare, Buckinghamshire, GB)
- Positive controls (DNA Analysis Unit, Brisbane, QLD, AU)
- TNE (DNA Analysis Unit, Brisbane, QLD, AU)
- Proteinase K (20mg/mL) (Sigma-Aldrich® Corporation, St Louis, MO, US)
- Dithiothreitol (Sigma-Aldrich® Corporation, St Louis, MO, US)
- Trigene (Medichem International, Kent, GB)
- Ethanol (Recochem Incorporated, Wynnum, QLD,AU)
- Bleach (Ionics Australasia Pty Ltd., Lytton, QLD, AU)
- Amphyl (Rickitt Benckiser Inc. Parsippany, NJ, US)
- Sarcosyl (Sigma-Aldrich® Corporation, St Louis, MO, US)
- Nanopure water (DNA Analysis Unit, Brisbane, QLD, AU)
- Quantifiler™ Human DNA Quantification kits (Life Technologies Applied Biosystems, Foster City, CA, US)
- AB 7500 Real Time PCR System (Life Technologies Applied Biosystems, Foster City, CA, US)
- GeneAmp® PCR system 9700 (Life Technologies Applied Biosystems, Foster City, CA, US)
- ABI 3130*xl* Genetic Analyzer (Life Technologies Applied Biosystems, Foster City, CA, US)
- Hi-Di™ Formamide (Life Technologies Applied Biosystems, Foster City, CA, US)
- 3130 POP-4™ Polymer (Life Technologies Applied Biosystems, Foster City, CA, US)
- Running Buffer (Life Technologies Applied Biosystems, Foster City, CA, US)

- DNA IQ™ Casework Pro Kit for Maxwell® 16 (Promega Corp., Madison, WI, US)
- Promega PowerPlex® 21 system (Promega Corp., Madison, WI, US)
- Promega CC5 Internal Lane Standard 500 (Promega Corp., Madison, WI, US)
- Promega PowerPlex 5 Dye Matrix Standard (Promega Corp., Madison, WI, US)
- Promega PowerPlex® 21 Allelic Ladder Mix (Promega Corp., Madison, WI, US)
- 2800M Control DNA, 10ng/µl (Promega Corp., Madison, WI, US)

Water amplification grade (Promega Corp., Madison, WI, US)

4 Methods

4.1 Sample Selection

All samples used in this validation were sourced from the internal DNA Analysis staff DNA database or Collaborative Testing Services (CTS) DNA testing samples and reference samples that had the National Criminal Investigation DNA Database (NCIDD) categories of Volunteer Unlimited Purpose (VUP) or Suspect (SCT). Permission to use reference samples from NCIDD was obtained from the Queensland Police Service (QPS).

4.2 Selection of Sub-Population samples

4.2.1 Aboriginal and Torres Strait Islanders Sub-Populations

Aboriginal samples:

Aboriginal samples previously profiled as part of the sub-population dataset for the validation of AmpFℓSTR® Profiler Plus® loci were recommended as the best samples to use for compilation of the Aboriginal sub-population dataset for the Promega PowerPlex®21 system. The samples are self-declared Aboriginal ethnicity and were collected over a number of years.

220 Aboriginal samples were randomly selected from the Aboriginal dataset (545 total) previously profiled with AmpFℓSTR® Profiler Plus®. Microsoft Excel RANDBETWEEN function was used and duplicates removed until 220 unique samples were identified for profiling.

These 220 samples were originally extracted using Chelex. The extracts for the 220 samples were viewed for sufficient volume. 201 samples with sufficient volume were identified and given new population dataset barcodes.

Torres Straits Islander samples:

A list of FTA™ samples previously profiled with AmpFℓSTR® Profiler Plus® resulting in a full profile and identified as self-declared Torres Strait Islander ethnicity in AUSLAB were compiled to be used for the Aboriginal sub population dataset.

599 samples were listed and after further filtering, including removing duplicates, 249 Torres Strait Islander samples remained. Of the 249 Torres Strait Islander samples listed 223 samples were randomly selected for processing. Samples were given new population dataset barcodes

4.2.2 Caucasian Sub-Population

A list of FTA™ samples previously profiled with AmpFℓSTR® Profiler Plus® resulting in a full profile and identified as Caucasian ethnicity in AUSLAB were compiled to be used for the Caucasian sub-population dataset.

From this list 210 samples were selected and 208 were selected for processing as two were deemed unsuitable. Samples were given new population database barcodes.

4.2.3 South East Asian Sub-Population

A list of FTA™ samples previously profiled with AmpFℓSTR® Profiler Plus® resulting in a full profile and identified as South East Asian ethnicity in AUSLAB were compiled to be used for the South East Asian population dataset.

157 samples were listed and after further filtering 141 South East Asian samples remained. These 141 samples were given new population database barcodes.

4.3 Collection Procedure for FTA™ cards

Where staff samples were entirely consumed during processing, additional samples were collected. New FTA™ samples were collected using FTA™ Collection kits. A foam swab was used to collect buccal cells from each cheek for one minute then applied to the FTA™ card[7]. The FTA™ card was stored at room temperature until required.

4.4 FTA™ punching method

1. PCR Amplification mix was created as required.
2. 25µL (full) or 12.5µL (half) of PCR amplification mix was added to a clean 0.2mL 96 well PCR plate.
3. Plate was sealed and centrifuged to ensure PCR amplification mix was at the bottom of the wells.
4. Each FTA™ sample was punched with the 1.2mm diameter die into the 96 well PCR plate using the BSD Duet 600 Series II.

5. 1µL of 2800M control DNA was added to the Positive control well.
6. 1 x 1.2mm punch of a blank FTA™ card was added to the blank control well
7. Amplification mix without FTA™ card was used as a negative control.
8. The plate was sealed and centrifuged briefly to pull the FTA™ cards to the bottom of the plate wells.

4.5 FTA® punching method 2

1. 7.5µL of amplification grade water was added to the required wells.
2. Plate was sealed and centrifuged to ensure the water was at the bottom of the wells.
3. Each FTA® sample was punched with the 1.2mm diameter die into the 96 well PCR plate using the BSD Duet 600 Series II.
4. 1µL of 2800M control DNA was added to the Positive control well.
5. 1 x 1.2mm punch of a blank FTA® card was added to the blank control well
6. PCR Amplification mix without FTA® card was used as a negative control.
7. PCR Amplification mix was created as required and 5µL added to each well required.
8. The plate was sealed and centrifuged briefly to pull the FTA® cards to the bottom of the plate wells.

4.6 Punching for extraction

FTA™ samples were prepared for extraction by punching four paper spots of 3.2mm diameter into 1.5mL/2mL tubes using the BSD Duet 600 according to standard operating procedure 24823 V4.0 "FTA™ Processing and Work Instructions".

4.7 Extraction

FTA™ samples requiring DNA extraction were processed using the DNA IQ™ Casework Pro Kit for Maxwell®16 according to standard operating procedure 29344 V4.0 "DNA IQ™ Extraction using the Maxwell®16".

4.8 Preparation of DNA stock solutions

Samples used to make dilution series required a stock solution to be prepared. FTA™ samples were selected and punched in duplicate for extraction (as outlined in section 4.5) then extracted (as outlined in section 4.6). The duplicate samples were pooled into a single tube and quantified twice (as outlined in section 4.9).

4.9 Procedure for creating a dilution series

The samples used to make dilution series were diluted with amplification grade water provided with the Promega PowerPlex®21 System. Spreadsheets for calculating the normalisation and dilution series were written to outline the serial dilutions required to obtain the specified concentrations (refer to Appendix A).

4.10 Quantification

All preparations of reactions were performed using MultiPROBE II plus HT EX platform according to standard operating procedure 19977 V8.0 "Automated Quantification of Extracted DNA using the Quantifiler™ Human DNA Quantitation Kit.

4.11 Amplification set up

For the experiments that used extracted DNA, all amplifications reactions were performed using a MultiPROBE II plus HT EX platform. A new protocol called PowerPlex 21 amp setup v1.0 was created using WinPrep® software and utilised for amplifications at 25µL and 12.5µL total PCR volumes. The protocol is saved and stored on the C drive of the MultiPROBE II plus HT EX platform computer. Table 2 outlines the components of the amplification mix per sample.

Table 2 - Amplification mix per sample.

Kit components	Volumes (µL)	Volumes (µL)
Master Mix	5.0	2.5
Primer pair	5.0	2.5
Sample	15	7.5
Total Volume	25	12.5

4.12 Amplification conditions

Table 3 lists the PCR cycling conditions used in this validation. All PCR reactions were carried out in 96 well plates (Axygen Inc.) on GeneAmp® 9700 thermal cyclers

Table 3 - PCR cycling conditions used for PowerPlex®21 system

PowerPlex® 21 Kit	Direct amp	Standard
GeneAmp 9700 mode	Max	Max
	25,26 or 27 cycles	30 cycles
Activation	96°C for 1 minute	96°C for 1 minute
Cycling	94°C for 10 seconds	94°C for 10 seconds

	59°C for 1 minute 72°C for 30 seconds	59°C for 1 minute 72°C for 30 seconds
Extension	60°C for 20 minutes	60°C for 10 minutes
	4°C Soak	4°C Soak

4.13 DNA fragment analysis

The plates for DNA fragment analysis were prepared as recommended by the manufacturer, using a combination of Hi-Di™ formamide, size standard and sample as outlined below.

Formamide: size standard mixture composed of

[(2.0µl CC5 ILS 500) x (number of injections)] + [(10.0µl Hi-Di™ formamide) x (number of injections)]

Formamide: size standard mixture **12µL**

PCR product or allelic ladder **1µL**

The prepared plate was then centrifuged to remove bubbles, denatured at 95°C for 3 minutes then chilled in an ice block in the freezer for 3 minutes. The prepared plates were then run on a 3130*xl* Genetic Analyzer.

The PCR fragments were separated by capillary electrophoresis (CE) using a 3130*xl* Genetic Analyzer set up according to manufacturer recommendations outlined in Table 4.

Table 4 - CE Protocol conditions.

Injection time	Injection voltage	Run time
5s	3kV	1500s

4.14 Profile Interpretation 1

All DNA profiles were analysed with GeneMapper® ID-X v1.1.1. The analysis panel used was PowerPlex_21_IDX_v1.0. The thresholds were set as follows:

1. Heterozygote threshold was set at 40RFU
2. Limit of Detection (negative controls) was set at 16RFU
3. Individual locus stutter thresholds were set as per Promega PowerPlex® 21 Stutter filter
4. Homozygote threshold was set to 200RFU

4.15 Profile Interpretation 2

All DNA profiles were analysed with GeneMapper® ID-X v1.1.1. The analysis panel used was PowerPlex_21_IDX_v1.0. The rules were set as follows:

1. Samples were analysed at 1RFU.
2. All known alleles, forward and back stutter (+/-4bp or +/-5bp) of known alleles, known artefacts and spectral pull-up were removed. As defined by Promega artefact peaks in the N-2bp and/or N+2bp position at D1S1656, D6S1043, D13S317, vWA, D21S11, D7S820, D5S818, D12S391 and D18S51 loci and in the N-1bp position at Amelogenin were also removed.
3. Any peaks determined to be carry over peaks were also removed. Carry-over is defined as the physical transfer of DNA from one injection to the next.

4.16 Profile Interpretation 3

All samples were analysed with GeneMapper ID-X v1.1.1 with the stutter thresholds set to zero. The analysis panel used was PowerPlex_21_IDX_v1.1.

1. Samples were analysed at 20RFU
2. Loci where the two main alleles were one repeat apart were excluded from analysis.

5 Experimental Design

5.1 Sub-Population Datasets

As part of the national approach to implementation of next generation STR amplification kits, the creation of three national sub-population datasets was undertaken. Each jurisdiction contributed DNA profiles for each sub-population Caucasian, Aboriginal and South East Asian to Jo-Anne Bright (ESR) and John Buckleton (ESR) for analysis.

5.1.1 Aboriginal dataset

In this experiment 201 Aboriginal samples were transferred to appropriate tubes and the DNA concentrations determined as outlined in Method 4.10.

The samples were amplified with the recommended DNA template input of 0.5ng in a 25µL total PCR volume. Three plates were amplified using the PowerPlex®21 system kit with each plate including a positive amplification control (2800M DNA) and a negative amplification control (amplification grade water). The three plates were prepared as per Method 4.11.

Standard amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13 and 4.14.

5.1.2 Torres Strait Islander dataset

In this experiment 223 Torres Strait Islander samples were punched across three 96 well plates as outlined in section 4.4. Each sample had one spot punched, a total PCR volume of 12.5µL and was directly amplified at 26 PCR cycles.

Amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13 and 4.14.

5.1.3 Caucasian dataset

In this experiment 208 Caucasian samples were punched across three 96 well plates as outlined in section 4.4. Each sample had two spots punched, a total PCR volume of 25µL and was directly amplified at 25 PCR cycles.

Caucasian samples that did not produce a full PowerPlex®21 profile were punched again using 2 spots, a total PCR volume of 25µL and was directly amplified at 26 PCR cycles.

Amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13 and 4.14.

5.1.4 South East Asian dataset

In this experiment 141 South East Asian samples were punched across two 96 well plates as outlined in section 4.5. Each sample had one spot punched, a total PCR volume of 12.5µL and was directly amplified at 26 PCR cycles.

South East Asian samples that did not produce a full PowerPlex®21 profile were punched for extraction, extracted, quantified and amplified as outlined in Methods 4.6, 4.7, 4.8 and 4.10.

Amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13 and 4.14.

5.2 Concordance

155 samples purchased from Collaborative Testing Services (CTS) as external Proficiency Tests were used to test the concordance of the PowerPlex® 21 system. These samples had previously been extracted, quantified and amplified with AmpF*l*STR® Profiler Plus® and AmpF*l*STR® COfiler® kits.

The samples were amplified with the recommended DNA template input of 0.5ng in a 12.5µL total PCR volume. Two plates were amplified using the PowerPlex®21 system kit with each plate including a positive amplification control (2800M DNA) and a negative amplification control (amplification grade water). The two plates were prepared as outlined in Method 4.11.

Amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13 and 4.14.

The alleles obtained from these samples were compared with the CTS published alleles. Three loci could not be compared as CTS did not publish results for the D12S391, D1S1656 and D6S1043 loci.

5.3 Baseline Determination

To determine the limit of detection (LOD) and the limit of reporting (LOR), the baseline (background) was assessed.

Ten samples from the Caucasian sub-population dataset that exhibited high heterozygosity were used for baseline determination.

The samples were prepared as Methods 4.6, 4.7, 4.8, 4.9, 4.10, 4.11.

Ten samples diluted in ten steps (10x10) outlined in table 5 were used for the baseline calculations. Each dilution set was amplified at 25µL and 12.5µL total PCR volumes.

50 negative samples were also amplified at 25µL and 12.5µL total PCR volumes.

Table 5 - Total DNA input for each dilution

Dilution	Total DNA (ng)
1	0.500
2	0.447
3	0.394
4	0.342
5	0.289
6	0.236
7	0.183
8	0.131
9	0.078
10	0.025

Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13, 4.14 and 4.15.

The average peak height RFU (μ_{Pk}) for each dye channel was calculated using the AVERAGE function (Arithmetic mean) in Microsoft Excel. The standard deviation (σ_{Pk}) was calculated using the STDEV function in Microsoft Excel.

The thresholds were calculated as follows:

The limit of detection (LOD) was calculated from Equation 1[8].

Equation 1

$LOD = \mu_{PK} + 3\sigma_{PK}$

The limit of reporting (LOR) also known as the analytical threshold (AT) was calculated from Equation 2[8].

Equation 2

$LOR = \mu_{PK} + 10\sigma_{PK}$

5.4 Sensitivity 1

This experiment tested the sensitivity of PowerPlex® 21 system at amplification volumes of 25µL and 12.5µL for DNA template inputs from 4ng to 1pg.

Two staff (one male and one female) with the most heterozygous DNA profile processed with AmpFℓSTR® Profiler Plus® and AmpFℓSTR COfiler® kits were selected for testing[9]. Heterozygous loci provide more information with respect to allele drop out and peak balance.

FTA™ cards were collected, processed, extracted, stock solutions prepared, quantified and dilution series prepared as outlined in Methods 4.6, 4.7, 4.8, 4.9 and 4.10.

Each donor had 9 dilutions prepared as outlined in Table 6. These dilutions were amplified in duplicate with a total amplification volume of 25µL and 12.5µL. Each amplification plate included the kit positive control (2800M DNA) and a negative control (amplification grade water).

Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.11, 4.12, 4.13 and 4.14.

Table 6 - Total DNA input for sensitivity 1

DNA Template Input (ng)
4
2
1
0.5
0.1
0.05
0.01
0.005
0.001

5.5 Sensitivity 2

To assess the differences between the two total PCR volumes with respect to low DNA extract concentrations a second sensitivity experiment was performed.

This experiment tested a dilution series of the same samples used in sensitivity 1 at low DNA templates outlined in table 7. Each dilution was amplified in duplicate at 25µL and 12.5µL.

Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.11, 4.12, 4.13 and 4.14.

Table 7 - Concentration, DNA template input for each dilution.

Concentration (ng/µL)	Volume of sample added to 25 µL reaction volume	Total DNA template input (ng)	Volume of Sample added to 12.5 µL volume reaction	Total DNA template input (ng)
0.01	15	0.15	7.5	0.075
0.005	15	0.075	7.5	0.0375
0.0025	15	0.0375	7.5	0.01875
0.00125	15	0.01875	7.5	0.009375
0.000625	15	0.009375	7.5	0.004688
0.0003125	15	0.004688	7.5	0.002344
0.00015625	15	0.002344	7.5	0.001172
0.000078125	15	0.001172	7.5	0.000586

5.6 Drop In

50 negative samples were amplified alongside the 10 x10 data at 25µL and 12.5µL. Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.11, 4.12, 4.13 and 4.15.

The negative samples were analysed at 1RFU using GeneMapper ID-X v1.1.1 to determine if any peaks above 20RFU were present. Known artefacts, carry-over and pull-up were removed and not included in the analysis.

5.7 Stutter

To determine the thresholds for forward and back stutter peaks 342 samples from the Aboriginal data set, 10 x10, sensitivity 1 and sensitivity 2 were amplified at 25µL and 255 samples from 155 CTS samples, 10 x 10, sensitivity 1 and sensitivity 2 samples were amplified at 12.5µL.

Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.11, 4.12, 4.13 and 4.16.

The stutter ratio (SR) was calculated for each locus as per Equation 3.

Equation 3

$$SR = E_S/E_A$$

SR = Stutter Ratio, E_S = Stutter Height, E_A = Allele Height

The stutter threshold (ST)[4] for each locus was calculated as per Equation 4.

Equation 4

$$ST = \mu_{SR} + 3\,\sigma_{SR}$$

ST = Stutter Threshold, μ_{SR} = average stutter ratio, σ_{SR} = standard deviation of stutter ratio.

The stutter results were also processed with a multiple regression analysis by Jo-Anne Bright for use within the STRmix™ validation and STRmix™ settings[10].

5.8 Peak balance

The samples from the 10 x10 (section 5.4) were used to calculate peak height ratios and an allelic imbalance threshold to be used for reference samples and as a guide for determining the number of contributors to a mixture.

5.8.1 Peak Height Ratio and Allelic imbalance threshold

Peak height ratios for heterozygote loci (1127 alleles for 12.5µL and 1094 alleles for 25 µL total PCR volumes) were determined by dividing the lower peak height by the higher peak height. Loci where the two main alleles were one repeat apart or were homozygous were excluded from analysis.

The peak height ratio (PHR) was calculated for each locus as per equation 5 [11].

Equation 5

PHR = LPH / HPH

PHR = Peak Height Ratio, LPH = Lower Peak Height, HPH = Higher Peak Height

The average peak heights and standard deviation of peak height ratio were calculated using the Microsoft Excel AVERAGE and STDEV worksheet functions.

The allelic imbalance threshold (AI) was calculated as per Equation 6[12, 13]

Equation 6

$$AI_{TH} = \mu_{PHR} - 3\sigma_{PHR}$$

AI_{TH} = Allelic Imbalance threshold, μ_{PHR}= overall average PHR, σ_{PHR} = standard deviation of the PHR.

5.8.2 Homozygote threshold

The homozygote threshold is the threshold above which you can be confident that a heterozygote locus will not be incorrectly called as a homozygote locus. It was calculated using the following methods

Method 1 – As previously described in the internal validation[14] of peak heights and allelic imbalance thresholds and illustrated below:

Equation 7

$$Th_{Hom} = LOR \times (1 / AI_{TH}) \times 2$$

The LOR used for this calculation is from 5.3 and AI_{TH} was determined in 5.8.2.

Method 2 – As described in the Promega Internal validation guidelines[15] determined from a plot of allelic imbalance versus the lower RFU of a heterozygote pair. The homozygote threshold is assigned at the point at which there is a rapid drop off in peak height ratio.

5.9 Drop out

To aid in determining the default total PCR volume and template DNA range a series of drop out analyses were performed on the 10 x 10 (section 5.4), sensitivity experiments (sections 5.3 & 5.5) and population datasets (section 5.2).

5.9.1 Drop out 1

The samples from the sensitivity 1 experiment (section 5.3) were used to determine at what RFU the partner of a heterozygote pair drops out. The data was interpreted as outlined in section 4.13. Homozygote peaks, excess samples and no size data were excluded from data analysis. Heat maps were used to summarise the data.

5.9.2 Drop Out 2

Samples processed at 25µL and 12.5µL were analysed to determine the threshold when an allele most frequently drops out.

334 DNA profiles amplified at 25µL (from section 5.1.1, 5.3, 5.4 and 5.5) and 279 DNA profiles amplified at 12.5µL (from section 5.2, 5.3, 5.4 and 5.5) were analysed as outlined in Method 4.13.

Homozygote peaks, excess samples and no size data were excluded from both sets of data.

5.9.3 Drop Out 3

The samples from the 10 x 10 (section 5.4) and sensitivity experiments (section 5.3 & 5.5) experiments (156 samples) were analysed to record the peak height at which a heterozygote paired allele was lost. The data was interpreted as outlined in Method 4.13.

Homozygote peaks, excess samples and no size data were excluded from data analysis.

5.10 Mixture Studies

In this experiment 4 samples, two female and two male samples with high heterozygosity were selected, from the Caucasian dataset and CTS samples, to be combined to make mixed DNA samples. The samples were created as Methods 4.3, 4.4, 4.6, 4.7 and 4.10.

One female sample was combined with one male profile to create a two person mixture, the same female sample was combined with the two male samples to create a three person mixture and two female samples and two male samples were combined to create a four person mixture. The amount of sample required from each contributor to create the mixture ratio was calculated using excel spreadsheets, refer to Appendix A. Varying contributor ratios were made for each of the mixture combinations as outlined in table 8. Each mixture combination was amplified in duplicate at a variety of DNA templates.

Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.11, 4.12, 4.13 and 4.16.

Table 8 - Mixture ratios

Mixture Ratio	Template (ng)
Female:Male	
50:1	0.500
	0.250
	0.125
30:1	0.500
20:1	0.500
	0.250
	0.125
10:1	0.500
	0.125
5:1	0.500
	0.125
2:1	0.500
	0.06
1:1	0.500
Female:Male:Male	
20:10:1	0.500
	0.125
10:5:1	0.500
5:2:1	0.500
	0.125
Female:Male:Male:Female	
5:3:2:1	0.500
	0.125

The mixture ratio was calculated for each DNA profile and compared to the admixture ratio to determine whether there is any variability and whether the mixture ratio can be expected to hold across the profile.

The DNA profiles were analysed to determine at what ratio the minor contributor would be expected to drop out.

6 Results and Discussion

6.1 Population datasets

Results were tabulated in the following format Unique Sample ID, Race ID, Marker, Allele 1 and Allele 2. Table 9 summarizes the number of profiles for each sub-population submitted for analysis.

Table 9 - Summary of number of profiles for each sub-population submitted.

	Caucasian	Aboriginal	SE Asian
DNA Analysis, FSS	**139**	**309**	**126**
Dataset total	**1707**	**1778**	**990**

Data generated for the three sub-population datasets were analysed by Jo Bright and John Buckleton and used in STRmix™ for statistical analysis[16, 17].

6.2 Concordance

All samples (number of alleles = 4644) tested were found to be concordant to the CTS reported DNA profiles. Table 10 displays the number of times a particular allele was seen at each locus within the laboratory.

Different DNA amplification kits may contain different primers for each locus. Comparison of allele calls (concordance) is required to ensure that each kit gives consistent allele designations between kits as mismatches or null alleles will affect matching on NCIDD or within a case. The current kits used by the DNA Analysis are AmpFℓSTR® Profiler Plus® and AmpFℓSTR COfiler® DNA amplification kits. Both of these use primers developed by and manufactured by Life technologies. There are known issues with these kits such as a reverse primer binding mutation at the D8S1179 locus[18], vWA locus[19] and FGA locus[20]. The PowerPlex® 21 kit uses different primer sequences. All alleles tested were found to be concordant. As primer binding mutations and null alleles have been observed within DNA Analysis, any resulting mismatches on NCIDD will need to be retested using PowerPlex® 21.

Table 10 - Observed number of allele concordances

Allele Size	D3S1358	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	D8s1179	D19S433	FGA
2.2								5									
3.2								2									
5			17					5	1								
6									44					7			
7			32				4	5	75			4	3	4			
8		23	22	4			8	9	42			68	6	133	1		
9		21	10	44			4	48	50			28	13	34	4		
9.3									69								
10		11	25	26	2		69	31	3			80	19	13	11	1	
10.3									1								
11		79	26	83	2		77	45		1		65	91	65	14	6	
11.2																1	
12	1	86	40	78	37		93	51				26	100	11	37	26	
12.2																4	
13	1	48	27	46	30		16	44		3		9	15	1	96	72	
13.2																5	
14	41	20	15	2	38	1	1	8		28			3		71	67	
14.2																9	
15	84		12		42	1		3		43					43	23	
15.2																8	
16	56		13		48	14		1		63					10	5	
16.2																4	
17	67		10		36	46				67					1		
17.2																1	
18	36		6		18	19				57					1		4
18.2																1	
19	4		2		13	33				20							23
20			1		10	28				2							39
20.2																	2
21			2		5	19				2							35
22			2		2	13				1							56
22.2																	3
23					1	20											48
24						13											36
25						22											28
26						8					3						10
27						1					7						4
28											61						
29											47						1
29.2											1						
29.3											1						
30											78						
30.2											10						
31											18						
31.2											22						
32											5						
32.2											25						
33.2											9						
35											2						

6.3 Baseline Determination

The thresholds determined by the baseline experiments are the limit of detection (LOD) and limit of reporting (LOR). The use of thresholds for reporting is essentially a risk assessment[21], if the thresholds are set too low then labelling of artefacts and noise may occur, if set too high then real peaks will not be labelled and information will be lost[1, 11].

Type 1 errors are defined as false labelling of noise peaks. LODs calculated from negative samples may not be optimal for medium-high template samples, as the baseline will differ between positives and negative samples[22].

Type 2 errors are defined as false non-labelling of alleles. If the LOD is set too high, then for low level samples may have a heterozygous locus called as a homozygous locus[1, 22-24].

The LOR is the threshold in which a peak can be confidently distinguished from the background fluorescence (baseline). Several methods can be used to determine this threshold.

For the method used here[8] the LOR is derived from the mean baseline plus ten standard deviations (Equation 2).

The LOD is the lowest signal that can be distinguished from the background fluorescence (baseline) and may vary between CE instruments.

Previously in DNA Analysis[14]; baseline for the AmpFℓSTR® Profiler Plus® kit was determined using the BatchExtract software v0.16. The LOD was calculated using Equation 1. This approach of using the mean and three standard deviations would account for 99.73% of baseline fluorescence.

The files generated by GeneMapper ID-X v1.1.1 are not compatible with the BatchExtract software without modification. For this validation an equivalent process for measuring the baseline as described by Promega was used with some modifications to the types of samples used. For this validation samples containing DNA were used to determine baseline fluorescence.

Table 11 shows the results determined from the baseline calculations when the samples were amplified at 25µL. The highest average peak height (5.74RFU) and the highest standard deviation (3.21) was in the TMR (yellow) channel from run 2 on 3130xl A. The TMR (yellow) channel for run 2 on 3130xl A also yielded the highest LOD (15.37) and highest LOR (37.84). The LOD was rounded to 16RFU and the LOR was rounded to 40RFU and is to be used for all dye channels for samples amplified using a total amplification volume of 25µL.

Table 11 - Baseline results for amplifications at 25µL

		3130xl A run 1	3130xl A run 2	3130xl B run 1	3130xl B run 2	Overall 3130xl A & B run 1 & 2
Fluorescin (Blue)	μ_{PK}	2.33	2.58	1.90	1.68	2.11
	σ_{PK}	1.55	2.05	1.01	0.89	1.52
	LOD	6.99	8.73	4.93	4.36	6.68
	LOR	17.86	23.07	12.01	10.59	17.35
JOE (Green)	μ_{PK}	3.51	3.83	2.25	2.16	2.94
	σ_{PK}	2.34	2.62	1.04	1.29	2.12
	LOD	10.54	11.68	5.37	6.02	9.30
	LOR	26.94	29.99	12.65	15.02	24.14
TMR (Yellow)	μ_{PK}	5.29	5.74	3.33	3.07	4.32
	σ_{PK}	2.73	3.21	1.27	1.66	2.68
	LOD	13.47	15.37	7.15	8.05	12.37
	LOR	**32.55**	**37.84**	**16.06**	**19.66**	**31.16**
CXR (Red)	μ_{PK}	2.22	2.44	2.02	1.78	2.09
	σ_{PK}	1.36	1.54	0.89	1.01	1.35
	LOD	6.29	7.05	4.69	4.81	6.16
	LOR	15.79	17.79	10.93	11.88	15.63
CC5 (Orange)	μ_{PK}	1.76	1.99	1.14	1.36	1.66
	σ_{PK}	1.30	1.80	0.44	1.39	2.44
	LOD	5.68	7.38	2.47	5.52	9.00
	LOR	14.81	19.94	5.58	15.24	26.11
Overall	μ_{PK}	3.41	3.72	2.44	2.22	2.79
	σ_{PK}	2.45	2.80	1.33	1.39	2.29
	LOD	10.76	12.13	6.23	6.40	9.65
	LOR	**27.91**	**31.76**	**15.54**	**16.14**	**25.65**

Table 12 shows the results determined from the baseline calculations when the samples were amplified at 12.5µL. The highest average peak height (6.06RFU) was in the TMR (yellow) channel from the run on 3130xl A and the highest standard deviation (4.41) was in the JOE (green) channel from the run on 3130xl A. The TMR (yellow) channel for the run on 3130xl A yielded the highest LOD (18.50) and the JOE (green) channel yielded the highest LOR (48.60). It was noted on 3130xl A the baseline was raised more than expected compared to other baseline runs on the same instrument and baseline runs on 3130xl B. This could be due to a prolonged period between spectral calibrations, aging reagents and arrays and was taken into consideration when setting thresholds. With natural variations, the results from run to run and instrument may vary, by using the mean + 10SD for the LOR, although the baseline itself may shift, the LOR will always be greater than the LOD even if baseline is either increased or decreased on any given run. By using an "over all" result, the standard deviation is increased due to the difference in fluorescence between instruments, and this then gets factored into the overall LOR.

The highest overall LOD (15.70) was in the TMR (yellow) channel and was rounded to 16RFU and the highest overall LOR (42.27) was in the JOE (green) channel and was rounded to 40RFU.

In an effort to eliminate error and confusion a single LOD and LOR value is to be used for both instruments.

Table 12 - Baseline results for amplifications at 12.5µL

		3130xl A 12.5µL	3130xl B 12.5µL	Overall 3130xl A & B 12.5µL
Fluorescin (Blue)	μ_{PK}	3.10	2.19	2.64
	σ_{PK}	3.66	2.72	2.99
	LOD	14.07	10.36	11.59
	LOR	39.67	29.42	32.49
JOE (Green)	μ_{PK}	4.46	2.69	3.62
	σ_{PK}	4.41	2.86	3.86
	LOD	17.70	11.26	15.22
	LOR	48.60	31.28	42.27
TMR (Yellow)	μ_{PK}	6.06	3.58	4.83
	σ_{PK}	4.15	2.43	3.63
	LOD	18.50	10.88	15.70
	LOR	**47.52**	**27.92**	**41.08**
CXR (Red)	μ_{PK}	2.87	2.10	2.49
	σ_{PK}	2.32	1.28	1.93
	LOD	9.84	5.94	8.27
	LOR	26.11	14.90	21.75
CC5 (Orange)	μ_{PK}	2.38	1.66	2.02
	σ_{PK}	2.31	1.87	2.14
	LOD	9.33	7.26	8.84
	LOR	25.53	20.33	23.90
Overall	μ_{PK}	3.94	2.54	3.32
	σ_{PK}	3.87	2.46	3.30
	LOD	15.56	9.91	13.21
	LOR	**42.68**	**27.10**	**36.28**

μ_{PK} = Average peak height, σ_{PK} = Standard Deviation, LOD = limit of detection, LOR = Limit of Reporting

6.4 Sensitivity

All PCR amplification kits are optimised for a particular total reaction volume by the manufacturer; but it is commonplace to reduce the total PCR reaction volume to increase the sensitivity[25-28] and reduce processing costs[27]. Two sensitivity experiments were performed, in addition to the 10x10 (baseline determination) dataset.

To contrast and compare the effect of total PCR volume on DNA profiles, the same dilution series were amplified at two different total PCR volumes (25µL and 12.5µL) using 30 PCR cycles.

The results for the amplification of the two donors at 25µL and 12.5µL are summarised in tables 13 and 14 respectively.

Table 13 - Summary of the 2 donors amplified at 25µL

Donor 1 25µL	Template	Av No. Alleles	Av PH (RFU)	Max PH	Min PH	AV PHR
Donor1	4ng	N/A	NAD XS	N/A	N/A	N/A
Donor1	2ng	N/A	XS	N/A	N/A	N/A
Donor1	1ng	42	2512.56	4661.00	1456.00	90.47
Donor1	0.5ng	42	1347.65	2492.00	172.00	85.58
Donor1	0.1ng	42	277.47	506.00	119.00	78.78
Donor1	50pg	41	153.39	387.00	48.00	67.09
Donor1	10pg	17	46.86	108.00	20.00	79.08
Donor1	5pg	6.5	39.57	78.00	20.50	0.00
Donor1	1pg	1.5	33.83	43.00	27.00	0.00
Donor 2 25µL	**Template**	**Av No. Alleles**	**Av PH (RFU)**	**Av Max PH**	**Av Min PH**	**AV PHR**
Donor2	4ng	N/A	XS	N/A	N/A	N/A
Donor2	2ng	N/A	XS	N/A	N/A	N/A
Donor2	1ng	42	2790.81	5126.00	1461.00	89.19
Donor2	0.5ng	42	1344.10	2878.00	431.00	86.91
Donor2	0.1ng	42	292.72	698.00	88.00	74.55
Donor2	50pg	41.5	157.40	479.00	47.00	68.59
Donor2	10pg	24.5	69.69	171.00	14.25	69.60
Donor2	5pg	5.5	44.95	75.00	23.00	96.79
Donor2	1pg	6	33.62	55.00	20.00	94.85

Av = Average, PH = Peak Height, No. = Number, Max = Maximum, Min = Minimum, PHR = Peak Height Ratio

Table 14 - Summary of the 2 donors amplified at 12.5µL.

Donor 1 12.5µL	Template	Av No. Alleles	Av PH (RFU)	Max PH	Min PH	AV PHR
Donor1	4ng	N/A	NAD XS	N/A	N/A	N/A
Donor1	2ng	N/A	XS	N/A	N/A	N/A
Donor1	1ng	N/A	XS	N/A	N/A	N/A
Donor1	0.5ng	42	3132.96	6719.00	1590.00	84.41
Donor1	0.1ng	42	780.57	2444.00	180.00	74.66
Donor1	50pg	42	346.67	931.00	58.00	68.88
Donor1	10pg	27	91.95	406.00	21.00	49.76
Donor1	5pg	12	48.20	91.50	20.00	71.22
Donor1	1pg	4.5	35.80	51.00	22.00	88.24
Donor 2 12.5µL	**Template**	**Av No. Alleles**	**Av PH (RFU)**	**Av Max PH**	**Av Min PH**	**AV PHR**
Donor2	4ng	N/A	XS	N/A	N/A	N/A
Donor2	2ng	N/A	XS	N/A	N/A	N/A
Donor2	1ng	N/A	XS	N/A	N/A	N/A
Donor2	0.5ng	42	2878.80	6159.00	1281.00	78.29
Donor2	0.1ng	42	742.73	1612.00	140.00	68.12
Donor2	50pg	42	333.38	892.00	93.00	60.88
Donor2	10pg	25	82.33	249.00	21.00	59.05
Donor2	5pg	13.5	51.47	121.00	21.00	67.89
Donor2	1pg	0	0.00	0.00	0.00	0.00

The amplifications at 25µL total PCR volume with DNA templates of 4ng and 2ng for both donors gave excess profiles resulting in the profiles being unable to be interpreted. The results from the excess samples were excluded from the data analysis. The average number of alleles and the

average peak height was similar for both donors when processed with an amplification volume of 25µL.

The amplifications at 12.5µL with DNA templates of 4ng, 2ng, 1ng and one replicate of the 0.5ng for both donors gave excess results. The results from the excess samples were excluded from the data analysis. The average number of alleles and average peak height was similar for both donors when processed with an amplification volume of 12.5µL.

Figure 1 displays the average number of alleles and average peak height ratio obtained for each donor at each template amplified at 25µL and 12.5µL.

Figure 2 displays the average peak height and average peak height ratio at each DNA template amplified for 25µL and 12.5µL.

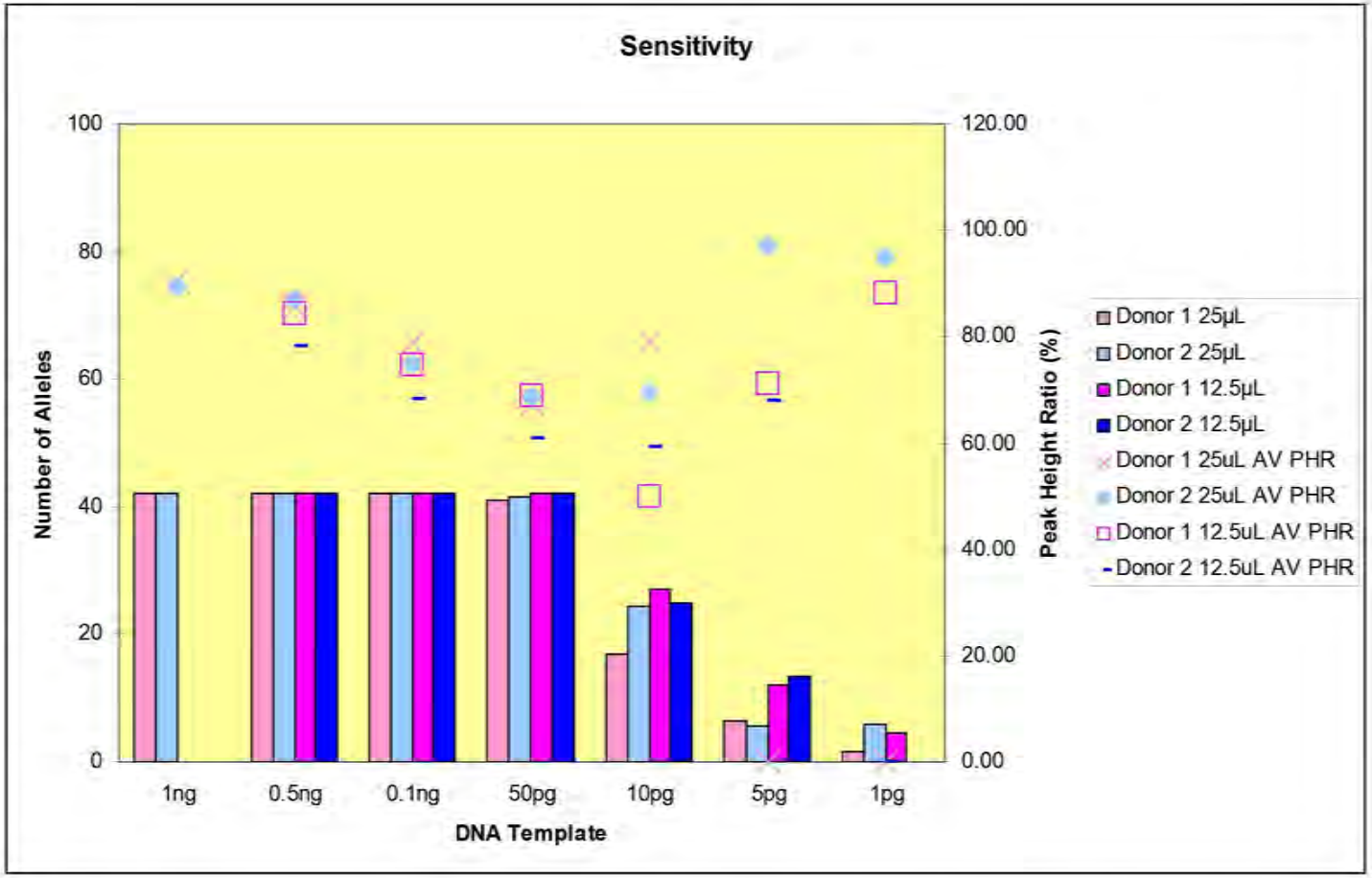


Figure 1 - Average number of alleles for each donor at each DNA template at amplification volumes of 25µL and 12.5µL. AV PHR = Average Peak Height Ratio

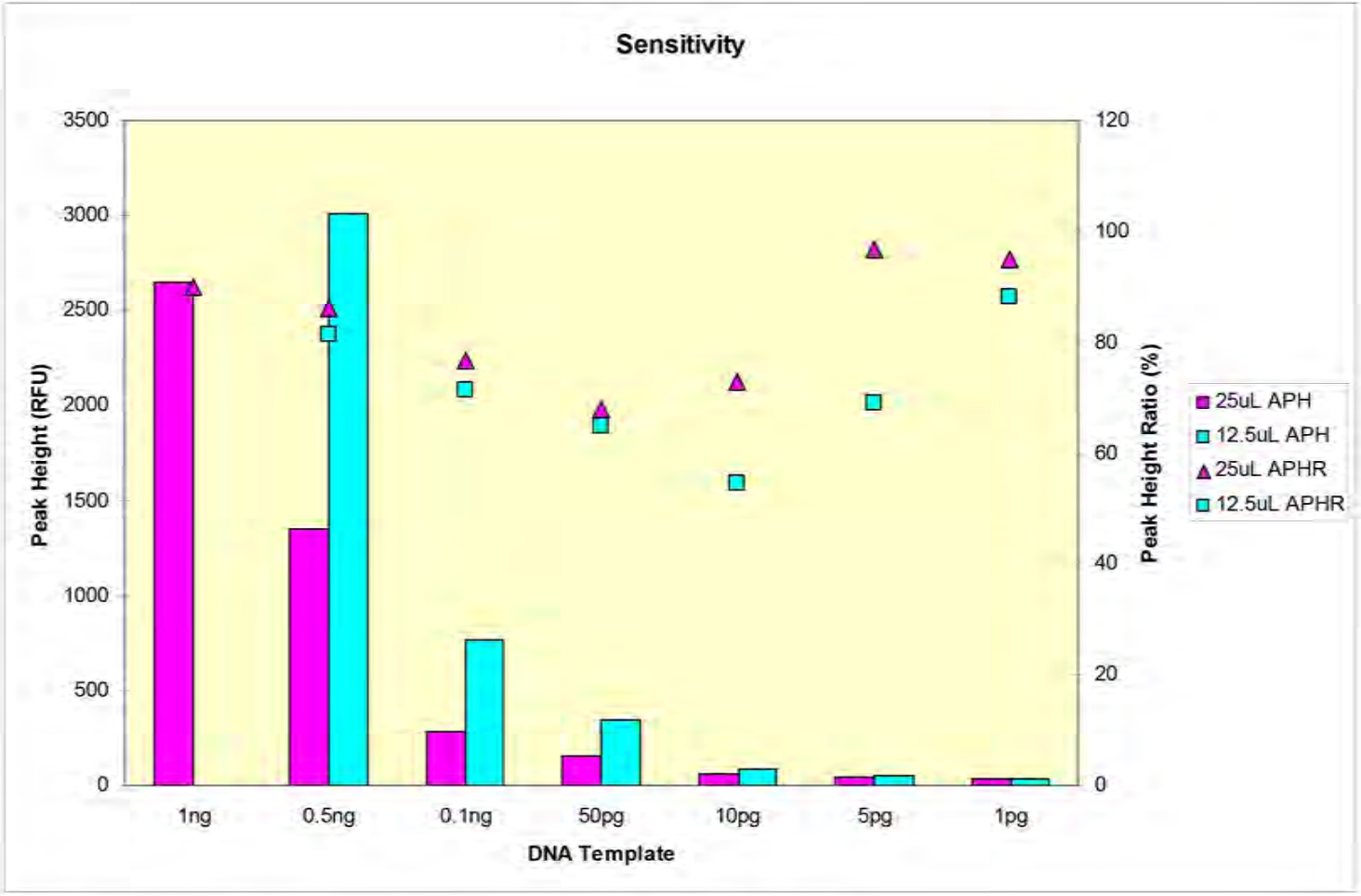


Figure 2 Average peak height and average peak height ratio for each DNA template

A full complement of alleles in the PowerPlex® 21 system was obtained for both donors at total DNA template inputs of 0.5ng and 0.1ng when amplified at both total PCR volumes. As expected the average number of alleles decreased as the DNA template decreased.

For both total PCR volumes, as the total DNA template decreased, the peak heights also decreased. The 12.5µL amplification gave higher peaks heights at the 0.5ng, 0.1ng and 50pg DNA template inputs compared with the 25µL amplification.

The average peak height ratio decreased as the DNA template decreased to 50pg. Below a DNA template of 50pg less heterozygote pairs were observed (as expected) which resulted in the peak height ratio becoming more variable and drop out being observed.

The samples from the 10x10 dataset ranged from template inputs of 0.5ng to 0.025ng. The results of these experiments are concordant with the first sensitivity experiment.

A full complement of alleles in the PowerPlex® 21 system was obtained for all samples between 0.5ng and 0.132ng DNA template inputs when amplified at both total PCR volumes.

The second sensitivity experiment was undertaken to enable direct comparison of the sample concentration when amplified at a total PCR volume of 25µL and 12.5µL rather than comparing the total DNA template input.

Figure 3 shows the results of low concentration samples amplified at 25µL and 12.5µL total PCR volumes with the vertical red line highlighting the limit of detection[29] (quantification) used for the AB 7500 Real Time PCR system. The numbers of alleles obtained at each concentration were counted using the LOR thresholds determined in section 6.4.

The DNA profiles exhibited increased allelic imbalance across different loci when the sample concentration dropped below 0.025ng/µL.

Overall the PowerPlex®21 system is a very sensitive STR amplification kit capable of detecting DNA amounts below what is generally considered low copy number (LCN). The data analyses indicate that the risk of type 2 errors will increase if the DNA template is too low for both total PCR volumes.

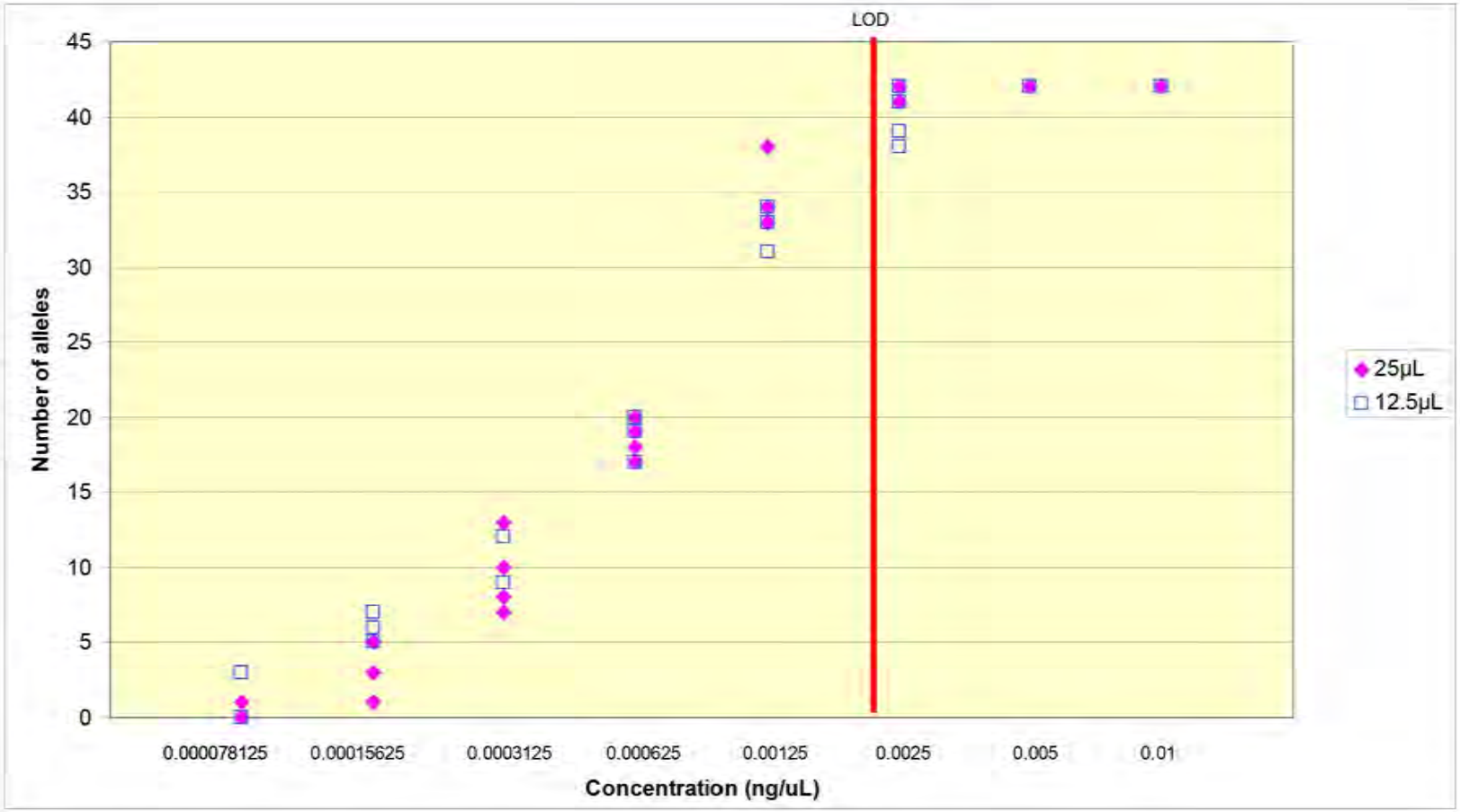


Figure 3 - Comparison of sample concentration vs allele count for 25µL and 12.5µL total PCR volumes.

6.5 Drop In

Allelic drop-in is due to spurious amplification products from unknown DNA, which makes allele drop-in a random event[30, 31]. The phenomenon of allelic drop-in is usually not reproducible and can be detected through testing samples multiple times[32].

For the 25µL amplifications processed on both 3130xl instruments 3 drop in events were noted. True drop-in alleles were seen in three negative controls at D16S539 as a 7 allele at 21RFU, D3S1358 as a 21 allele at 19RFU and at TH01 as a 5 allele at 19RFU.

For 12.5 µL amplifications on both 3130xl instruments no drop in events were noted.

Drop in data was sent to John Buckleton for fit to a Poisson distribution and tested. This data is required for STRmix™ validation and STRmix™ settings.

The rate of drop in events for 25µL volume amplifications (3 events in 1050 alleles above 15RFU) was calculated for STRmix™ by John Buckleton, see figure 4.

STRmix™ uses the model for drop-in ae-bx where the values for a and b are the drop-in parameters in STRmix™. John Buckleton's calculations determined that a=b=0.393. The maximum drop-in seen at any one locus is determined in RFU; this means that if two peaks were seen at one locus the drop-in would be the total height of both peaks. Since only one drop-in peak was observed at any one locus and the highest of these events was 21RFU, then our drop-in setting for STRmix™ would be 21RFU. Since our LOR was determined to be 40RFU, it seemed reasonable to set the drop-in level to 40RFU.

Although no drop-in events were observed for half volume amplifications, the same parameters will be applied.

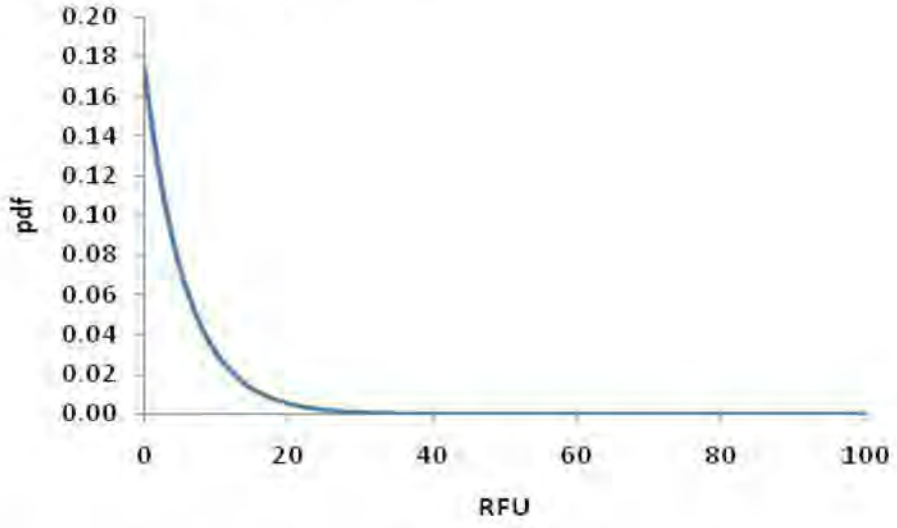


Figure 4 - Probability of Drop in for 25µL total PCR volume.

6.6 Stutter

Stutter peaks are Polymerase Chain Reaction (PCR) artefacts commonly observed in all STR analysis[4, 33]. They are usually observed as a peak one repeat unit smaller in size than the true allele peak[33]. The stutter mechanism has been attributed to slippage of the DNA strand during replication.

Over stutter is observed as a peak one repeat unit more in size than the true allele. Figure 5 shows an example of stutter and over stutter.

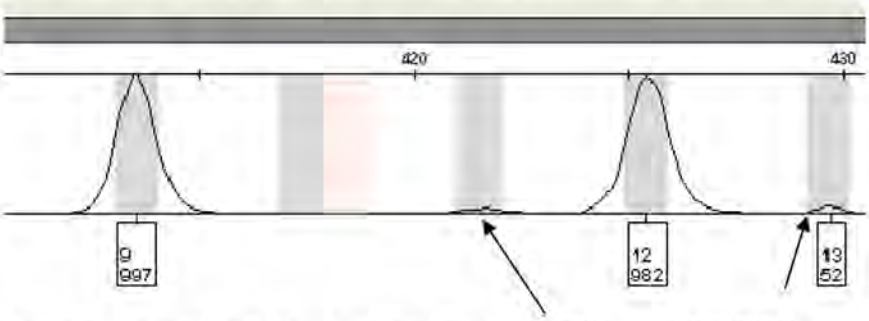


Figure 5 - Example of stutter and over stutter.

Promega supplied a stutter text file (using μ + 3σ[4]) for GeneMapper ID-X v.1.1.1. We have used the same calculation as it incorporates 99.73% of the data assuming normal distribution.

The data for the observed stutter ratios (forward and over) for samples amplified at 25μL are listed in table 15 and for 12.5μL are listed in table16.

Over stutter was observed for all loci when amplified at 25μL and therefore a threshold was able to be calculated for each locus. Over stutter was not observed for all loci when amplified at 12.5μL and therefore a threshold was only able to be calculated for those loci at which over stutter was observed. Over stutter will be continued to be monitored until enough data is obtained to review the thresholds set in this validation.

Most calculated stutter thresholds were higher than the Promega supplied stutter filter file both for 25μL and 12.5μL. The exceptions were D6S1043, D18D51, D2S1338, and Penta D for 25μL and D6S1043, Penta E, D18D51, D2S1338, and Penta D for 12.5uL.

When comparing the calculated stutter thresholds for the 25μL and 12.5μL total PCR volumes, they appear to be similar.

Table 15 - 25µL Calculated stutter thresholds.

Locus	μ_{SR}	σ_{SR}	Stutter Ratio (%)	μ_{OSR}	σ_{OSR}	Over stutter Ratio (%)
D3S1358	0.0868	0.0184	14.2	0.0131	0.0100	4.3
D1S1656	0.0910	0.0269	17.2	0.0183	0.0163	6.7
D6S1043	0.0685	0.0171	12.0	0.0164	0.0192	7.4
D13S317	0.0496	0.0228	11.8	0.0185	0.0184	7.4
Penta E	0.0457	0.0203	10.7	0.0113	0.0018	1.7
D16S539	0.0686	0.0173	12.1	0.0133	0.0099	4.3
D18S51	0.0873	0.0244	16.0	0.0144	0.0116	4.9
D2S1338	0.0878	0.0203	14.9	0.0196	0.0150	6.5
CSF1PO	0.0640	0.0244	13.7	0.0155	0.0096	4.4
Penta D	0.0245	0.0190	8.2	0.0306	0.0193	8.8
TH01	0.0325	0.0181	8.7	0.0085	0.0041	2.1
vWA	0.0782	0.0246	15.2	0.0157	0.0135	5.6
D21S11	0.0809	0.0199	14.1	0.0175	0.0177	7.1
D7S820	0.0485	0.0218	11.4	0.0207	0.0124	5.8
D5S818	0.0595	0.0202	12.0	0.0165	0.0132	5.6
TPOX	0.0381	0.0174	9.0	0.0235	0.0130	6.3
D8S1179	0.0790	0.0177	13.2	0.0176	0.0123	5.5
D12S391	0.0948	0.0311	18.8	0.0146	0.0128	5.3
D19S433	0.0666	0.0205	12.8	0.0211	0.0165	7.1
FGA	0.0702	0.0227	13.8	0.0182	0.0135	5.9

Stutter thresholds higher than the recommended stutter thresholds from Promega =

μ_{SR} = mean stutter ratio, σ_{SR} = standard deviation of stutter ratio, μ_{OSR} = mean over stutter ratio, σ_{OSR} = standard deviation of over stutter ratio

Table 16 - 12.5µL calculated stutter thresholds.

Locus	μ_{SR}	σ_{SR}	Stutter Ratio (%)	μ_{OSR}	σ_{OSR}	Over stutter Ratio (%)
D3S1358	0.0880	0.0194	14.6	0.0113	0.0067	3.2
D1S1656	0.0909	0.0247	16.5	0.0138	0.0055	3.0
D6S1043	0.0738	0.0153	12.0	0.0141	0.0088	4.0
D13S317	0.0544	0.0197	11.3	0.0148	0.0070	3.6
Penta E	0.0389	0.0141	8.1	0.0289	0.0111	6.2
D16S539	0.0690	0.0195	12.8	0.0120	0.0049	2.7
D18S51	0.0827	0.0258	16.0	0.0167	0.0125	5.4
D2S1338	0.0909	0.0218	15.6	0.0298	0.0241	10.2
CSF1PO	0.0721	0.0258	14.9	0.0145	0.0071	3.6
Penta D	0.0262	0.0093	5.4	0.0324	0.0005	3.4
TH01	0.0252	0.0120	6.1	0.0071	0.0000	0.0
vWA	0.0836	0.0212	14.7	0.0149	0.0097	4.4
D21S11	0.0839	0.0199	14.4	0.0256	0.0132	6.5
D7S820	0.0508	0.0232	12.0	0.0250	0.0108	5.7
D5S818	0.0675	0.0230	13.7	0.0163	0.0139	5.8
TPOX	0.0346	0.0179	8.8	0.0145	0.0000	0.0
D8S1179	0.0818	0.0208	14.4	0.0173	0.0125	5.5
D12S391	0.1026	0.0313	19.6	0.0135	0.0083	3.8
D19S433	0.0689	0.0185	12.4	0.0129	0.0032	2.2
FGA	0.0700	0.0218	13.5	0.0192	0.0223	8.6

6.7 Peak balance

6.7.1 Peak Height Ratio and Allelic Imbalance Threshold

Peak height ratio (PHR) is the ratio between the two peaks in a heterozygous pair. Under optimal conditions the amplification of a pair of alleles should result in equal peak heights however, input DNA, inhibitors and quality of DNA will affect the amplification [34, 35].

The method used in Equation 4 is recommended in the SWGDAM guidelines [11]and well represented in the literature [36], although other methods have been published by Kelly et al [37].

By assigning a threshold of the mean minus three standard deviations, this incorporates 99.73% of the data, resulting in a conservative threshold. This threshold was rounded up to the nearest RFU. Use of this method to produce a threshold is a low risk to reference samples, as samples that deviate would be reprocessed.

Table 17 shows the summary of PHR and AI_{Th} data calculated. The overall average PHR for 12.5µL and 25µL total PCR volumes are 78.9% and 80.4% respectively. These values are consistent with other kits listed in the literature [12, 38]. Although the average peak height ratios are similar to those reported in the literature, given the wide standard deviation

observed in our data, the calculated AI_{Th} of 31.1% for 12.5uL and 38.6% for 25uL reaction volumes are considered low.

Figures 6 and 7 display the data obtained from the 10 x10 experiments for 25µL and 12.5µL total PCR volumes respectively. For both total PCR volumes, as the amount of DNA input is decreased from the recommended 0.5ng template DNA, the average peak height ratio (μ_{PHR}) decreases and the standard deviation of the peak height ratio (σ_{PHR}) increases.

When the mean PHR are calculated for each DNA template, between 0.183ng and 0.5ng inputs there is no significant difference between total PCR volumes although the standard deviation is higher for the 12.5µL total PCR volume, resulting in a much lower threshold. Refer to table.

Figures 10 -19 show observed PHR for different template DNA amounts. The PHR range is separated into 0.1 increments plotted against number of allele pairs. Figure 10 is lowest template DNA amount. This shows that at the low template DNA range, the PHR varies unpredictably for both the 25µL and 12.5µL total PCR volumes. As the template DNA amount increases, the PHR converges towards the ideal of 1.0.

The μ_{PHR_25} at 25pg input was 0.736 and at 0.5ng input was 0.851 compared with the $\mu_{PHR\_12.5}$, at 25pg input was 0.598 and at 0.5ng was 0.832.

The results of our validation are consistent with previous published findings referring to low template DNA and reduced volume amplifications [13, 34, 39].

Stochastic effects were obvious in this experiment in data from templates below 0.132ng. Stochastic effects are the result of random, uneven amplification of heterozygous allele pairs from low template samples (SWGDAM 2010 interpretation) which is displayed by low peak heights or allele/locus dropout. At 0.132ng DNA template is approaching what is usually defined as low copy number (LCN) (~0.100ng to 0.150ng).

Supportive experimental data is displayed in figure 20 AI_{TH} vs input graph, which displays a rapid drop off the AI_{TH} after 0.132ng DNA template. The calculated AI_{TH} drops below 0 for 0.02475ng DNA template because the standard deviation is so large. The rapid drop off is likely to increase the number of type 2 errors if AI_{TH} is used calculated from the entire dataset due to the large standard deviation. Exclusion of data from templates below 0.132ng increases the μ_{PHR} and decreases σ_{PHR}.

A multiple regression analysis was performed by Jo-Anne Bright, Duncan Taylor and John Buckleton to calculate the peak height variance for use in STRmix™[40].

The peak height ratios calculated here are for use with reference samples that have been amplified from extracted DNA and as a guideline to help determine the number of contributors for mixture interpretation as required for STRmix™ analysis.

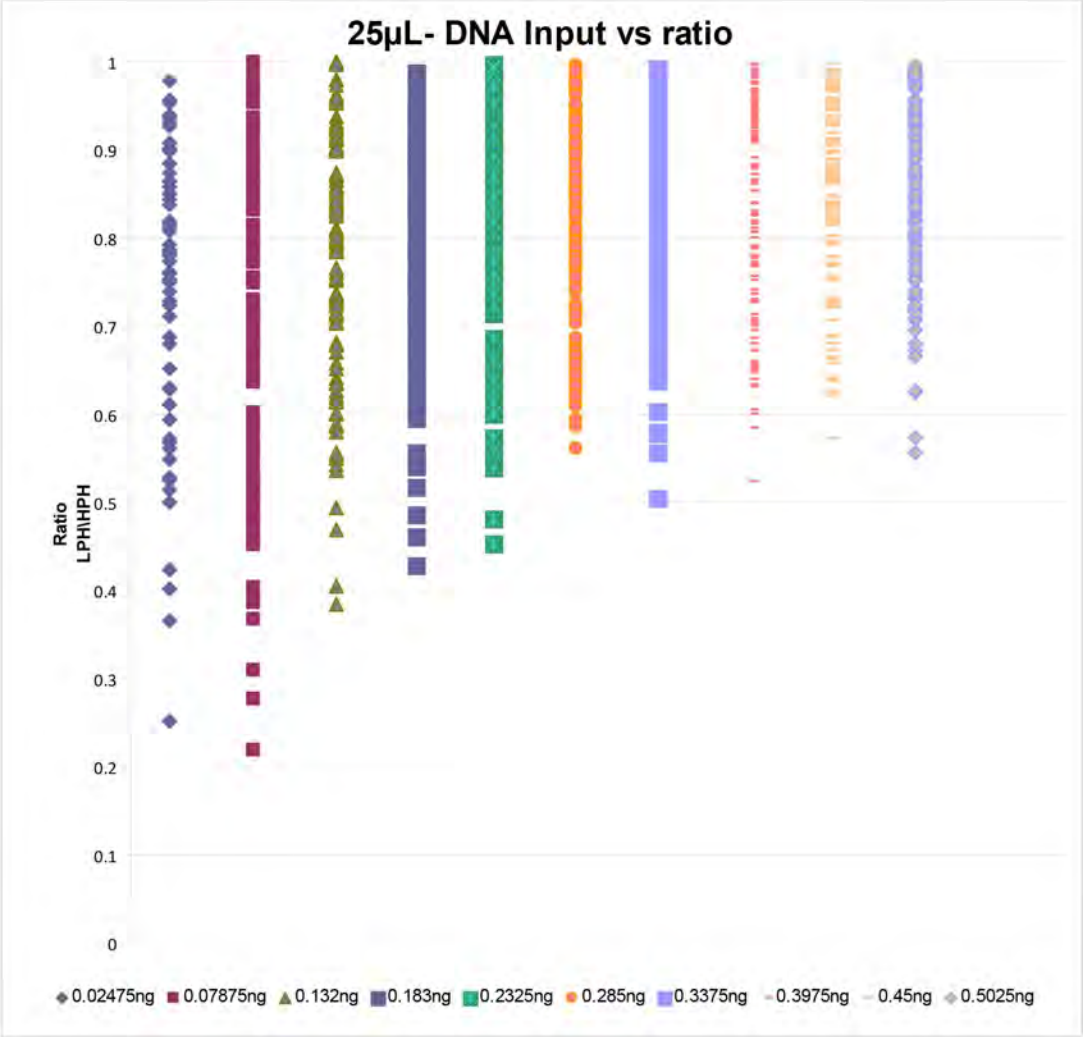


Figure 6 - 25µL total PCR volume, Peak balance vs total input DNA

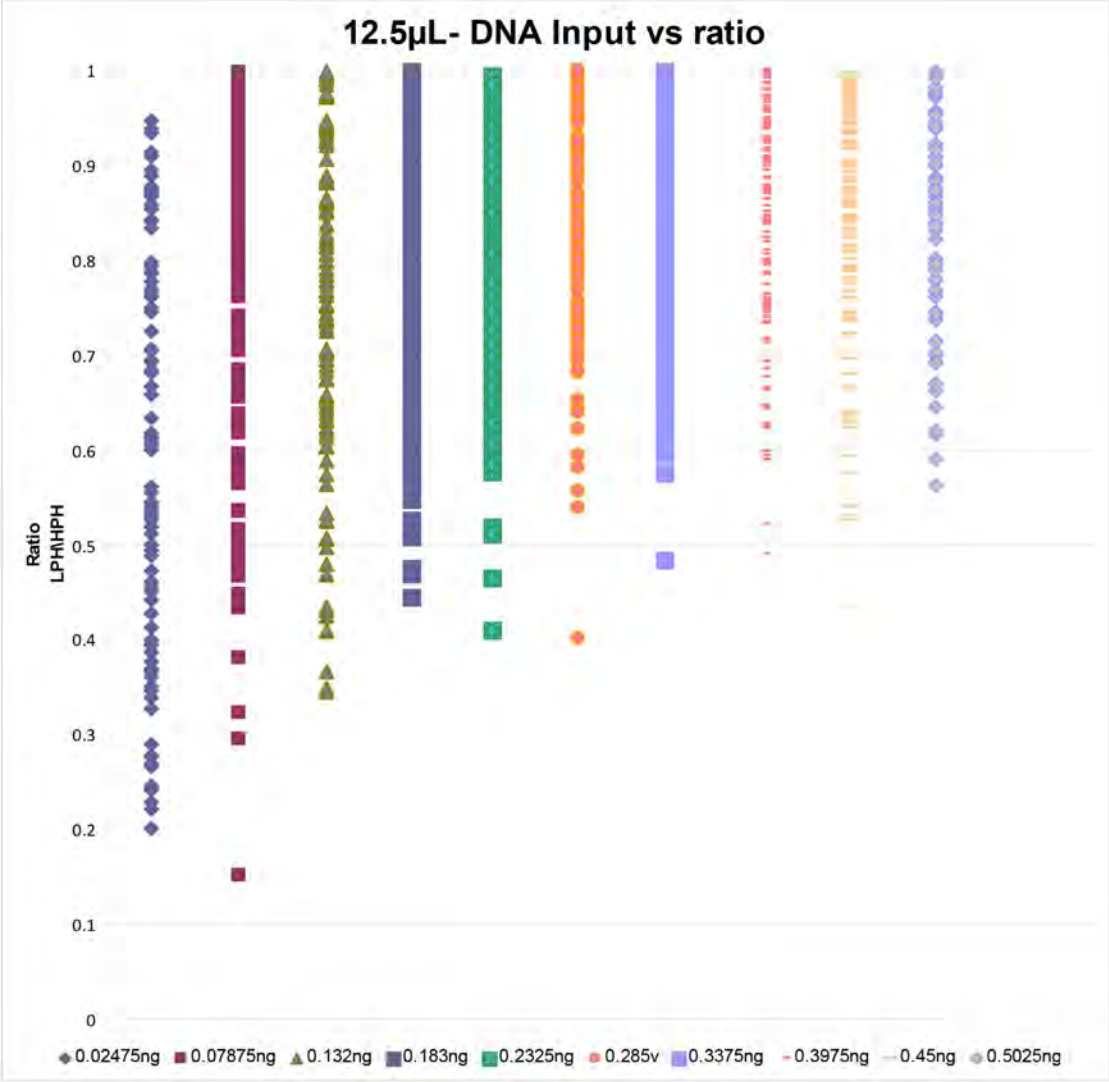


Figure 7 - 12.5µL Total PCR volume - Peak balance vs total input DNA.

Table 17 - Summary of calculated AI_{TH}.

	12.5µL			25µL		
	All Data	0.132 - 0.50	0.183- 0.50	All Data	0.132 - 0.50	0.183- 0.50
µ	0.789	0.814	0.825	0.804	0.824	0.830
σ	0.160	0.134	0.124	0.140	0.123	0.119
AI_{TH}	0.311	0.414	0.452	0.386	0.455	0.472

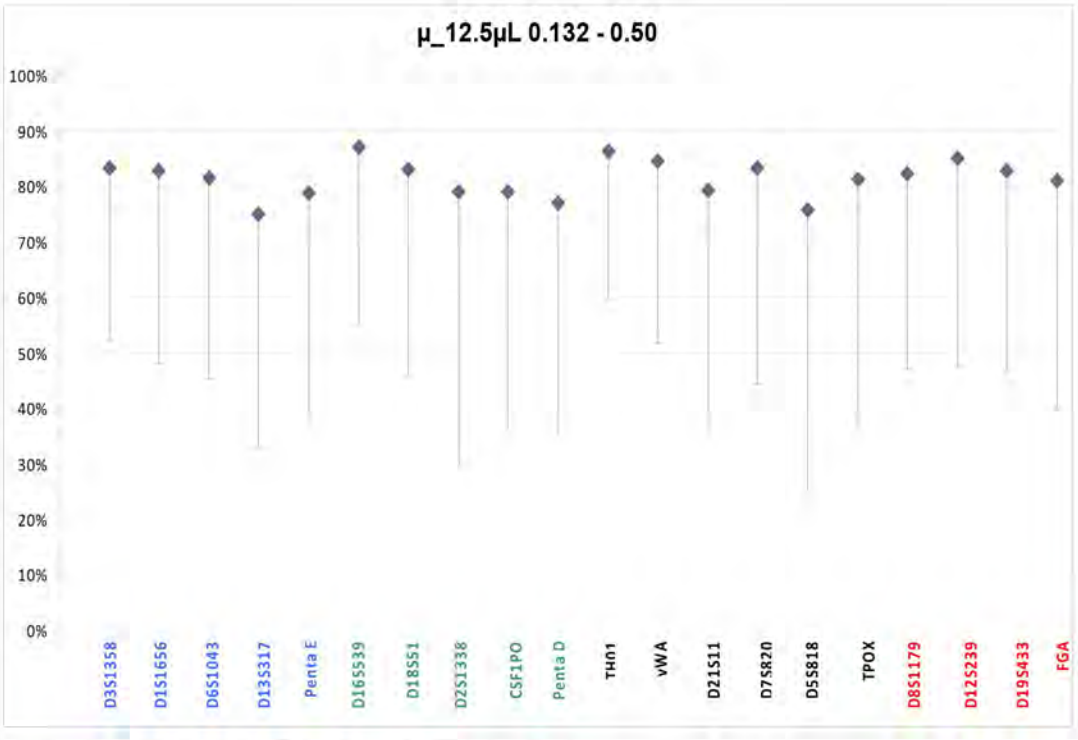


Figure 8 - 12.5µL total PCR volume µPHR per Loci

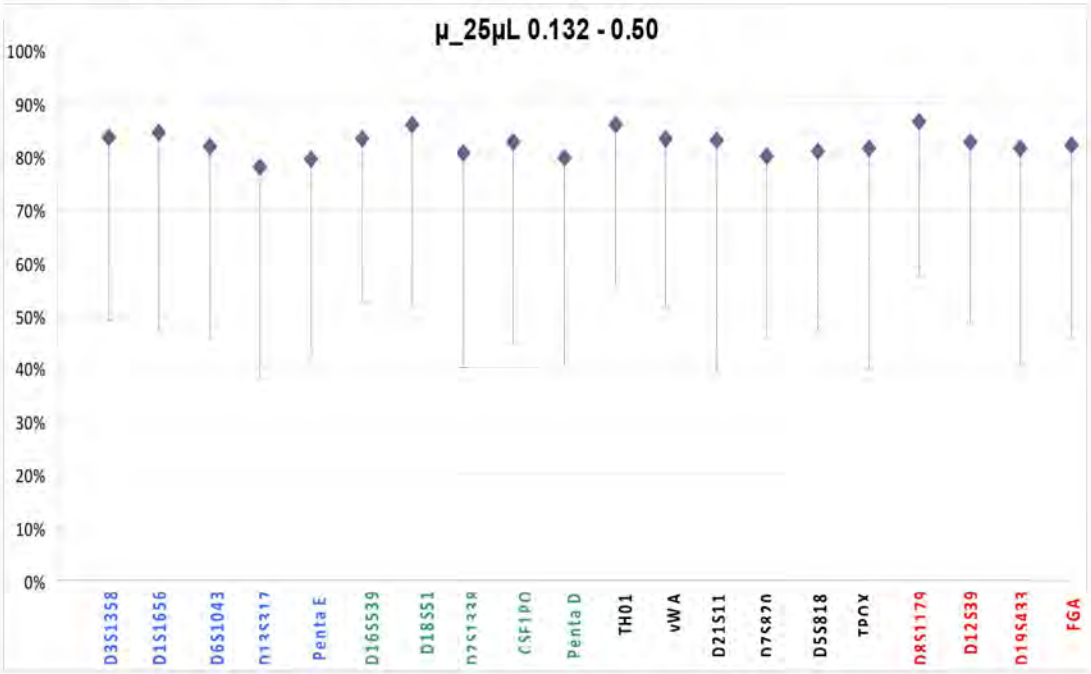


Figure 9 - 25µL total PCR volume µPHR per Loci

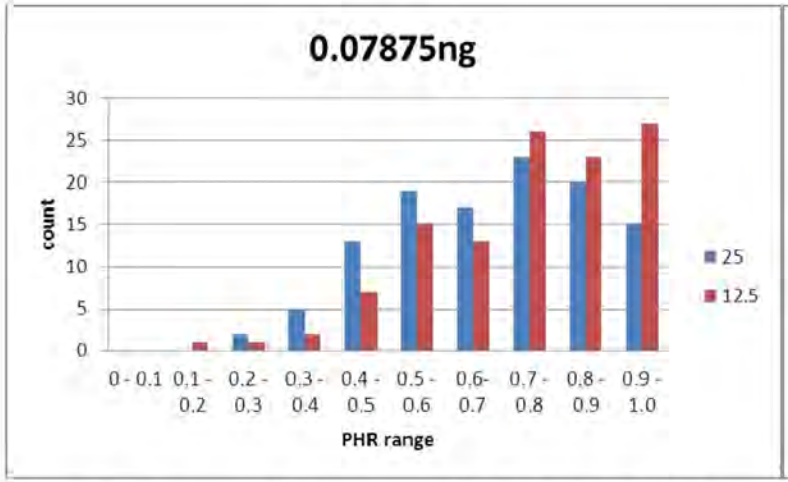


Figure 10 - The count of allele pairs per 0.1 PHR bin for 0.02475ng.

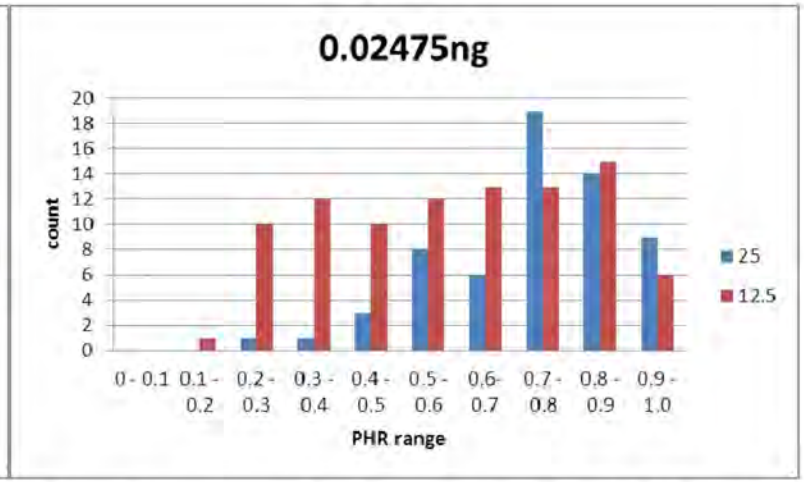


Figure 11 - The count of allele pairs per 0.1 PHR bin for 0.07875ng.

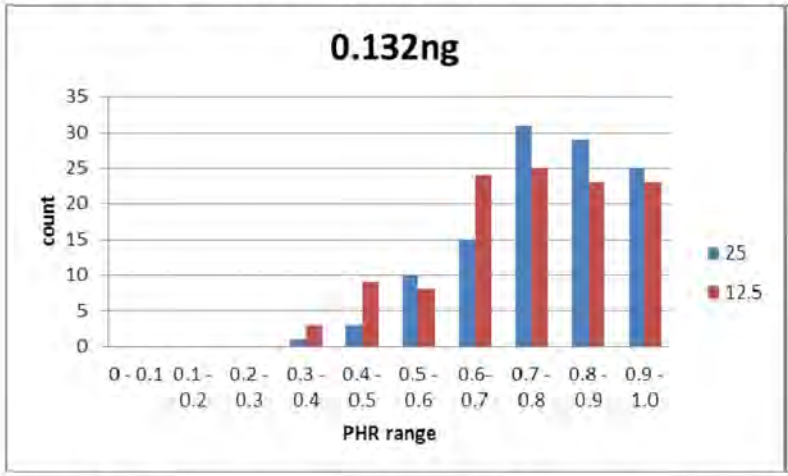


Figure 12 - The number of allele pairs per 0.1 PHR bin for 0.132ng.

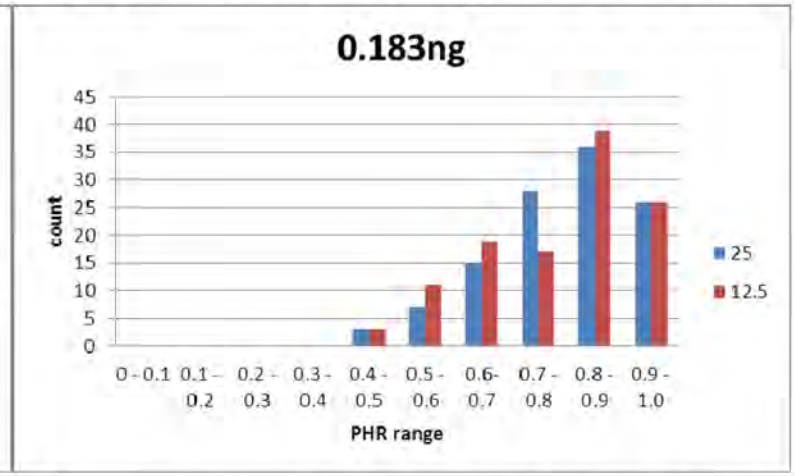


Figure 13 - The count of allele pairs per 0.1 PHR bin for 0.183ng.

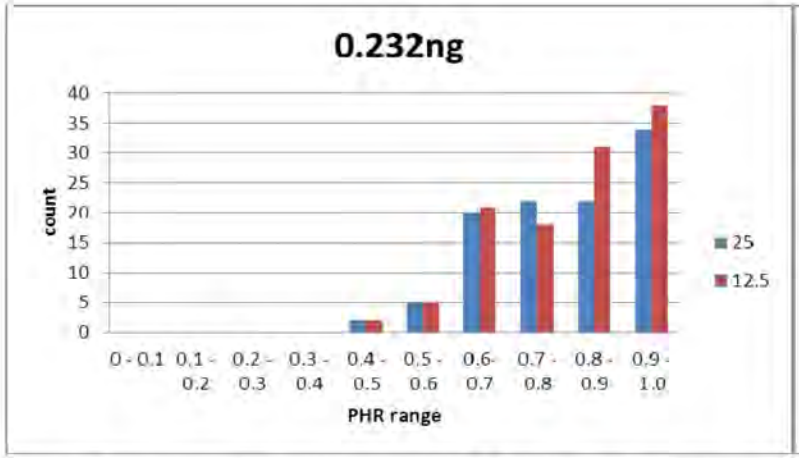


Figure 14 - The count of allele pairs per 0.1 PHR bin for 0.232ng.

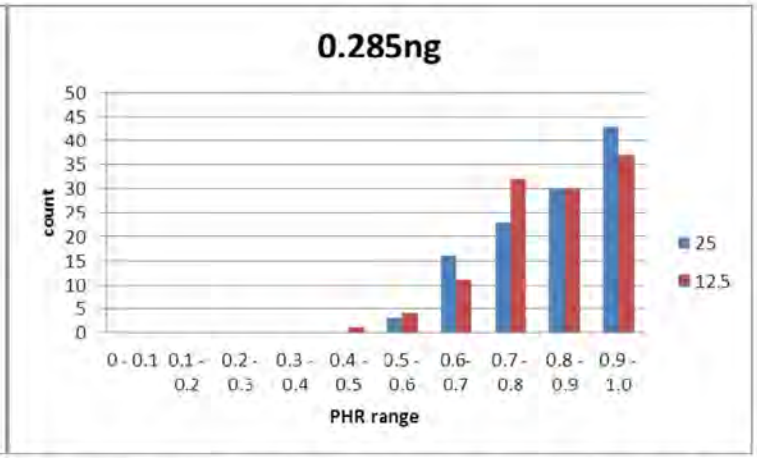


Figure 15 - The number of allele pairs per 0.1 PHR bin for 0.285ng.

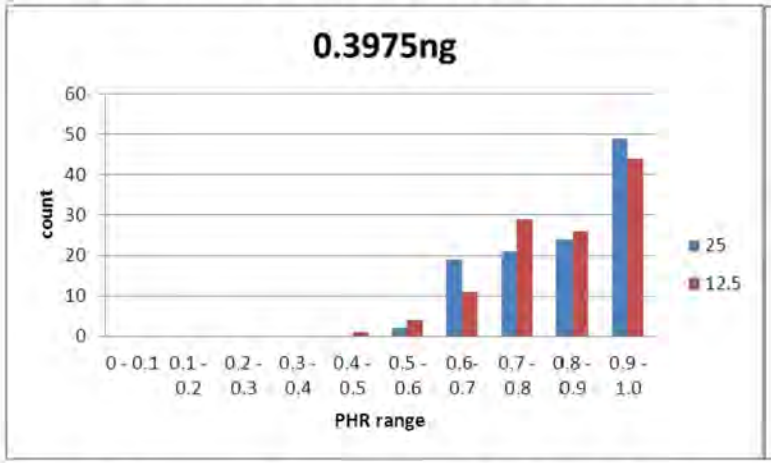


Figure 16 - The count of allele pairs per 0.1 PHR bin for 0.3375ng.

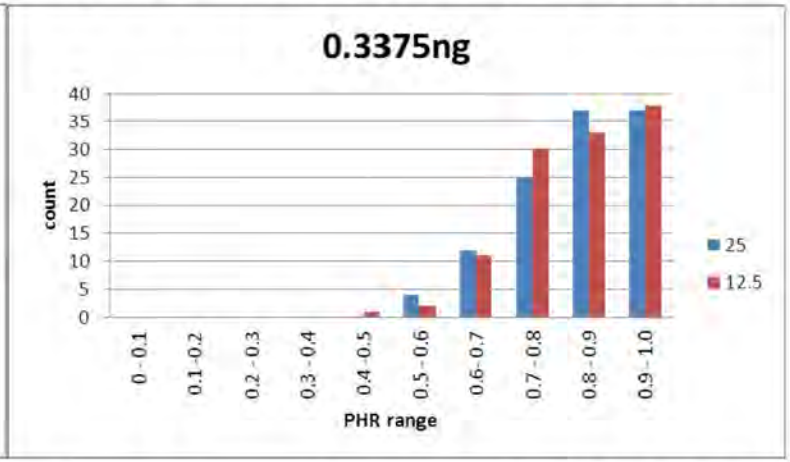


Figure 17 - The count of allele pairs per 0.1 PHR bin for 0.3975ng.

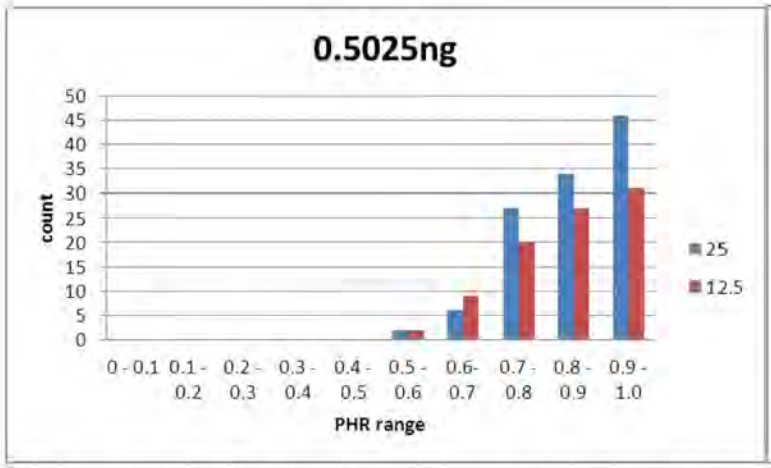


Figure 18 - The count of allele pairs per 0.1 PHR bin for 0.45ng.

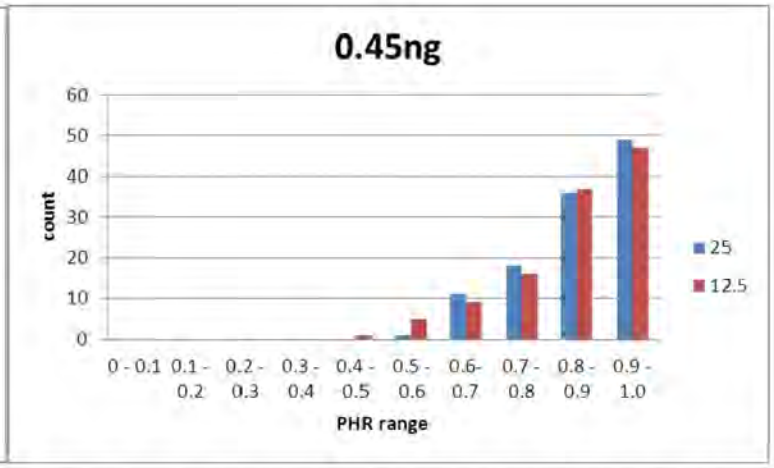


Figure 19 - The count of allele pairs per 0.1 PHR bin for 0.5025ng.

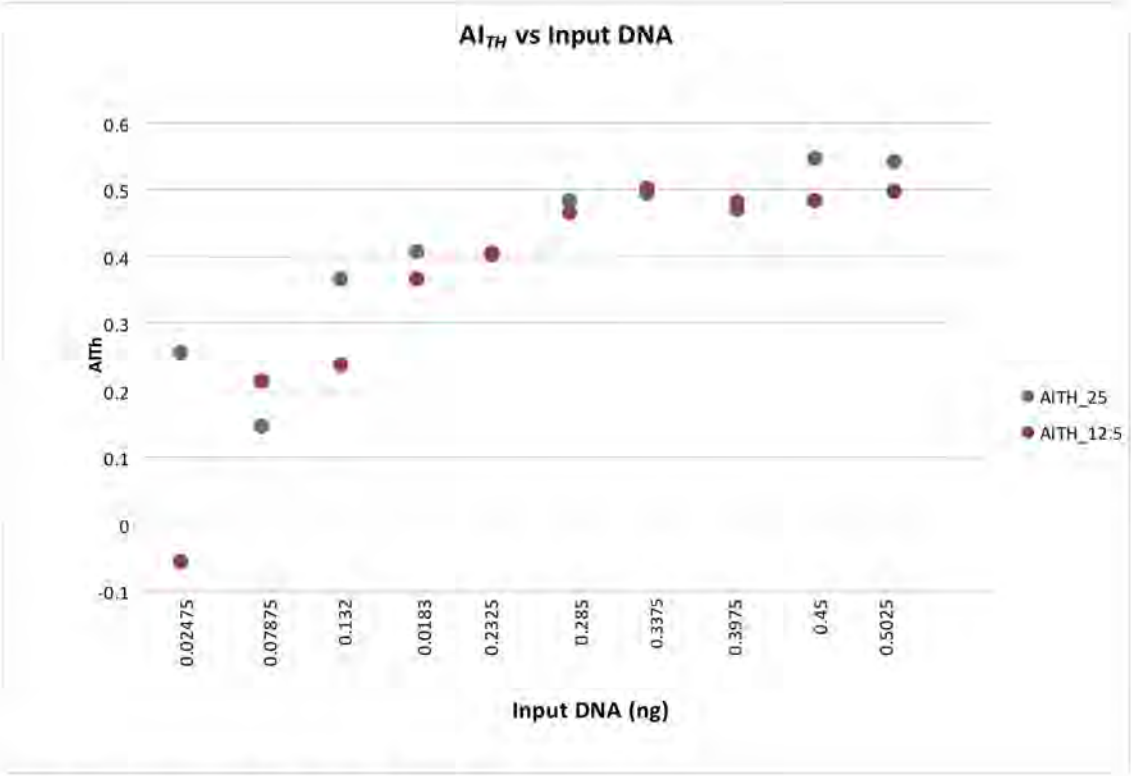


Figure 20 - Calculated AI_{TH} vs DNA template

6.7.2 Homozygote thresholds

The homozygote threshold is the threshold above which you can be confident that a heterozygote locus will not be incorrectly called as a homozygote locus.

Setting the homozygous threshold too high will result in excessive reworking of samples as a partial DNA profile would be called. Conversely, setting the threshold too low could result in false exclusions [1, 11, 23].

The method for determining the homozygote threshold varies in the literature. Traditionally, it had been arbitrarily designated at a particular level above the LOR. As already mentioned the risk of Type 1 and Type 2 errors should be balanced. Literature describes the setting of Th_{Hom} with respect to casework samples [21, 41, 42].

Previously in DNA Analysis, the Th_{Hom} was calculated as described in section 5.10 Equation 7. Using this method a figure of 176RFU for 25µL and 193FU for 12.5µL was calculated. These thresholds have been calculated excluding data below 0.132ng DNA template.

Another method of determining the Th_{Hom} is described in the Promega Internal Validation of STR systems reference manual[15]. This plots the peak height ratio for heterozygous loci against the lower RFU peak. The

threshold is defined as the point at which peak height ratio drops off significantly. Figures 21 and 22 display the data, the average AI_{TH} calculated for the range 0.132ng-0.5ng in section 6.7.1 for 25µL and 12.5µL respectively. An RFU that encompasses the majority of the data that falls below the average AI_{TH} calculated.

Unlike data reported in other publications[21, 43] there is not a rapid drop off of peak height ratios observed in the PowerPlex® 21 system, most likely due to the exclusion of the lower template data that exhibits extreme allelic imbalance. We have observed that the PowerPlex® 21 system loci tend to completely drop out completely compared to partially dropping out.

As both methods used give similar results, it is recommended the homozygote threshold be set at 200RFU for 25µL and 250RFU for 12.5µL.

These methods are subjective but when considered with the observed drop out data in figures 23-32, Th_{Hom} of 200RFU would result in no type 2 errors. Additionally the threshold is more than three times the LOR threshold so Type 1 errors would also be addressed.

The homozygote threshold calculated in this validation will be used for extracted reference samples as case work samples do not require a homozygote threshold for STRmix™ analysis.

To ensure all of the thresholds set for this validation are appropriate a post implementation review of the thresholds will be performed. If the thresholds are found to be too conservative and have resulted in additional processing the review will provide an opportunity to re-adjust the thresholds based on empirical data.

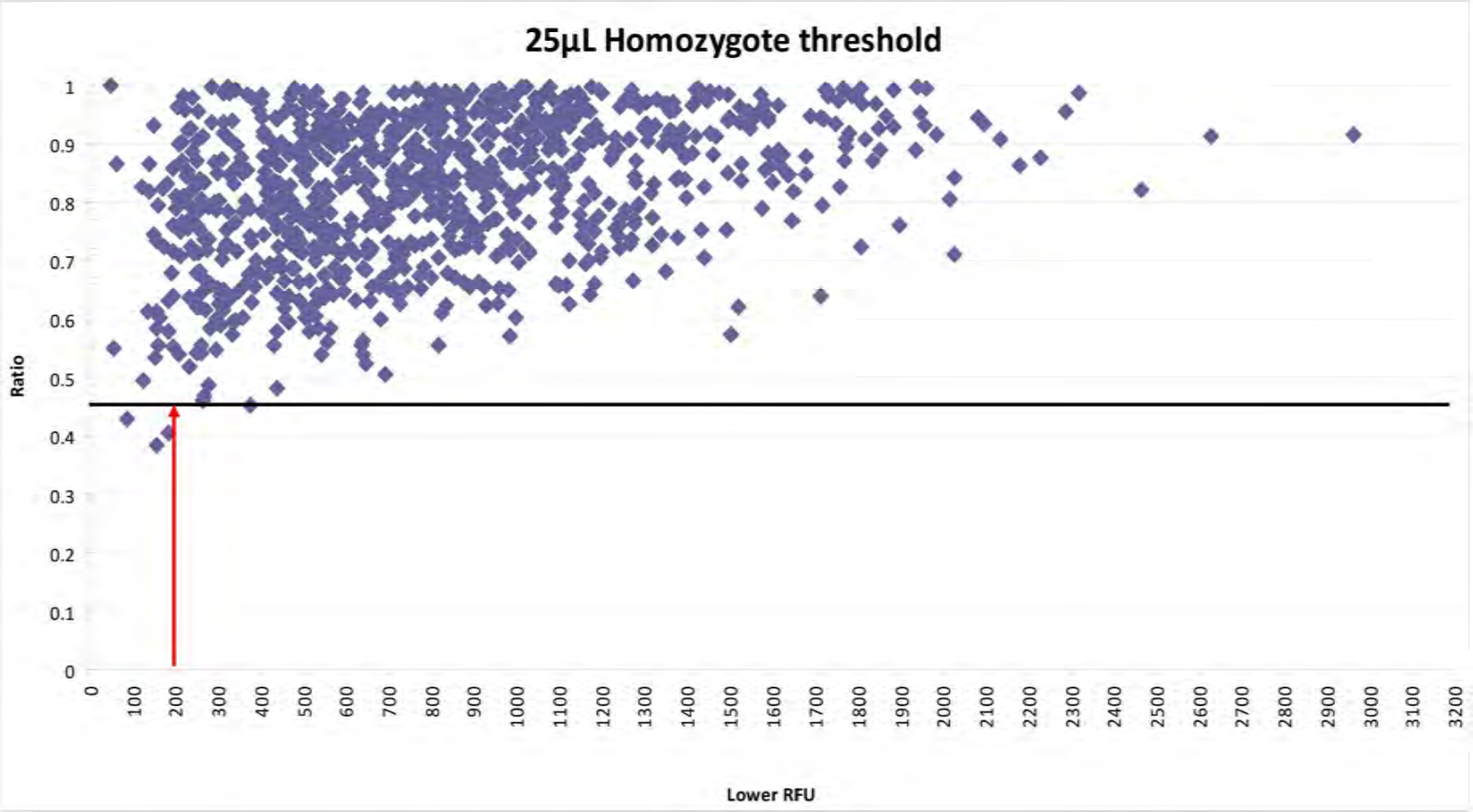


Figure 21 - plot of the peak height ratio vs RFU of lower peak for 25µL. The black horizontal line is the AI_{TH}. The red vertical line is set to encompass the majority of points that fall below the AI_{TH}.

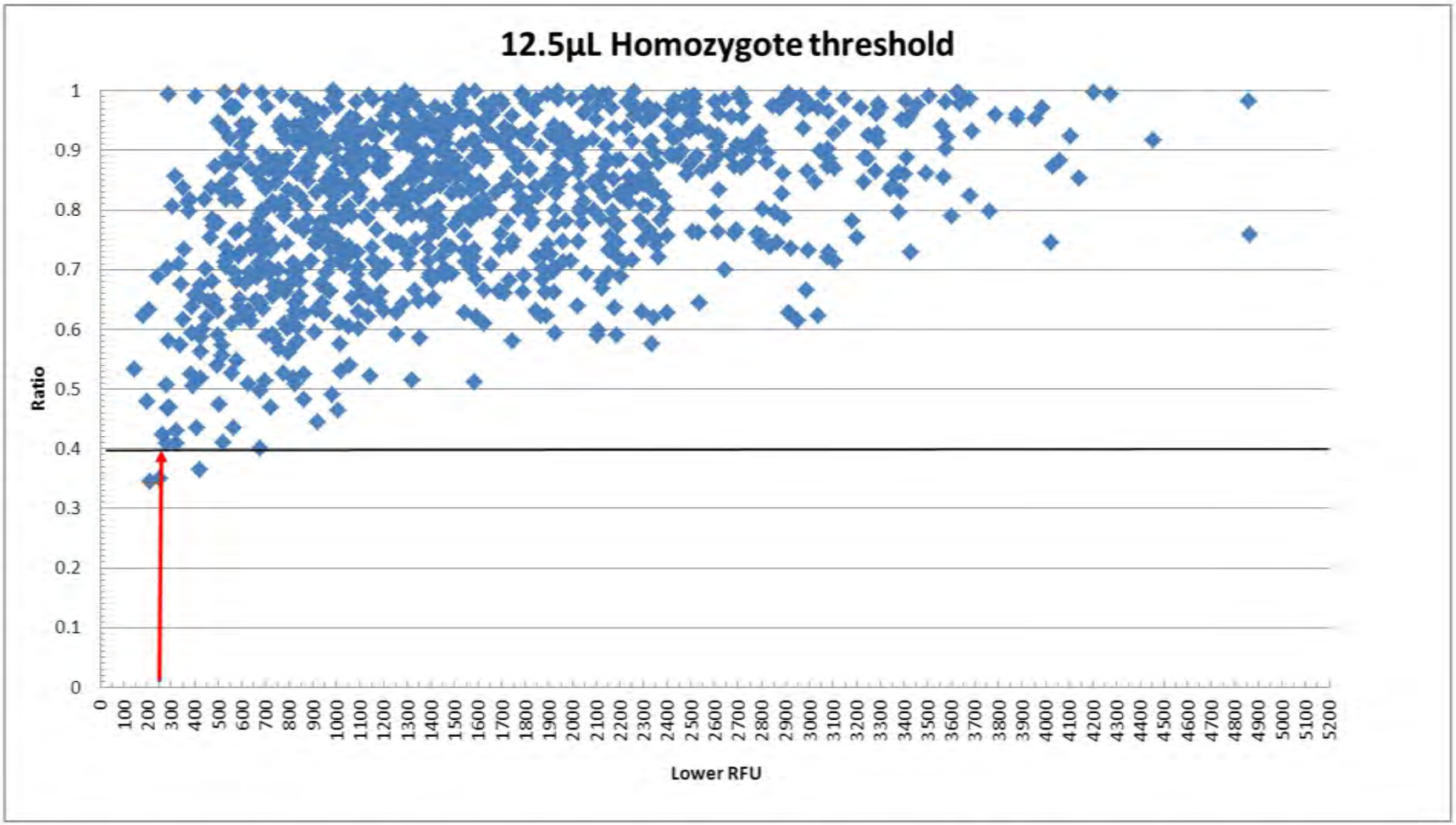


Figure 22 - plot of the peak height ratio vs RFU of lower peak for 12.5µL. The black horizontal line is the AI_{TH}. The red vertical line is set to encompass the majority of points that fall below the AI_{TH}

6.8 Dropout Experiments

Allelic dropout is when one allele of a heterozygous pair has not appeared or has a very low peak height[44]. One cause of dropout is one allele of a heterozygous pair is preferentially amplified thus giving the false impression of a homozygous allele at a particular locus[31].

This experiment used sensitivity 1 data of the two donors from 1ng to 1pg the 4ng and 2ng data was excluded due to the excess nature of the profiles. The heat maps shown in figures 23, 24, 25 and 26 summarise the data to quickly compare the drop out events observed.

The data for the 25µL amplification shows 62 drop out events occurred across both donors from dilutions 0.001ng to 0.05ng. Figure 24 shows the highest peak height (RFU) where a heterozygous pair dropped out was at 160RFU for the 0.01ng dilution for donor 2 amplified at 25µL total PCR volume.

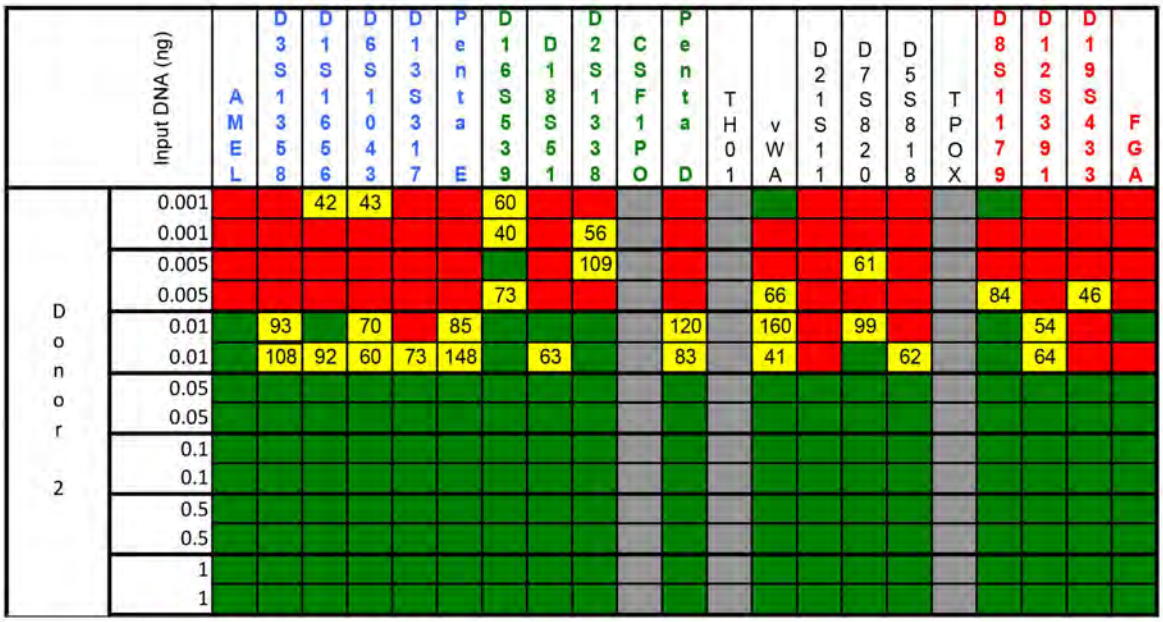
The data for the 12.5µL amplification shows 70 drop out events occurred across both donors from dilutions 0.001ng to 0.05ng. Figure 26 shows the highest peak height (RFU) where a heterozygous pair dropped out was at 399RFU for the 0.01ng dilution for donor 2.



Locus dropout
Allele dropout (surviving allele RFU)
Complete heterozygous locus
Homozygous locus

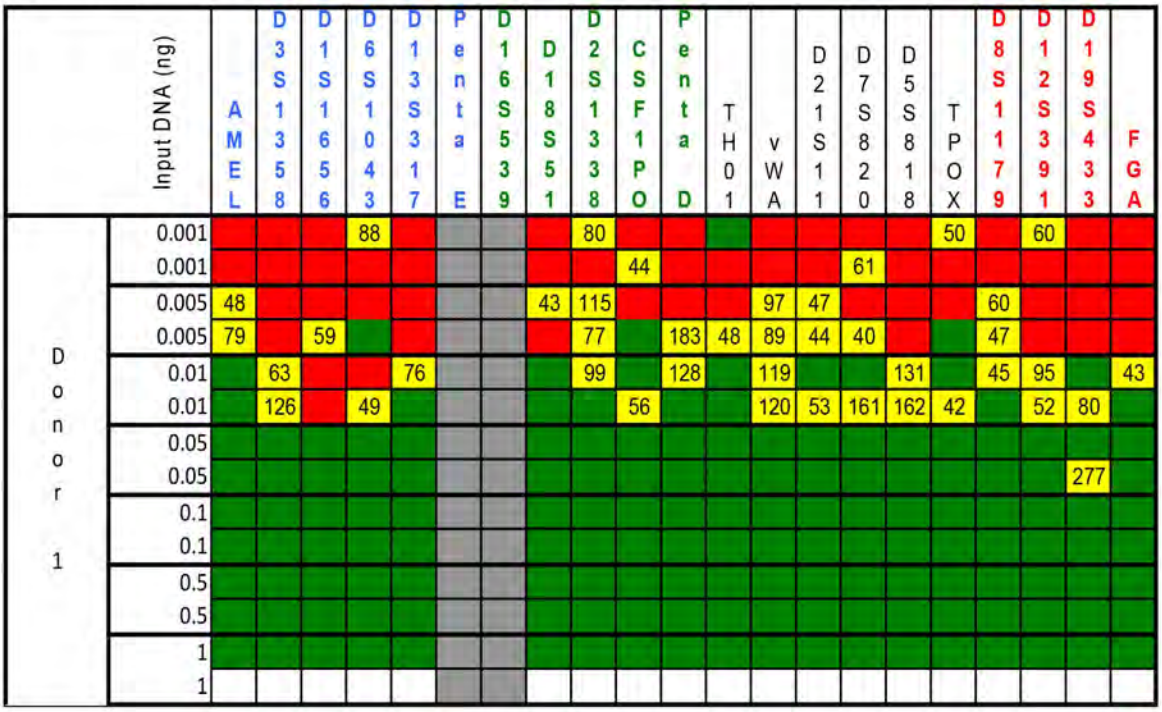
	Input DNA (ng)	AMEL	D3S1358	D1S1656	D6S1043	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	D8S1179	D12S391	D19S433	FGA
Donor 1	0.001										54											
	0.001								43													
	0.005	83												50		96					69	
	0.005	41		46		61								46				54	70			
	0.01	100	76	73						58	67	49		65	51		90	103	140			
	0.01	89								47			120		41	87	42		50	40	88	63
	0.05																131					
	0.05																					
	0.1																					
	0.1																					
	0.5																					
	0.5																					
	1																					
	1																					

Figure 23 - Heat map - Donor 1 - 25µL total PCR volume



	Input DNA (ng)	AMEL	D3S1358	D1S1656	D6S1043	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	D8S1179	D12S391	D19S433	FGA
Donor 2	0.001			42	43			60														
	0.001							40		56												
	0.005									109						61						
	0.005							73						66					84		46	
	0.01		93		70		85					120		160		99				54		
	0.01		108	92	60	73	148		63			83		41			62			64		
	0.05																					
	0.05																					
	0.1																					
	0.1																					
	0.5																					
	0.5																					
	1																					
	1																					

Figure 24 - Heat map - Donor 2 - 25µL total PCR volume



	Input DNA (ng)	AMEL	D3S1358	D1S1656	D6S1043	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	D8S1179	D12S391	D19S433	FGA
Donor 1	0.001				88					80								50		60		
	0.001										44					61						
	0.005	48							43	115				97	47				60			
	0.005	79		59						77		183	48	89	44	40			47			
	0.01		63			76				99		128		119			131		45	95		43
	0.01		126		49						56			120	53	161	162	42		52	80	
	0.05																					
	0.05																				277	
	0.1																					
	0.1																					
	0.5																					
	0.5																					
	1																					
	1																					

Figure 25 - Heat map - Donor 1 - 12.5µL total PCR volume

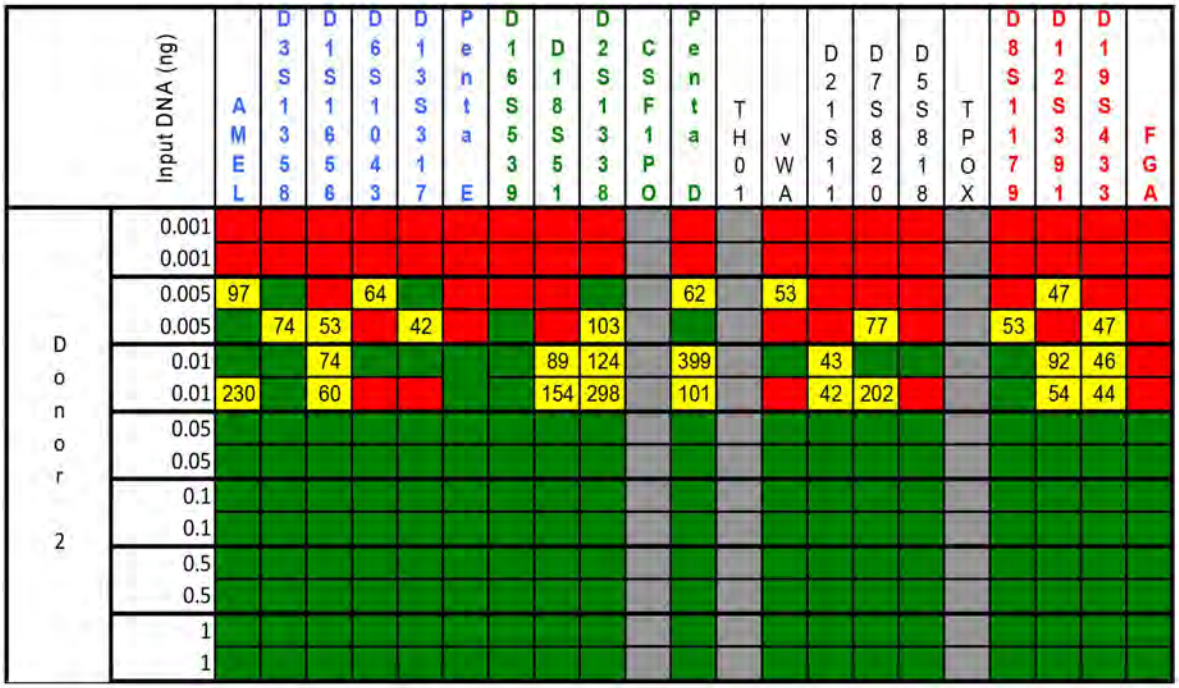


Figure 26 - Heat Map – Donor 2 - 12.5µL total PCR volume

6.8.1 Drop Out 2

Analysis for drop out 2 used the data obtain from the Aboriginal dataset, 10 x10 and both sensitivity experiments for 25µL total PCR volume and the 10 x10, both sensitivity experiments and concordance for 12.5µL total PCR volume. The dropout 2 results are displayed in figures 27 and 28. Figure 27 shows the dropout events for all samples amplified at 25µL total PCR volume. Figure 28 shows the dropout events for all samples amplified at 12.5µL total PCR volume.

For both 25µL and 12.5µL total PCR volume amplifications there are more drop out events of whole loci compared with a single allele drop out event

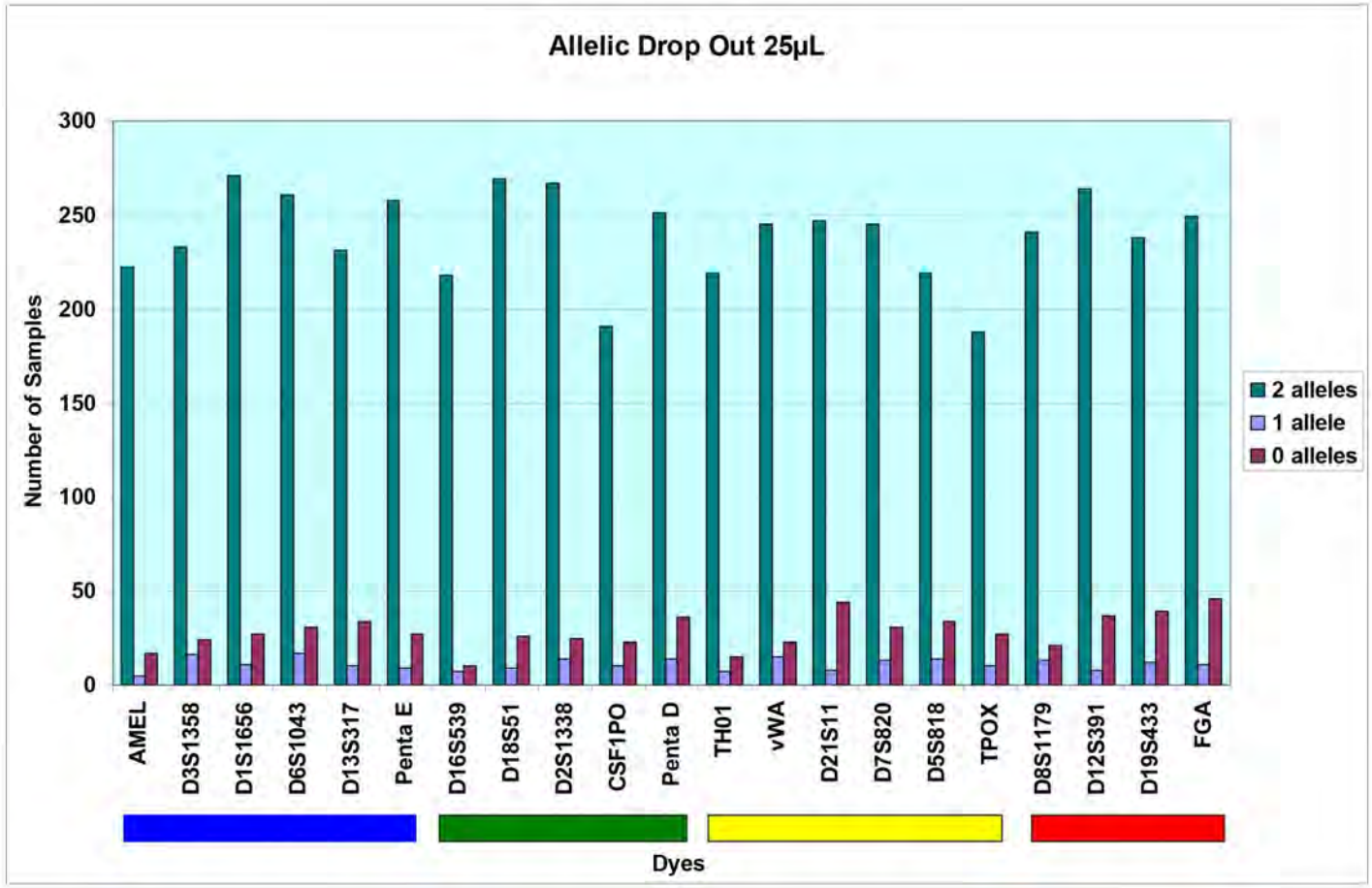


Figure 27 - Dropout events for samples amplified at 25µL

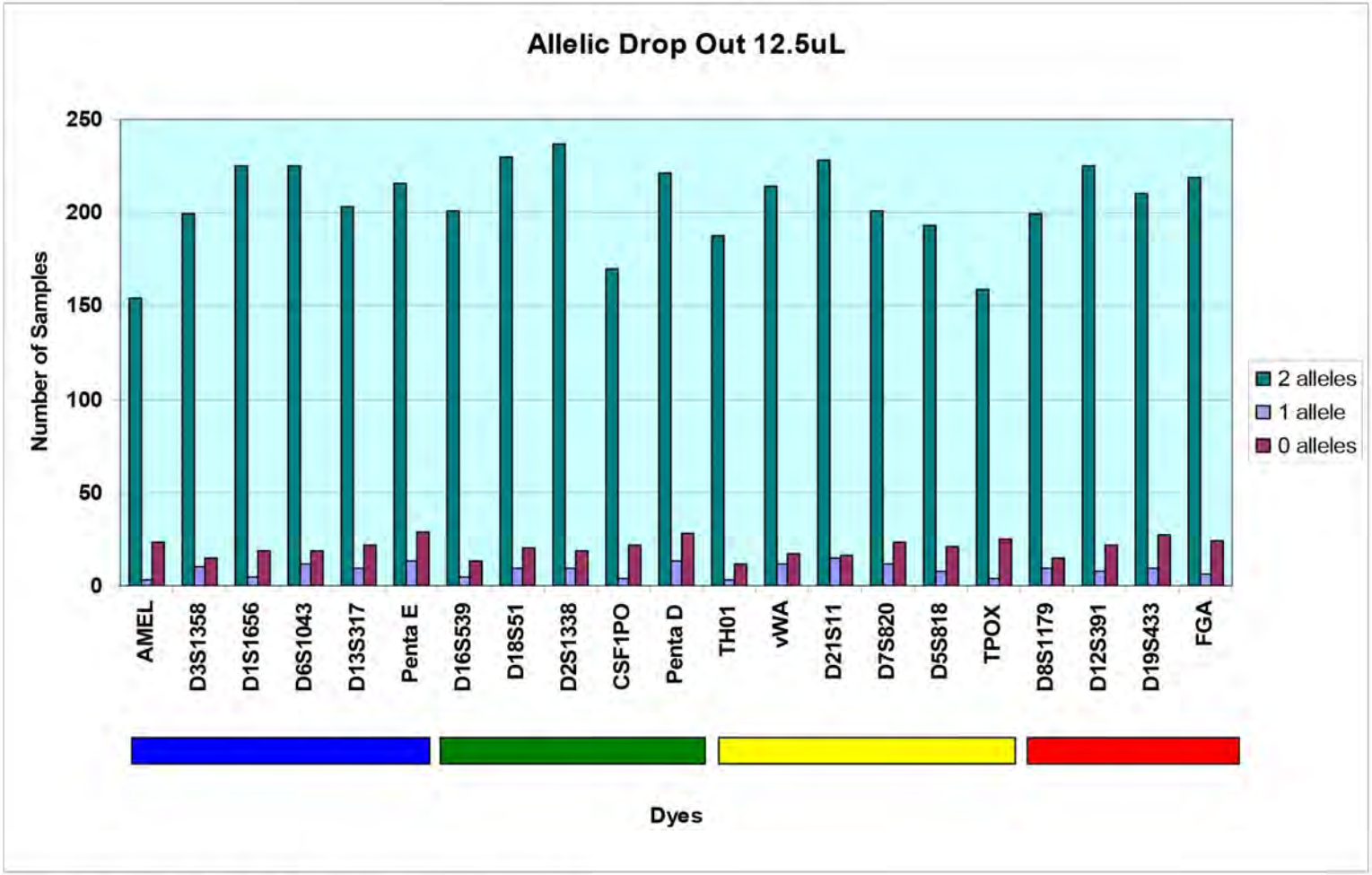


Figure 28 - Dropout events for samples amplified at 12.5µL

6.8.2 Drop Out 3

Analysis for drop out 3 used the data from the baseline (10 x 10) and both sensitivity experiments at both 25µL and 12.5µL total PCR volume. There were 215 drop out events observed for the 25µL total PCR volume compared to198 drop out events observed at 12.5µL total PCR volume. Figure 29 shows the number of drop out events for a range of peak heights. This shows the majority of drop out events occur below 150RFU for 25µL total PCR volume and below 180RFU for 12.5µL total PCR volume.

Figures 30, 31 and 32 show the peak heights where one of the heterozygote pairs has dropout at each DNA template. Figure 30 shows one dropout event occurred at 226RFU for the 12.5µL total PCR volume at a DNA template of 0.131ng whereas 17 dropout events occurred at 25 µL total PCR volume at the same DNA template, however these dropout events occurred under 80RFU. The highest drop out seen for 12.5µL total PCR volume was at 234RFU at a DNA template of 0.025ng and for 25µL total PCR volume was at 106RFU. The total number of dropout events seen for the 10 x10 at 25µL total PCR volume was 68 and 30 at 12.5µL total PCR volume.

Figure 31 (Sensitivity 1) shows the highest drop out for 12.5µL total PCR volume was seen at 399RFU at a DNA template of 0.01ng and 160RFU at DNA template 0.01ng for the 25µL total PCR volume. The total number of dropout events seen for the sensitivity 1 experiment at 25µL total PCR volume was 58 and 66 at 12.5µL total PCR volume.

Figure 32 (Sensitivity 2) shows the highest drop out for 12.5µL total PCR volume was seen at 246RFU at a DNA template of 0.0094ng and 249RFU at a DNA template of 0.0375ng for the 25µL total PCR volume. The total number of dropout events seen for the sensitivity 2 experiment at 25µL total PCR volume was 89 and 102 at 12.5µL total PCR volume.

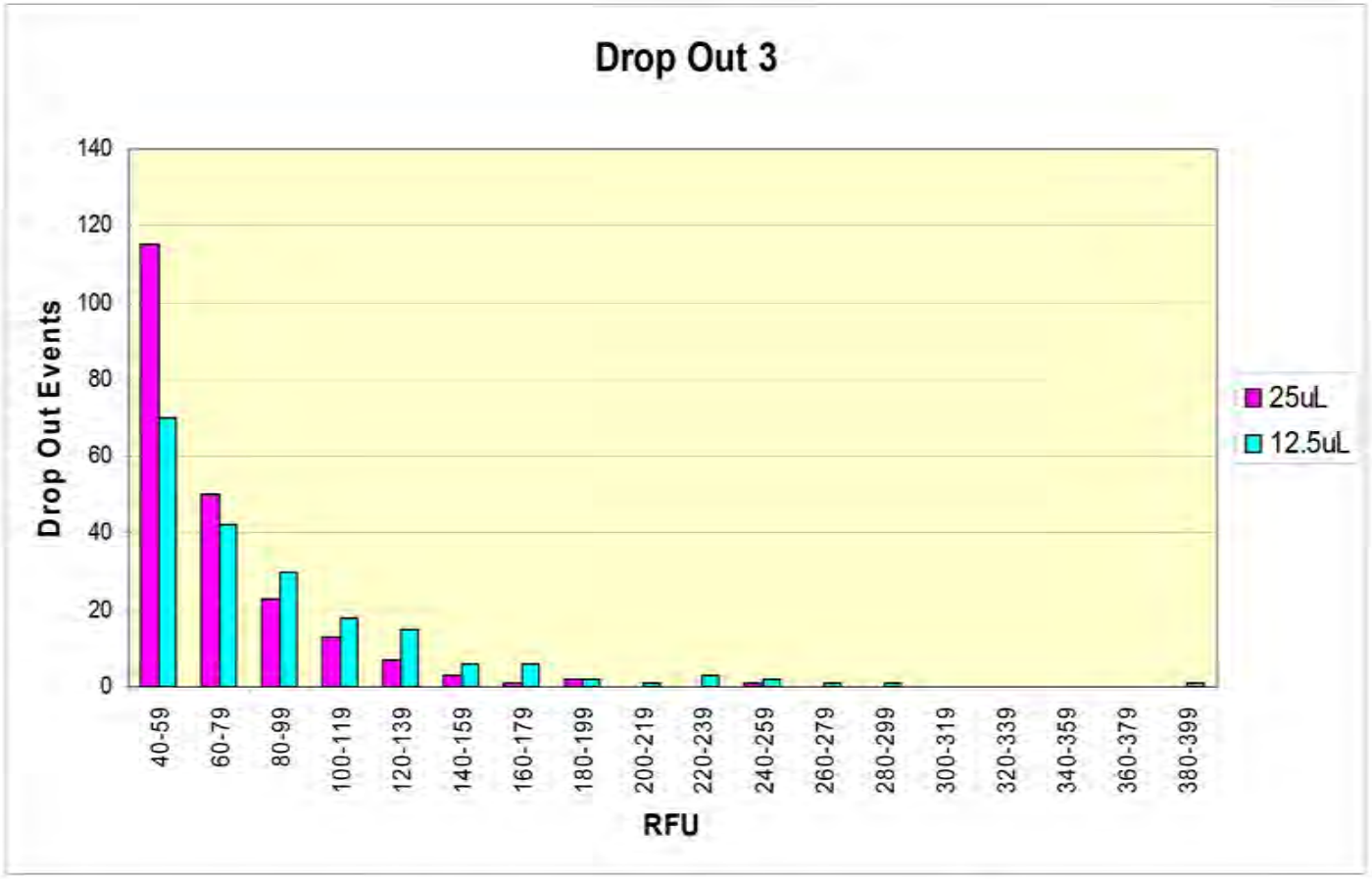


Figure 29 - Number of drop out events seen within peak height ranges at 25µL and 12.5µL amplifications

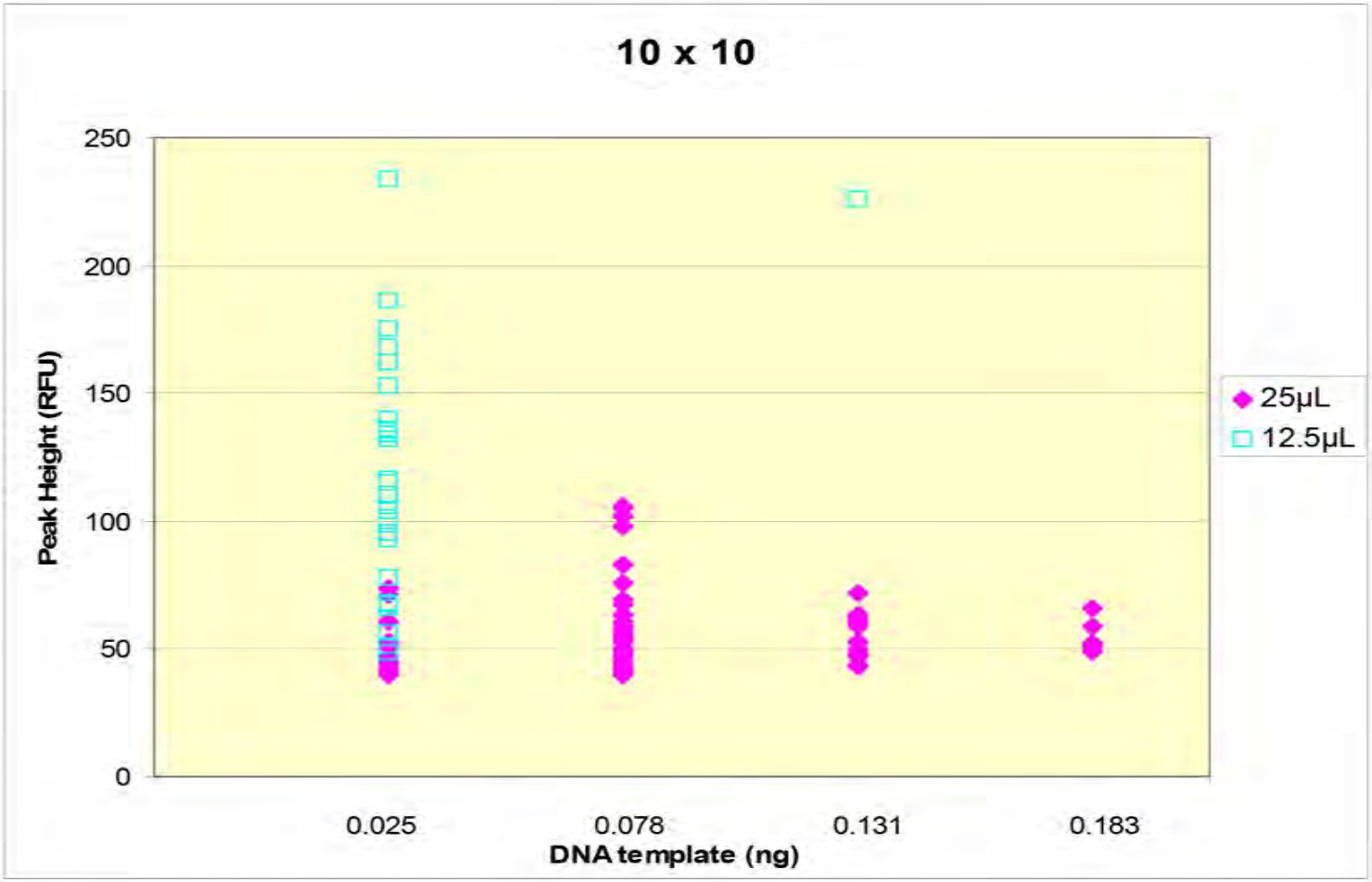


Figure 30 - Peak heights where the heterozygote pair has dropped out at different DNA templates for 12.5uL and 25uL using the baseline data (10 x10)

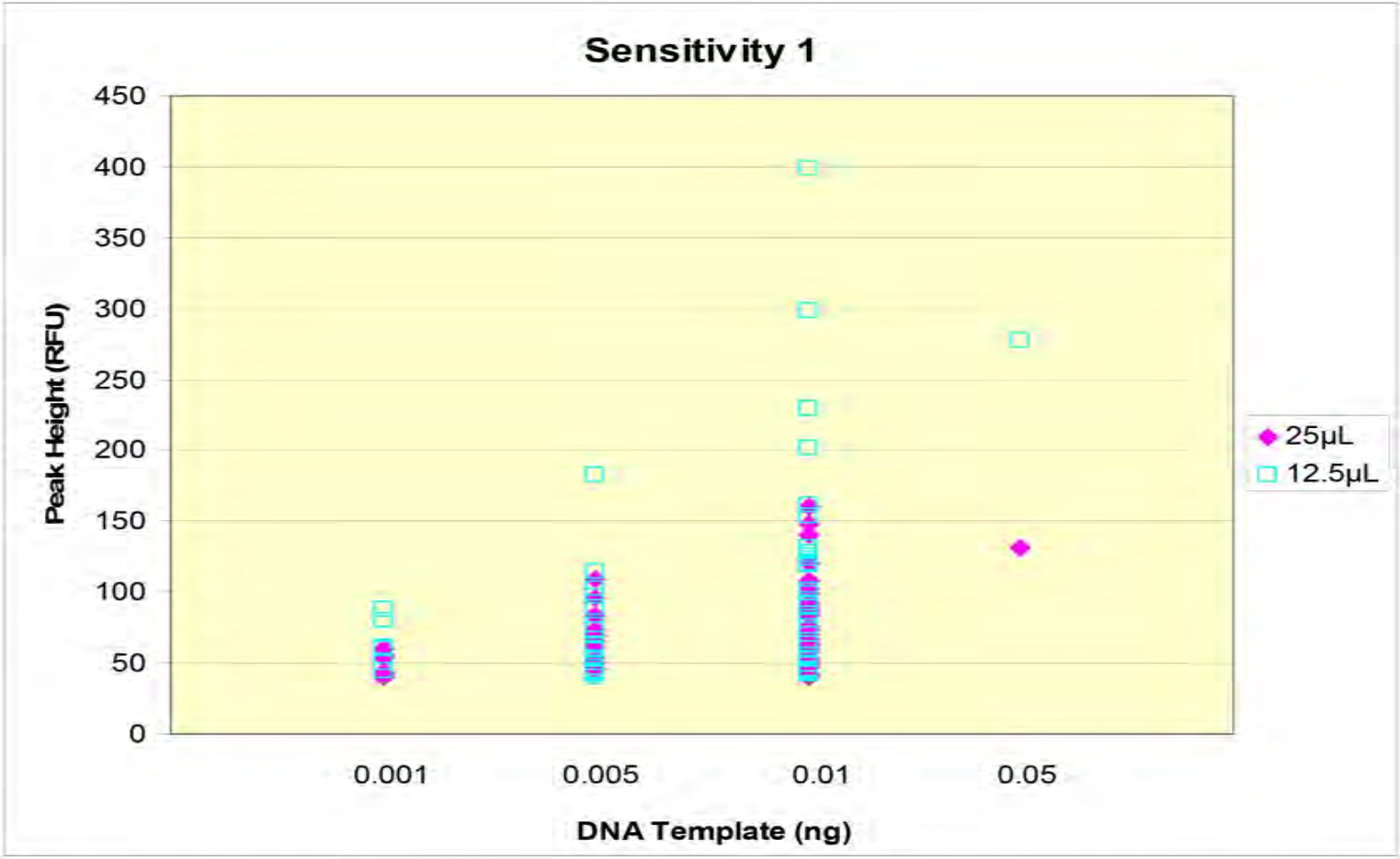


Figure 31 - Peak heights where the heterozygote pair has dropped out at different DNA templates for 12.5uL and 25uL using sensitivity 1 data

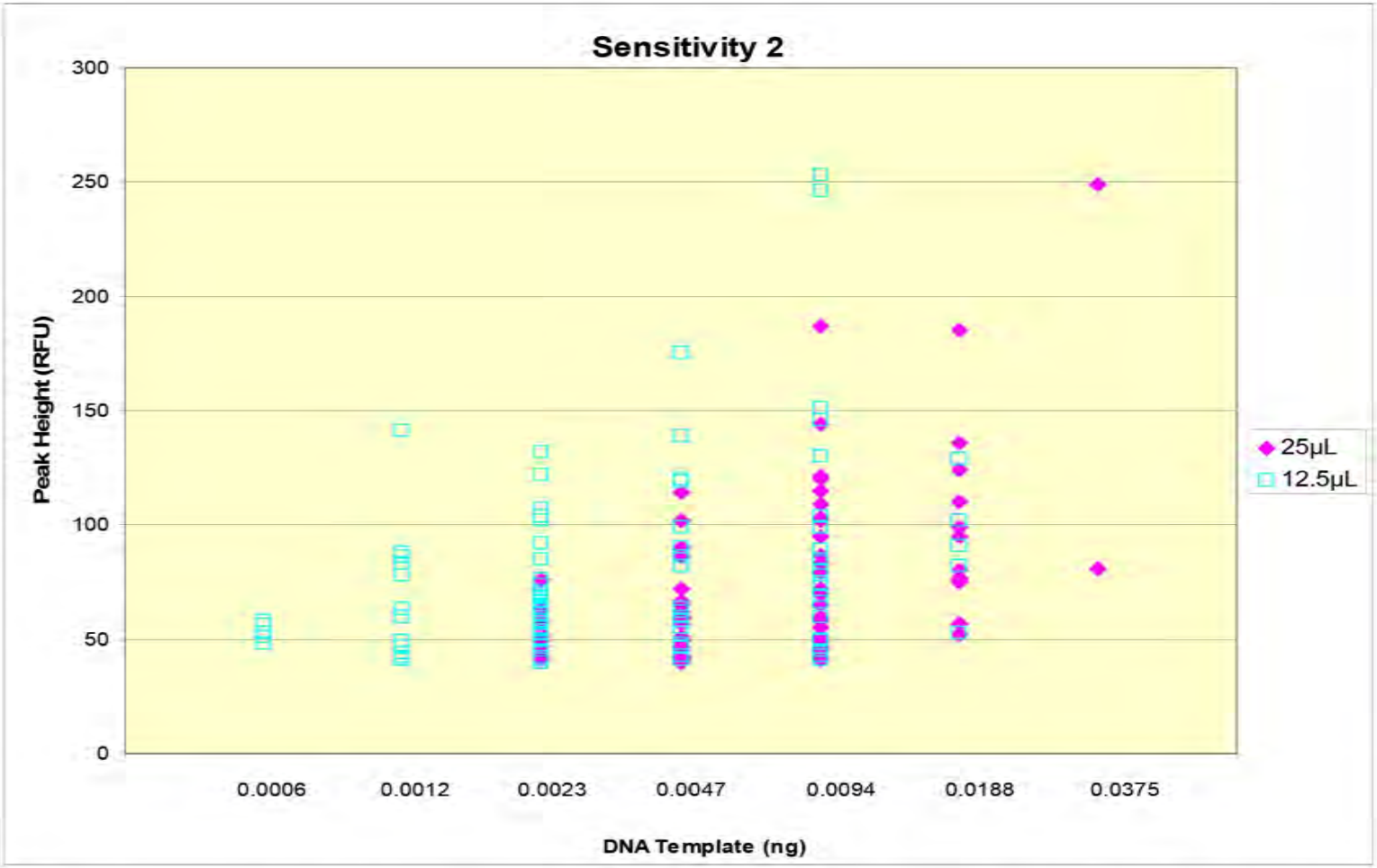


Figure 32 - Peak heights where the heterozygote pair has dropped out at different DNA templates for 12.5uL and 25uL using sensitivity 2 data

6.9 Mixture Studies

At a total input template of 0.5ng, for both 25µL and 12.5µL, all alleles were detected for the mixtures with ratios of 1:1, 2:1 and 5:1. Any allelic imbalance was observed at a level of greater than 40%.

When the template was decreased to 0.125ng for 5:1 mixtures, drop-out of the lower level contributor was observed for both 25µL and 12.5µL volumes. At this template level, allelic imbalance of down to 35% was observed for the lower level contributor at both 25µL and 12.5µL volumes, however, one of these peaks fell into the stutter position of the larger contributor.

When the template was decreased to 0.06ng for 2:1 mixtures, drop-out of the lower level contributor was observed for both 25µL and 12.5µL volume with the partner allele being as high as 562RFU. At this template level, allelic imbalance of down to 20% was observed for the lower level contributor and 23% for the higher level contributor.

For the remaining mixtures with ratios of 10:1, 20:1, 30:1 and 50:1 of varying template levels (maximum 0.5ng), the lower contributors exhibited, sometimes quite marked, stochastic variation. This included drop-out with peaks up to 392RFU and allelic imbalance as low as 20%.

The tables 16 and 17 show the approximate mixture ratio of the profile compared with the mixture ratio of the sample. For the 2 person mixtures this was averaged over all loci where there was no allele sharing between the two contributors and where the alleles did not fall into a stutter position. For the 3 person mixtures, the ratio was averaged over all loci where there was no allele sharing between the three contributors, however it was not possible to exclude loci where the alleles fell into stutter positions as there were no loci fulfilling this criteria. It was not possible to accurately calculate mixture ratios for the four person mixtures.

The data shows that the mixture ratio after DNA amplification is approximately equal to the mixture ratio of the initial sample for both 25µL and 12.5µL volumes at all ratios. The mixture ratio deviates more as the ratio increases most likely due to the stochastic effects of the lower contributor. The mixture ratios for the 25µL volume amp appear to be slightly lower than for the12.5µL volume amp.

Although mixture ratios have not been calculated for the four person mixtures, the alleles obtained are consistent with expected profiles.

Table 18 - 12.5µL total PCR volume mixture studies

Mixture Ratio of Sample	Total Input Template (ng)	Approximate Mixture Ratio of Profile
2 Person Mixtures		
1:1	0.500	1.2:1
2:1	0.500	2.2:1
	0.060	2.9:1
5:1	0.500	6.1:1
	0.125	6.1:1
10:1	0.500	12:1
	0.125	11:1
20:1	0.500	24:1
	0.250	16:1
	0.125	19:1
30:1	0.500	21:1
50:1	0.500	35:1
	0.250	49:1
	0.125	Unable to calculate
3 Person Mixtures		
5:2:1	0.500	4.2:1.3:1
	0.125	Unable to calculate
10:5:1	0.500	13:9.1:1
20:10:1	0.500	10:5.7:1
	0.125	Unable to calculate
4 Person Mixtures		
5:3:2:1	0.500	Unable to calculate
	0.125	Unable to calculate

Table 19 - 25µL total PCR mixture studies

Mixture Ratio of Sample	Total Input Template (ng)	Approximate Mixture Ratio of Profile
2 Person Mixtures		
1:1	0.500	1.2:1
2:1	0.500	1.8:1
	0.060	1.7:1
5:1	0.500	4.1:1
	0.125	4.8:1
10:1	0.500	8.5:1
	0.125	6.3:1
20:1	0.500	22:1
	0.250	17:1
	0.125	10:1
30:1	0.500	15:1
50:1	0.500	26:1
	0.250	9.2:1
	0.125	6.7:1
3 Person Mixtures		
5:2:1	0.500	2.9:1.5:1
	0.125	2.7:1.1:1
10:5:1	0.500	7.4:5.4:1
20:10:1	0.500	10:6.4:1
	0.125	10:4.7:1
4 Person Mixtures		
5:3:2:1	0.500	Unable to calculate
	0.125	Unable to calculate

7 Conclusion

The results from this validation support that Promega's PowerPlex®21 System is suitable for analysis of STRs.

Despite slight differences observed between the two 3130xl analysers, the use of single LOD and LOR of 16RFU and 40RFU is more practical for use in DNA Analysis.

The PowerPlex21® System displays full concordance with all alleles observed in testing being concordant.

The three national population datasets (Caucasian, Aboriginal and SE Asian) created collaboratively within Australia, have been externally validated and will be implemented in conjunction with STRmix™ for statistical interpretation.

12.5µL total PCR volumes gave higher peak heights than their 25µL counterparts at the same DNA template.

The PowerPlex®21 system is a very sensitive amplification kit when used at either the standard amplification volume (25µL) or reduced volume amplification (12.5µL); however the increased sensitivity does not necessarily result in more reliable information.

The two sensitivity experiments explored the range on DNA template inputs from very large inputs (4ng) to very small inputs (0.00059ng). Within this validation complete PowerPlex® 21 DNA profiles were obtained with as little as 0.01875ng of template DNA. However, the PHR data indicate that as the amount of template DNA decreases the μ_{PHR} decreases and σ_{PHR} increases. The risk of type 2 errors is greatly increased from template DNA amounts of less than 0.132ng for both 25µL and 12.5µL total PCR volumes, which is supported by the experimental drop out data.

The data presented within this report indicates that input templates less than 0.132ng total DNA (concentrations 0.0176ng/µL if using 12.5µL total PCR volume or 0.0088ng/µL for 25µL total PCR volume) may result in increased stochastic effects.

As previously documented in DNA Analysis[45, 46], the Quantifiler™ Human DNA Quantification kit gives an estimate of the DNA concentration. Careful consideration of the DNA profile is required before reporting because the precision within a quantification method and between different quantification methods may vary.

For the range of DNA templates specified above, significant differences between 12.5µL and 25µL total PCR volumes was not observed. The use of 12.5µL total amplification volume as the default protocol with DNA Analysis is indicated. The disadvantage of the 12.5µL total PCR volume are the physical constraints of the process i.e. a maximum of 7.5µL of sample can be used compared with 15µL for the 25µL total PCR volume. However, higher peak heights and the cost savings associated with reduced volume amplifications even with additional processes to increase the sample concentration, mitigate the disadvantage.

The implementation of PowerPlex® 21 for amplification of DNA extracts will coincide with the implementation of STRmix™. The combination of the two processes will apply a continuous biological model rather than a binary model to DNA interpretation. STRmix™ models stutter, drop out, heterozygote balance and homozygote threshold for case work samples.

The rate of drop in events has been calculated for both total PCR volumes and will be implemented in conjunction with STRmix™.

At a total input template of 0.5ng, for 25µL and 12.5µL total PCR volumes, all alleles were detected for the mixtures with ratios of 1:1, 2:1 and 5:1.

For the remaining mixtures with ratios of 10:1, 20:1, 30:1 and 50:1 of varying template levels (maximum 0.5ng), the lower contributors exhibited, sometimes quite marked, stochastic variation.

Mixture interpretation is beyond the scope of this validation and will be dealt with in the STRmix™ validation report.

8 Recommendations

1. A common LOD/LOR (16RFU/40RFU) will be used for both 3130xl instruments as outline in section 6.4.
2. The default total PCR volume will be 12.5µL. Samples can also be amplified at 25µL total PCR volume.
3. Initially samples with concentrations below 0.01ng/µL will not be routinely processed in the first instance. If necessary, these samples may undergo post extraction concentration via centrifugal filter concentration procedure to increase the concentration.
4. Initially samples with concentrations between 0.01ng/µL and 0.0176ng/µL will not be routinely amplified. These samples are considered as candidates for post extraction concentration via centrifugal filter concentration procedure to increase the concentration to the point that stochastic effects are minimized.
5. Initially samples with concentrations between 0.0176ng/µL and 0.0244ng/µL will be amplified and assessed for stochastic effects during case management to ensure the suitability of these DNA profiles for reporting.
6. Samples with concentrations above 0.0244ng/µL will be routinely amplified.
7. AI_{TH} to be set at 40% and Hom_{TH} 250RFU for extracted reference, environmental and quality control samples amplified at 12.5µL total PCR volume.
8. AI_{TH} to be set at 45% and Hom_{TH} 200RFU for extracted reference, environmental and quality control samples amplified at 25µL total PCR volume.

9. Adoption of the national Caucasian, Asian and Aboriginal sub-population datasets that DNA Analysis contributed to as part of this validation for use within statistical calculations.
10. Adoption of the locus specific stutter filter as per results section.
11. Thresholds listed in 7 and 8 are to be used as a guidelines when assessing the number of contributors in a mixture.
12. A post implementation review should be performed to review the appropriateness of points 3 – 8. The review will at minimum examine the outcomes of samples amplified within 0.0176ng/µL and 0.0244ng/µL concentration range. Similarly, all of the extracted reference samples will be reviewed with regards to the AI_{TH} and homozygote threshold.

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10 Appendix A

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PowerPlex®21 – Amplification of Extracted DNA Validation v2.0

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1 Abstract

To meet Queensland legislative requirements and core business needs, DNA Analysis has validated the PowerPlex® 21 system DNA profiling Kit. All Australian jurisdictions are expected to implement a new DNA profiling kit by the end of 2012. This project came about through the Australian and New Zealand Policing Advisory Agency (ANZPAA).

The loci within the AmpFℓSTR® Profiler Plus® and AmpFℓSTR® COfiler® kits, which are currently used in DNA Analysis, are represented within the PowerPlex® 21 system loci. This allows concordance of the kit for direct comparison and matching against existing AmpFℓSTR® Profiler Plus® crime scene and reference DNA profiles.

This validation has demonstrated that the PowerPlex® 21 system kit is fit for purpose for the amplification of extracted DNA samples processed in the Forensic DNA Analysis laboratory. A limit of reporting threshold of 40 RFU will be adopted for analysis of extracted DNA samples amplified at either 25 µL or 12.5 µL total PCR volumes. This updated validation report supports the validity of samples processed with 5 s and 3 s injection times. However, the recommendation is that the 5 s injection time is the default injection time as it results in higher peak height RFU.

The sensitivity of this next generation STR kit has greatly increased, however the increased sensitivity does not necessarily result in increased information. The results of this validation indicates that Promega's PowerPlex® 21 system is a very sensitive STR amplification kit, but to reduce the risk of type 2 errors (calling a heterozygous locus homozygous[1]) consideration needs to be given to restricting the range of DNA template added. Single source samples with DNA templates of greater than 0.5ng overload the PowerPlex® 21 system resulting in DNA profiles being unable to be interpreted. Generally samples with lower templates (reaching the often termed 'low copy number' level of 100-150pg) tend to exhibit enhanced stochastic effects as one would expect. Therefore, it should be considered whether samples around this input template level should be amplified given that interpretation of the results could be unwieldy. It would be possible to increase the template levels of samples that fall into this category by post extraction concentration or increase the total PCR volume.

At a total DNA input template of 0.5 ng, for 25 µL and 12.5 µL total PCR volumes, all alleles were detected for the mixtures with ratios of 1:1, 2:1 and 5:1.

The results from this validation support that the Promega PowerPlex®21 System is suitable for analysis of short tandem repeats (STR).

2 Introduction

To meet Queensland legislative requirements and core business needs, DNA Analysis has validated the PowerPlex® 21 system DNA profiling Kit. All Australian jurisdictions are expected to implement a new DNA profiling kit by the end of 2012. This expectation has been directed by ANZPAA, which comprises a Police Commissioner from each jurisdiction.

The initial plan endorsed by the members of the Biological Specialist Advisory Group (BSAG) involved a series of experiments designed to enable each jurisdiction to choose an appropriate STR amplification kit but using the same methodology (national approach to STR kit validation)[2].

This plan included:

1. Sensitivity and amplification volume determination
2. Population studies
3. Concordance
4. Mixture studies
5. Baseline determinations, peak balance, stutter thresholds, minimum reporting threshold and probability of drop in. This last series of experiments were devised by the Statistics Scientific Working Group (StatSWG)[3].

The plans created by BSAG and StatSWG are a significant development with respect to STR validation and interpretation within Australia. In line with current research, these plans involve the move away from a binary approach to DNA profile interpretation to a continuous model. To achieve this, a new DNA profile interpretation software (STRmix™) has been developed by forensic DNA experts & statisticians from Australia and New Zealand forensic laboratories. The validation of the STRmix™ software will be covered in the STRmix™ validation document to be issued subsequent to this report.

The PowerPlex® 21 system[4] is a new short tandem repeat (STR) kit made available to the Australian forensic laboratories in early 2012. The kit has all of the nine loci amplified in AmpFℓSTR® Profiler Plus®[5] and the six loci amplified in AmpFℓSTR® COfiler®[6] and an additional seven loci. See Table 1 for kit loci.

Table 1 - Comparison of loci in three different kits

(dye colour indicated by colour text)

PowerPlex® 21 System	AmpFℓSTR® Profiler Plus®	AmpFℓSTR® COfiler®
AMEL	AMEL	AMEL
D3S1358	D3S1358	D3S1358
D1S1656		
D6S1043		
D13S317	D13S317	
Penta E		
D16S539		D16S539
D18S51	D18S51	
D2S1338		
CSF1PO		CSF1PO
Penta D		
TH01		TH01
vWA	vWA	
D21S11	D21S11	
D7S820	D7S820	D7S820
D5S818	D5S818	
TPOX		TPOX
D8S1179	D8S1179	
D12S391		
D19S433		
FGA	FGA	

The scope of this validation is to determine for the PowerPlex® 21 system, the limit of detection (LOD), limit of reporting (LOR), the optimal total PCR amplification volume, the range of DNA template, ensure concordance of the PowerPlex® 21 system against the AmpFℓSTR® Profiler Plus® and COfiler® kits, observe the performance of mixed DNA samples and create population datasets required for statistical calculations. Secondary to this, this validation provides the data necessary for STRmix™ validation.

3 Materials

The following materials were used within this validation:

- BSD Duet 600 Series II (BSD Robotics, Brisbane, QLD,AU)
- STORstar instrument (Process Analysis & Automation, Hampshire, GB)
- MultiPROBE II PLUS HT EX with Gripper Integration Platform (PerkinElmer, Downers Grove, IL, US)
- Sterile conductive filtered Roborack 25µL disposable tips (PerkinElmer, Downers Grove, IL, USA)
- 5804 centrifuge (Eppendorf AG, Hamburg, DE)
- 5424 centrifuge (Eppendorf AG, Hamburg, DE)
- Thermomixer (Eppendorf AG, Hamburg, DE)

- MixMate (Eppendorf AG, Hamburg, DE)
- Vortex (Ratek Instruments Pty Ltd, Melbourne, VIC, AU)
- Micro centrifuge (Tomy, Tokyo, JP)
- 1.5 mL screw-cap tubes (Axygen Inc. Union City, CA, US)
- Pipettes (Eppendorf, Hamburg, DE and Thermo Fisher Scientific(Finnpipette), Waltham, MA, US)
- Pipette tips (VWR International LLC Radnor, PA, US and Molecular Bioproducts Inc., San Diego, CA, US)
- 96-well PCR plates(Axygen Inc. Union City, CA, US)
- 2.0 mL sterile screw-cap tubes (Axygen Inc. Union City, CA, US)
- Plate septas (Axygen Inc. Union City, CA, US)
- Adhesive film (QIAGEN, Hilden, DE)
- FTA™ collection kits (Whatman™ GE Healthcare, Buckinghamshire, GB)
- Positive controls (DNA Analysis Unit, Brisbane, QLD, AU)
- TNE (DNA Analysis Unit, Brisbane, QLD, AU)
- Proteinase K (20 mg/mL) (Sigma-Aldrich® Corporation, St Louis, MO, US)
- Dithiothreitol (Sigma-Aldrich® Corporation, St Louis, MO, US)
- Trigene (Medichem International, Kent, GB)
- Ethanol (Recochem Incorporated, Wynnum, QLD,AU)
- Bleach (Ionics Australasia Pty Ltd., Lytton, QLD, AU)
- Amphyl (Rickitt Benckiser Inc. Parsippany, NJ, US)
- Sarcosyl (Sigma-Aldrich® Corporation, St Louis, MO, US)
- Nanopure water (DNA Analysis Unit, Brisbane, QLD, AU)
- Quantifiler™ Human DNA Quantification kits (Life Technologies Applied Biosystems, Foster City, CA, US)
- AB 7500 Real Time PCR System (Life Technologies Applied Biosystems, Foster City, CA, US)
- GeneAmp® PCR system 9700 (Life Technologies Applied Biosystems, Foster City, CA, US)
- ABI 3130*xl* Genetic Analyzer (Life Technologies Applied Biosystems, Foster City, CA, US)
- Hi-Di™ Formamide (Life Technologies Applied Biosystems, Foster City, CA, US)
- 3130 POP-4™ Polymer (Life Technologies Applied Biosystems, Foster City, CA, US)
- Running Buffer (Life Technologies Applied Biosystems, Foster City, CA, US)

- DNA IQ™ Casework Pro Kit for Maxwell® 16 (Promega Corp., Madison, WI, US)
- Promega PowerPlex® 21 system (Promega Corp., Madison, WI, US)
- Promega CC5 Internal Lane Standard 500 (Promega Corp., Madison, WI, US)
- Promega PowerPlex 5 Dye Matrix Standard (Promega Corp., Madison, WI, US)
- Promega PowerPlex® 21 Allelic Ladder Mix (Promega Corp., Madison, WI, US)
- 2800M Control DNA, 10ng/µl (Promega Corp., Madison, WI, US)
- Water, Amplification Grade (Promega Corp., Madison, WI, US)

4 Methods

4.1 Sample Selection

All samples used in this validation were sourced from the internal DNA Analysis staff DNA database, Collaborative Testing Services (CTS) DNA testing samples, or reference samples that had the National Criminal Investigation DNA Database (NCIDD) categories of Volunteer Unlimited Purpose (VUP) or Suspect (SCT). Permission to use reference samples from NCIDD was obtained from the Queensland Police Service (QPS).

4.2 Selection of Sub-Population Samples

4.2.1 Aboriginal and Torres Strait Islanders Sub-Populations

Aboriginal samples:

Aboriginal samples previously profiled as part of the sub-population dataset for the validation of AmpFℓSTR® Profiler Plus® loci were recommended as the best samples to use for compilation of the Aboriginal sub-population dataset for the Promega PowerPlex®21 system. The samples are self-declared Aboriginal ethnicity and were collected over a number of years.

220 Aboriginal samples were randomly selected from the Aboriginal dataset (545 total) previously profiled with AmpFℓSTR® Profiler Plus®. Microsoft Excel RANDBETWEEN function was used and duplicates removed until 220 unique samples were identified for profiling.

These 220 samples were originally extracted using Chelex. The extracts for the 220 samples were viewed for sufficient volume. 201 samples with sufficient volume were identified and given new population dataset barcodes.

Torres Straits Islander samples:

A list of FTA™ samples previously profiled with AmpF*l*STR® Profiler Plus® resulting in a full profile and identified as self-declared Torres Strait Islander ethnicity in AUSLAB were compiled to be used for the Aboriginal sub population dataset.

599 samples were listed and after further filtering, including removing duplicates, 249 Torres Strait Islander samples remained. Of the 249 Torres Strait Islander samples listed 223 samples were randomly selected for processing. Samples were given new population dataset barcodes

4.2.2 Caucasian Sub-Population

A list of FTA™ samples previously profiled with AmpF*l*STR® Profiler Plus® resulting in a full profile and identified as Caucasian ethnicity in AUSLAB were compiled to be used for the Caucasian sub-population dataset.

From this list 210 samples were selected and 208 were selected for processing as two were deemed unsuitable. Samples were given new population database barcodes.

4.2.3 South East Asian Sub-Population

A list of FTA™ samples previously profiled with AmpF*l*STR® Profiler Plus® resulting in a full profile and identified as South East Asian ethnicity in AUSLAB were compiled to be used for the South East Asian population dataset.

157 samples were listed and after further filtering 141 South East Asian samples remained. These 141 samples were given new population database barcodes.

4.3 Collection Procedure for FTA™ Cards

Where staff samples were entirely consumed during processing, additional samples were collected. New FTA™ samples were collected using FTA™ Collection kits. A foam swab was used to collect buccal cells from each cheek for one minute then applied to the FTA™ card[7]. The FTA™ card was stored at room temperature until required.

4.4 FTA™ Punching Method

1. PCR Amplification mix was created as required.
2. 25 µL (full) or 12.5 µL (half) of PCR amplification mix was added to a clean 0.2 mL 96 well PCR plate.
3. Plate was sealed and centrifuged to ensure PCR amplification mix was at the bottom of the wells.

4. Each FTA™ sample was punched with the 1.2 mm diameter die into the 96 well PCR plate using the BSD Duet 600 Series II.
5. 1 µL of 2800M Control DNA was added to the Positive control well.
6. 1 x 1.2 mm punch of a blank FTA™ card was added to the blank control well
7. Amplification mix without FTA™ card was used as a negative control.
8. The plate was sealed and centrifuged briefly to pull the FTA™ cards to the bottom of the plate wells.

4.5 FTA® Punching Method 2

1. 7.5 µL of Water, Amplification Grade was added to the required wells.
2. Plate was sealed and centrifuged to ensure the water was at the bottom of the wells.
3. Each FTA® sample was punched with the 1.2 mm diameter die into the 96 well PCR plate using the BSD Duet 600 Series II.
4. 1 µL of 2800M Control DNA was added to the Positive control well.
5. 1 x 1.2 mm punch of a blank FTA® card was added to the blank control well
6. PCR Amplification mix without FTA® card was used as a negative control.
7. PCR Amplification mix was created as required and 5 µL added to each well.
8. The plate was sealed and centrifuged briefly to pull the FTA® cards to the bottom of the plate wells.

4.6 Punching for Extraction

FTA™ samples were prepared for extraction by punching four paper spots of 3.2 mm diameter into 1.5 mL/2 mL tubes using the BSD Duet 600 according to standard operating procedure 24823 V4.0 "FTA™ Processing and Work Instructions".

4.7 Extraction

FTA™ samples requiring DNA extraction were processed using the DNA IQ™ Casework Pro Kit for Maxwell®16 according to standard operating procedure 29344 V4.0 "DNA IQ™ Extraction using the Maxwell®16".

4.8 Preparation of DNA Stock Solutions

Samples used to make dilution series required a stock solution to be prepared. FTA™ samples were selected and punched in duplicate for

extraction (as outlined in section 4.6) then extracted (as outlined in section 4.7). The duplicate samples were pooled into a single tube and quantified twice (as outlined in section 4.9).

4.9 Procedure for Creating a Dilution Series

The samples used to make dilution series were diluted with Water, Amplification Grade provided with the Promega PowerPlex®21 System. Spreadsheets for calculating the normalisation and dilution series were written to outline the serial dilutions required to obtain the specified concentrations

4.10 Quantification

All preparations of reactions were performed using MultiPROBE II plus HT EX platform according to standard operating procedure 19977 V8.0 "Automated Quantification of Extracted DNA using the Quantifiler™ Human DNA Quantitation Kit".

4.11 Amplification Set up

For the experiments that used extracted DNA, all amplification reactions were performed using a MultiPROBE II plus HT EX platform. A new protocol called PowerPlex® 21 amp setup v1.0 was created using WinPrep® software and utilised for amplifications at 25 µL and 12.5 µL total PCR volumes. The protocol is saved and stored on the C drive of the MultiPROBE II plus HT EX platform computer. Table 2 outlines the components of the amplification mix per sample.

Table 2 - Amplification mix per sample.

Kit components	Volumes (µL)	Volumes (µL)
PowerPlex® 21 5x Master Mix	5.0	2.5
PowerPlex® 21 5x Primer Pair	5.0	2.5
Sample	15	7.5
Total Volume	25	12.5

4.12 Amplification Conditions

Table 3 lists the PCR cycling conditions used in this validation. All PCR reactions were carried out in 96 well plates (Axygen Inc.) on GeneAmp® 9700 thermal cyclers

Table 3 - PCR cycling conditions used for PowerPlex®21 system

PowerPlex® 21 Kit	Direct amp	Standard
thermal cycler mode	Max	Max
	25,26 or 27 cycles	30 cycles
Activation	96 °C for 1 minute	96 °C for 1 minute
Cycling	94 °C for 10 seconds 59 °C for 1 minute 72 °C for 30 seconds	94 °C for 10 seconds 59 °C for 1 minute 72 °C for 30 seconds
Extension	60 °C for 20 minutes	60 °C for 10 minutes
	4 °C Soak	4 °C Soak

4.13 DNA Fragment Analysis

The plates for DNA fragment analysis were prepared as recommended by the manufacturer, using a combination of Hi-Di™ formamide, size standard and sample as outlined below.

Formamide: size standard mixture composed of

[(2.0 µl CC5 Internal Lane Standard 500) x (number of injections)] + [(10.0 µL Hi-Di™ formamide) x (number of injections)]

Formamide: size standard mixture **12 µL**

PCR product or allelic ladder **1 µL**

The prepared plate was then centrifuged to remove bubbles, denatured at 95 °C for 3 minutes then chilled in an ice block in the freezer for 3 minutes. The prepared plates were then run on a Applied Biosystems 3130*xl* Genetic Analyzer.

The PCR fragments were separated by capillary electrophoresis (CE) using a Applied Biosystems 3130*xl* Genetic Analyzer set up as outlined in Table 4.

Table 4 - CE Protocol conditions.

Injection time	Injection voltage	Run time
5 s	3 kV	1500 s
3 s	3 kV	1500 s

4.14 Profile Interpretation 1

All DNA profiles were analysed with GeneMapper® ID-X v1.1.1. The analysis panel used was PowerPlex_21_IDX_v1.0. The thresholds were set as follows:

1. Heterozygote threshold was set at 40 RFU
2. Limit of Detection (negative controls) was set at 16 RFU
3. Individual locus stutter thresholds were set as per Promega PowerPlex® 21 Stutter filter
4. Homozygote threshold was set to 200 RFU

4.15 Profile Interpretation 2

All DNA profiles were analysed with GeneMapper® ID-X v1.1.1. The analysis panel used was PowerPlex_21_IDX_v1.0. The rules were set as follows:

1. Samples were analysed at 1 RFU.
2. All known alleles, -1 repeat and +1 repeat stutter (+/-4 bp or +/-5 bp) of known alleles, known artefacts and spectral pull-up were removed. As defined by Promega artefact peaks in the N-2 bp and/or N+2 bp position at D1S1656, D6S1043, D13S317, vWA, D21S11, D7S820, D5S818, D12S391 and D18S51 loci and in the N-1 bp position at Amelogenin were also removed.
3. Any peaks determined to be CE carry over peaks were also removed. CE carry-over is defined as the physical transfer of DNA from one injection to the next.

4.16 Profile Interpretation 3

All samples were analysed with GeneMapper ID-X v1.1.1 with the stutter thresholds set to zero. The analysis panel used was PowerPlex_21_IDX_v1.1.

1. Samples were analysed at 20 RFU
2. Loci where the two main alleles were one repeat apart were excluded from analysis.

4.17 Profile Interpretation 4

All samples were analysed with GeneMapper ID-X v1.1.1 with the stutter thresholds set to zero. The analysis panel used was PowerPlex_21_IDX_v1.1.

1. Samples were analysed at 20 RFU
2. -2 repeat stutter peaks were recorded if they were distinct from baseline and not in a pull-up or +1 repeat stutter position.

5 Experimental Design

5.1 Sub-Population Datasets

As part of the national approach to implementation of next generation STR amplification kits, the creation of three national sub-population datasets was undertaken. Each jurisdiction contributed DNA profiles for each sub-population Caucasian, Aboriginal and South East Asian to Jo-Anne Bright (ESR) and John Buckleton (ESR) for analysis.

5.1.1 Aboriginal dataset

In this experiment 201 Aboriginal samples were transferred to appropriate tubes and the DNA concentrations determined as outlined in Method 4.10.

The samples were amplified with the recommended DNA template input of 0.5 ng in a 25 µL total PCR volume. Three plates were amplified using the PowerPlex®21 system kit with each plate including a positive amplification control (2800M Control DNA) and a negative amplification control (Water, Amplification Grade). The three plates were prepared as per Method 4.11.

Standard amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13 and 4.14.

5.1.2 Torres Strait Islander dataset

In this experiment 223 Torres Strait Islander samples were punched across three 96 well plates as outlined in section 4.4. Each sample had one spot punched, a total PCR volume of 12.5 µL and was directly amplified at 26 PCR cycles.

Amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13 and 4.14.

5.1.3 Caucasian dataset

In this experiment 208 Caucasian samples were punched across three 96 well plates as outlined in section 4.4. Each sample had two spots punched, a total PCR volume of 25 µL and was directly amplified at 25 PCR cycles.

Caucasian samples that did not produce a full PowerPlex®21 profile were punched again using 2 spots, a total PCR volume of 25 µL and was directly amplified at 26 PCR cycles.

Amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13 and 4.14.

5.1.4 South East Asian dataset

In this experiment 141 South East Asian samples were punched across two 96 well plates as outlined in section 4.5. Each sample had one spot punched, a total PCR volume of 12.5 µL and was directly amplified at 26 PCR cycles.

South East Asian samples that did not produce a full PowerPlex®21 profile were punched for extraction, extracted, quantified and amplified as outlined in Methods 4.6, 4.7, 4.8 and 4.10.

Amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13 and 4.14.

5.2 Concordance

155 samples purchased from Collaborative Testing Services (CTS) as external Proficiency Tests were used to test the concordance of the PowerPlex® 21 system. These samples had previously been extracted, quantified and amplified with AmpFℓSTR® Profiler Plus® and AmpFℓSTR® COfiler® kits.

The samples were amplified with the recommended DNA template input of 0.5 ng in a 12.5 µL total PCR volume. Two plates were amplified using the PowerPlex®21 system kit with each plate including a positive amplification control (2800M DNA) and a negative amplification control (amplification grade water). The two plates were prepared as outlined in Method 4.11.

Amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13 and 4.14.

The alleles obtained from these samples were compared with the CTS published alleles. Three loci could not be compared as CTS did not publish results for the D12S391, D1S1656 and D6S1043 loci.

5.3 Baseline Determination

To determine the limit of detection (LOD) and the limit of reporting (LOR), the baseline (background) was assessed.

Ten samples from the Caucasian sub-population dataset that exhibited high heterozygosity were used for baseline determination.

The samples were prepared as Methods 4.6, 4.7, 4.8, 4.9, 4.10, 4.11.

Ten samples diluted in ten steps (10x10) outlined in Table 5 were used for the baseline calculations. Each dilution set was amplified at 25 µL and 12.5 µL total PCR volumes.

50 negative samples were also amplified at 25µL and 12.5µL total PCR volumes.

Table 5 - Total DNA input for each dilution

Dilution	Total DNA (ng)
1	0.500
2	0.447
3	0.394
4	0.342
5	0.289
6	0.236
7	0.183
8	0.131
9	0.078
10	0.025

Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13, 4.14 and 4.15.

The average peak height RFU (μ_{Pk}) for each dye channel was calculated using the AVERAGE function (Arithmetic mean) in Microsoft Excel. The standard deviation (σ_{Pk}) was calculated using the STDEV function in Microsoft Excel.

The thresholds were calculated as follows:

The limit of detection (LOD) was calculated from Equation 1[8].

Equation 1

$$LOD = \mu_{PK} + 3\sigma_{PK}$$

The limit of reporting (LOR) also known as the analytical threshold (AT) was calculated from Equation 2[8].

Equation 2

$$LOR = \mu_{PK} + 10\sigma_{PK}$$

5.4 Sensitivity 1

This experiment tested the sensitivity of PowerPlex® 21 system at amplification volumes of 25 µL and 12. 5µL for DNA template inputs from 4 ng to 1 pg. These were all processed with a 5 s injection time.

Two staff (one male and one female) with the most heterozygous DNA profile processed with AmpFℓSTR® Profiler Plus® and AmpFℓSTR COfiler® kits were selected for testing[9]. Heterozygous loci provide more information with respect to allele drop out and peak balance.

FTA™ cards were collected, processed, extracted, stock solutions prepared, quantified and dilution series prepared as outlined in Methods 4.6, 4.7, 4.8, 4.9 and 4.10.

Each donor had 9 dilutions prepared as outlined in Table 6. These dilutions were amplified in duplicate with a total amplification volume of 25 µL and 12.5 µL. Each amplification plate included the kit positive control (2800M Control DNA) and a negative control (Water, Amplification Grade).

Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.11, 4.12, 4.13 and 4.14.

Table 6 - Total DNA input for sensitivity 1

DNA Template Input (ng)
4
2
1
0.5
0.1
0.05
0.01
0.005
0.001

5.5 Sensitivity 2

To assess the differences between the two total PCR volumes with respect to low DNA extract concentrations a second sensitivity experiment was performed.

This experiment tested a dilution series of the same samples used in sensitivity 1 at low DNA templates outlined in Table 7. Each dilution was amplified in duplicate at 25 µL and 12.5 µL. These were all processed with a 5 s injection time.

Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.11, 4.12, 4.13 and 4.14.

Table 7 - Concentration, DNA template input for each dilution.

Concentration (ng/µL)	Volume of sample added to 25 µL reaction volume	Total DNA template input (ng)	Volume of Sample added to 12.5 µL volume reaction	Total DNA template input (ng)
0.01	15	0.15	7.5	0.075
0.005	15	0.075	7.5	0.0375
0.0025	15	0.0375	7.5	0.01875
0.00125	15	0.01875	7.5	0.009375
0.000625	15	0.009375	7.5	0.004688
0.0003125	15	0.004688	7.5	0.002344
0.00015625	15	0.002344	7.5	0.001172
0.000078125	15	0.001172	7.5	0.000586

5.6 Drop In

50 negative samples were amplified alongside the baseline (10x10) samples at 25 µL and 12.5 µL. Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.11, 4.12, 4.13 and 4.15.

The negative samples were analysed at 1 RFU using GeneMapper ID-X v1.1.1 to determine if any peaks above 20 RFU were present. Known artefacts, carry-over and pull-up were removed and not included in the analysis.

5.7 Stutter

To determine the thresholds for -1repeat and +1repeat stutter peaks 342 samples from the Aboriginal data set, baseline samples (10 x10), sensitivity 1 and sensitivity 2 were amplified at 25µL and 255 samples from 155 CTS samples and baseline samples were amplified at 12.5 µL.

Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.11, 4.12, 4.13 and 4.16.

The stutter ratio (SR) was calculated for each locus as per Equation 3.

Equation 3

$$SR = E_S/E_A$$

SR = Stutter Ratio, E_S = Stutter Height, E_A = Allele Height

The stutter threshold (ST)[4] for each locus was calculated as per Equation 4.

Equation 4

$$ST = \mu_{SR} + 3\,\sigma_{SR}$$

ST = Stutter Threshold, μ_{SR} = average stutter ratio, σ_{SR} = standard deviation of stutter ratio.

The stutter results were also processed with a multiple regression analysis by Jo-Anne Bright for use within the STRmix™ validation and STRmix™ settings[10].

To determine thresholds for -2 repeat stutter peaks, 243 samples (155 CTS and 88 reference samples) were amplified at 12.5 µL and 25 µL. Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.11, 4.12, 4.13 and 4.17.

The stutter ratio (SR) was calculated for each locus using Equations 5 & 6, modified versions of Equation 3.

Equation 5

$$SR = E_{S-2}/E_{S-1}$$

SR = Stutter Ratio, E_{S-2} = -2 repeat stutter Height, E_{S-1} = -1 repeat Stutter Height

Equation 6

$$SR = E_{S-2}/E_A$$

SR = Stutter Ratio, E_{S-2} = -2 repeat stutter Height, E_A = Allele Height

The -2 repeat stutter threshold (ST) [4] for each locus was calculated as per Equation 4 from the main allele peak.

5.8 Peak Balance

The samples from the baseline experiment (10 x10 in section 5.3) were used to calculate peak height ratios and an allelic imbalance threshold to be used for reference samples and as a guide for determining the number of contributors to a mixture.

5.8.1 Peak Height Ratio and Allelic imbalance threshold

Peak height ratios for heterozygote loci (1127 alleles for 12.5 µL and 1094 alleles for 25 µL total PCR volumes) were determined by dividing the lower peak height by the higher peak height. Loci where the two main alleles were one repeat apart or were homozygous were excluded from analysis.

The peak height ratio (PHR) was calculated for each locus as per equation 5 [11].

Equation 7

PHR = LPH / HPH

PHR = Peak Height Ratio, LPH = Lower Peak Height, HPH = Higher Peak Height

The average peak heights and standard deviation of peak height ratio were calculated using the Microsoft Excel AVERAGE and STDEV worksheet functions.

The allelic imbalance threshold (AI) was calculated as per Equation 6[12, 13]

Equation 8

$$AI_{TH} = \mu_{PHR} - 3\sigma_{PHR}$$

AI_{TH} = Allelic Imbalance threshold, μ_{PHR}= overall average PHR, σ_{PHR} = standard deviation of the PHR.

5.8.2 Homozygote threshold

The homozygote threshold is the threshold above which you can be confident that a heterozygote locus will not be incorrectly called as a homozygote locus. It was calculated using the following methods

Method 1 – As previously described in the internal validation[14] of peak heights and allelic imbalance thresholds and illustrated below:

Equation 9

$$Th_{Hom} = LOR \times (1 / AI_{TH}) \times 2$$

The LOR used for this calculation is from 5.3 and AI_{TH} was determined in 5.8.2.

Method 2 – As described in the Promega Internal validation guidelines[15] determined from a plot of allelic imbalance versus the lower RFU of a heterozygote pair. The homozygote threshold is assigned at the point at which there is a rapid drop off in peak height ratio.

5.9 Drop Out

To aid in determining the default total PCR volume and template DNA range a series of drop out analyses were performed on the baseline samples (section 5.4), sensitivity experiments (sections 5.3 & 5.5) and population datasets (section 5.2).

5.9.1 Drop out 1

The samples from the sensitivity 1 experiment (section 5.3) were used to determine at what RFU the partner of a heterozygote pair drops out. The data was interpreted as outlined in section 4.13. Homozygote peaks, excess samples and no size data were excluded from data analysis. Heat maps were used to summarise the data.

5.9.2 Drop out 2

Samples processed at 25 µL and 12.5 µL were analysed to determine the threshold when an allele most frequently drops out.

334 DNA profiles amplified at 25 µL (from section 5.1.1, 5.3, 5.4 and 5.5) and 279 DNA profiles amplified at 12.5µL (from section 5.2, 5.3, 5.4 and 5.5) were analysed as outlined in Method 4.13.

Homozygote peaks, excess samples and no size data were excluded from both sets of data.

Data was split between 3 s injection times and 5 s injection times

5.9.3 Drop out 3

The samples from the baseline samples (section 5.4) and sensitivity experiments (section 5.3 & 5.5) experiments (156 samples) were analysed to record the peak height at which a heterozygote paired allele was lost. The data was interpreted as outlined in Method 4.13.

Homozygote peaks, excess samples and no size data were excluded from data analysis.

Data was split between 3 s injection times and 5 s injection times

5.10 Mixture Studies 1

In experiment 4 samples, two female and two male samples with high heterozygosity were selected, from the Caucasian dataset and CTS samples, to be combined to make mixed DNA samples. The samples were created as Methods 4.3, 4.4, 4.6, 4.7 and 4.10.

One female sample was combined with one male profile to create a two person mixture, the same female sample was combined with the two male samples to create a three person mixture and two female samples and two male samples were combined to create a four person mixture. The amount of sample required from each contributor to create the mixture ratio was calculated using excel spreadsheets . Varying contributor ratios were made for each of the mixture combinations as outlined in Table 8. Each mixture combination was amplified in duplicate at a variety of DNA templates.

Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.11, 4.12, 4.13 and 4.16.

Table 8 - Mixture ratios

Mixture Ratio	Template (ng)
Female:Male	
50:1	0.500
	0.250
	0.125
30:1	0.500
20:1	0.500
	0.250
	0.125
10:1	0.500
	0.125
5:1	0.500
	0.125
2:1	0.500
	0.06
1:1	0.500
Female:Male:Male	
20:10:1	0.500
	0.125
10:5:1	0.500
5:2:1	0.500
	0.125
Female:Male:Male:Female	
5:3:2:1	0.500
	0.125

The mixture ratio was calculated for each DNA profile and compared to the admixture ratio to determine whether there is any variability and whether the mixture ratio can be expected to hold across the profile.

The DNA profiles were analysed to determine at what ratio the minor contributor would be expected to drop out.

6 Results and Discussion

6.1 Population Datasets

Results were tabulated in the following format Unique Sample ID, Race ID, Marker, Allele 1 and Allele 2. Table 9 summarises the number of profiles for each sub-population submitted for analysis. The total number refers to the size of the Australian combined sub-population datasets.

Table 9 - Summary of number of profiles for each sub-population submitted.

	Caucasian	Aboriginal	SE Asian
DNA Analysis, FSS	139	309	126
Dataset total	1707	1778	990

Data generated for the three sub-population datasets were analysed by Jo Bright and John Buckleton and used in STRmix™ for statistical analysis[16, 17].

6.2 Concordance

All samples (number of alleles = 4644) tested were found to be concordant to the CTS reported DNA profiles. Table 10 displays the number of times a particular allele was seen at each locus within the laboratory.

Different DNA amplification kits may contain different primers for each locus. Comparison of allele calls (concordance) is required to ensure that each kit gives consistent allele designations, as mismatches or null alleles will affect matching on NCIDD or within a case. The current kits used by the DNA Analysis are AmpFℓSTR® Profiler Plus® and AmpFℓSTR COfiler® DNA amplification kits. Both of these use primers developed by, and manufactured by Life technologies. There are known issues with these kits such as a reverse primer binding mutation at the D8S1179 locus[18], vWA locus[19] and FGA locus[20]. The PowerPlex® 21 kit uses different primer sequences. All alleles tested were found to be concordant. As primer binding mutations and null alleles have been observed within DNA Analysis, any resulting mismatches on NCIDD will need to be retested using PowerPlex® 21.

Table 10 - Observed number of allele concordances

Allele Size	D3S1358	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	D8s1179	D19S433	FGA
2.2								5									
3.2								2									
5			17					5	1								
6									44					7			
7			32				4	5	75			4	3	4			
8		23	22	4			8	9	42			68	6	133	1		
9		21	10	44			4	48	50			28	13	34	4		
9.3									69								
10		11	25	26	2		69	31	3			80	19	13	11	1	
10.3									1								
11		79	26	83	2		77	45		1		65	91	65	14	6	
11.2																1	
12	1	86	40	78	37		93	51				26	100	11	37	26	
12.2																4	
13	1	48	27	46	30		16	44		3		9	15	1	96	72	
13.2																5	
14	41	20	15	2	38	1	1	8		28			3		71	67	
14.2																9	
15	84		12		42	1		3		43					43	23	
15.2																8	
16	56		13		48	14		1		63					10	5	
16.2																4	
17	67		10		36	46				67					1		
17.2																1	
18	36		6		18	19				57					1		4
18.2																1	
19	4		2		13	33				20							23
20			1		10	28				2							39
20.2																	2
21			2		5	19				2							35
22			2		2	13				1							56
22.2																	3
23					1	20											48
24						13											36
25						22											28
26						8					3						10
27						1					7						4
28											61						
29											47						1
29.2											1						
29.3											1						
30											78						
30.2											10						
31											18						
31.2											22						
32											5						
32.2											25						
33.2											9						
35											2						

6.3 Baseline Determination

The thresholds determined by the baseline experiments are the limit of detection (LOD) and limit of reporting (LOR). The use of thresholds for reporting is essentially a risk assessment[21], if the thresholds are set too low then labelling of artefacts and noise may occur, if set too high then real peaks will not be labelled and information will be lost[1, 11].

Type 1 errors are defined as false labelling of noise peaks. LODs calculated from negative samples may not be optimal for medium-high template samples, as the baseline will differ between positives and negative samples[22].

Type 2 errors are defined as false non-labelling of alleles. If the LOD is set too high, then low level samples may have a heterozygous locus called as a homozygous locus[1, 22-24].

The LOR is the threshold in which a peak can be confidently distinguished from the background fluorescence (baseline). Several methods can be used to determine this threshold.

For the method used here[8] the LOR is derived from the mean baseline plus ten standard deviations (Equation 2).

The LOD is the lowest signal that can be distinguished from the background fluorescence (baseline) and may vary between CE instruments.

Previously in DNA Analysis [14] baseline for the AmpF*l*STR® Profiler Plus® kit was determined using the BatchExtract software v0.16. The LOD was calculated using Equation 1. This approach of using the mean and three standard deviations would account for 99.73% of baseline fluorescence.

The files generated by GeneMapper ID-X v1.1.1 are not compatible with the BatchExtract software without modification. For this validation an equivalent process for measuring the baseline as described by Promega was used with some modifications to the types of samples used. For this validation samples containing DNA were used to determine baseline fluorescence.

Table 11 shows the results determined from the baseline calculations when the samples were amplified at 25 µL. The highest average peak height (5.74 RFU) and the highest standard deviation (3.21) was in the TMR (yellow) channel from run 2 on 3130*xl* A. The TMR (yellow) channel for run 2 on 3130*xl* A also yielded the highest LOD (15.37) and highest LOR (37.84). The LOD was rounded to 16 RFU and the LOR was rounded to 40 RFU and is to be used for all dye channels for samples amplified using a total amplification volume of 25 µL.

Table 11 - Baseline results for amplifications at 25 µL

		3130*xl* A run 1	3130*xl* A run 2	3130*xl* B run 1	3130*xl* B run 2	Overall 3130*xl* A & B run 1 & 2
Fluorescin (Blue)	μ_{PK}	2.33	2.58	1.90	1.68	2.11
	σ_{PK}	1.55	2.05	1.01	0.89	1.52
	LOD	6.99	8.73	4.93	4.36	6.68
	LOR	17.86	23.07	12.01	10.59	17.35
JOE (Green)	μ_{PK}	3.51	3.83	2.25	2.16	2.94
	σ_{PK}	2.34	2.62	1.04	1.29	2.12
	LOD	10.54	11.68	5.37	6.02	9.30
	LOR	26.94	29.99	12.65	15.02	24.14
TMR (Yellow)	μ_{PK}	5.29	5.74	3.33	3.07	4.32
	σ_{PK}	2.73	3.21	1.27	1.66	2.68
	LOD	13.47	15.37	7.15	8.05	12.37
	LOR	**32.55**	**37.84**	**16.06**	**19.66**	**31.16**
CXR (Red)	μ_{PK}	2.22	2.44	2.02	1.78	2.09
	σ_{PK}	1.36	1.54	0.89	1.01	1.35
	LOD	6.29	7.05	4.69	4.81	6.16
	LOR	15.79	17.79	10.93	11.88	15.63
CC5 (Orange)	μ_{PK}	1.76	1.99	1.14	1.36	1.66
	σ_{PK}	1.30	1.80	0.44	1.39	2.44
	LOD	5.68	7.38	2.47	5.52	9.00
	LOR	14.81	19.94	5.58	15.24	26.11
Overall	μ_{PK}	3.41	3.72	2.44	2.22	2.79
	σ_{PK}	2.45	2.80	1.33	1.39	2.29
	LOD	10.76	12.13	6.23	6.40	9.65
	LOR	**27.91**	**31.76**	**15.54**	**16.14**	**25.65**

Table 12 shows the results determined from the baseline calculations when the samples were amplified at 12.5 µL. The highest average peak height (6.06 RFU) was in the TMR (yellow) channel from the run on 3130xl A and the highest standard deviation (4.41) was in the JOE (green) channel from the run on 3130*xl* A. The TMR (yellow) channel for the run on 3130*xl* A yielded the highest LOD (18.50) and the JOE (green) channel yielded the highest LOR (48.60). It was noted on 3130*xl* A the baseline was raised more than expected compared to other baseline runs on the same instrument and baseline runs on 3130*xl* B. This could be due to a prolonged period between spectral calibrations, aging reagents and arrays and was taken into consideration when setting thresholds. With natural variations, the results from run to run and instrument may vary, by using the mean + 10SD for the LOR, although the baseline itself may shift, the LOR will always be greater than the LOD even if baseline is either increased or decreased on any given run. By using an "over all" result, the standard deviation is increased due to the difference in fluorescence between instruments, and this then gets factored into the overall LOR.

The highest overall LOD (15.70) was in the TMR (yellow) channel and was rounded to 16 RFU and the highest overall LOR (42.27) was in the JOE (green) channel and was rounded to 40RFU.

In an effort to eliminate error and confusion a single LOD and LOR value is to be used for both instruments.

Table 12 - Baseline results for amplifications at 12.5 µL

		3130x/ A 12.5 µL	3130x/ B 12.5 µL	Overall 3130x/ A & B 12.5 µL
Fluorescin (Blue)	μ_{PK}	3.10	2.19	2.64
	σ_{PK}	3.66	2.72	2.99
	LOD	14.07	10.36	11.59
	LOR	39.67	29.42	32.49
JOE (Green)	μ_{PK}	4.46	2.69	3.62
	σ_{PK}	4.41	2.86	3.86
	LOD	17.70	11.26	15.22
	LOR	48.60	31.28	42.27
TMR (Yellow)	μ_{PK}	6.06	3.58	4.83
	σ_{PK}	4.15	2.43	3.63
	LOD	18.50	10.88	15.70
	LOR	**47.52**	**27.92**	**41.08**
CXR (Red)	μ_{PK}	2.87	2.10	2.49
	σ_{PK}	2.32	1.28	1.93
	LOD	9.84	5.94	8.27
	LOR	26.11	14.90	21.75
CC5 (Orange)	μ_{PK}	2.38	1.66	2.02
	σ_{PK}	2.31	1.87	2.14
	LOD	9.33	7.26	8.84
	LOR	25.53	20.33	23.40
Overall	μ_{PK}	3.94	2.54	3.32
	σ_{PK}	3.87	2.46	3.30
	LOD	15.56	9.91	13.21
	LOR	**42.68**	**27.10**	**36.28**

μ_{PK} = Average peak height, σ_{PK} = Standard Deviation, LOD = limit of detection, LOR = Limit of Reporting

Additional baseline calculations have been performed since the initial validation was performed [25-28] as critical components of the ABI 3130xl instruments such as the lasers and IAD filters have been replaced. See Table 13 below.

Table 13 – Summary of baseline experiments

Instrument	Description	inj time (s)	μ peak height (RFU)	σ peak height (RFU)	LOD (RFU)	LOR (RFU)	PCR vol (μL)
3130xlA	Original	5	3.41	2.45	11	28	25
3130xlA	Original	5	3.32	3.30	13	36	12.5
3130xlA	Rerun	5	3.72	2.80	12	32	25
3130xlA	Post laser	5	3.34	2.47	11	28	25
3130xlA	Post laser	5	3.89	3.80	15	42	12.5
3130xlB	Original	3	2.44	1.33	6	16	25
3130xlB	Rerun	3	2.22	1.39	6	16	25
3130xlB	Post IAD filter	3	2.23	1.21	6	14	25
3130xlB	Post IAD filter	3	2.49	1.94	8	22	12.5
3130xlB	Injection time change	5	2.96	1.92	9	22	25
3130xlB	Injection time change	5	3.54	3.16	13	35	12.5
3130xlB	Post laser	5	3.78	2.91	12	33	25
3130xlB	Original	3	2.54	2.46	10	27	12.5

Although the results obtained from these experiments vary slightly from the initial validation all have been below the threshold set within this validation report.

6.4 Sensitivity

All PCR amplification kits are optimised for a particular total reaction volume by the manufacturer; but it is commonplace to reduce the total PCR reaction volume to increase the sensitivity[29-32] and reduce processing costs[31]. Two sensitivity experiments were performed, in addition to the baseline experiments.

To contrast and compare the effect of total PCR volume on DNA profiles, the same dilution series were amplified at two different total PCR volumes (25 μL and 12.5 μL) using 30 PCR cycles.

The results for the amplification of the two donors at 25 μL and 12.5 μL are summarised in Table 14 .

Table 14 - Summary of the 2 donors amplified at 25 µL and 12.5 µL (Supplementary data files specified in 10.6.1) $\mu_{Alleles}$ – average number of alleles called, μ_{PH} – the average peak height, Max_{PH}- maximum peak height, Min_{PH} – minimum peak height, μ_{PHR}- average peak height ratio

	Template (ng)	$\mu_{Alleles}$	μ_{PH} (RFU)	Max_{PH} (RFU)	Min_{PH} (RFU)	μ_{PHR} (RFU)
Donor1_25 µL	4	N/A	NAD XS	N/A	N/A	N/A
	2	N/A	XS	N/A	N/A	N/A
	1	42	2512.558	4661	1456	90.47371
	0.5	42	1347.647	2492	172	85.58243
	0.1	42	277.4744	506	119	78.77696
	0.05	41	153.3896	387	48	67.09085
	0.01	17	46.86111	108	20	79.08416
	0.005	6.5	39.57143	78	20.5	0
	0.001	1.5	33.83333	43	27	0
Donor2_25 µL	4	N/A	XS	N/A	N/A	N/A
	2	N/A	XS	N/A	N/A	N/A
	1	42	2790.808	5126	1461	89.18818
	0.5	42	1344.103	2878	431	86.90558
	0.1	42	292.7179	698	88	74.55354
	0.05	41.5	157.3974	479	47	68.58833
	0.01	24.5	69.69271	171	14.25	69.5993
	0.005	5.5	44.95455	75	23	93.58974
	0.001	6	33.61538	55	20	94.84848
Donor1_12.5 µL	4	N/A	NAD XS	N/A	N/A	N/A
	2	N/A	XS	N/A	N/A	N/A
	1	N/A	XS	N/A	N/A	N/A
	0.5	42	3132.963	6719	1590	84.41101
	0.1	42	780.5732	2444	180	74.65676
	0.05	42	346.6667	931	58	68.87677
	0.01	27	91.94737	406	21	49.76132
	0.005	12	48.19643	91.5	20	71.22325
	0.001	4.5	35.8	51	22	88.23529
Donor2_12.5 µL	4	N/A	XS	N/A	N/A	N/A
	2	N/A	XS	N/A	N/A	N/A
	1	N/A	XS	N/A	N/A	N/A
	0.5	42	2878.8	6159	1281	78.28704
	0.1	42	742.7313	1612	140	68.11695
	0.05	42	333.375	892	93	60.88416
	0.01	25	82.33	249	21	59.05469
	0.005	13.5	51.46552	121	21	67.89194
	0.001	0	0	0	0	0

The amplifications at 25 µL total PCR volume with DNA templates of 4 ng and 2 ng for both donors gave excess profiles resulting in the profiles being unable to be interpreted. The results from the excess samples were excluded from the data analysis. The average number of alleles and the average peak height was similar for both donors when processed with an amplification volume of 25 µL.

The amplifications at 12.5 µL with DNA templates of 4 ng, 2 ng, 1 ng and one replicate of the 0.5 ng for both donors gave excess results. The results from the excess samples were excluded from the data analysis. The average number of alleles and average peak height was similar for both donors when processed with an amplification volume of 12.5 µL.

Figure 1 displays the average number of alleles and average peak height ratio obtained for each donor at each template amplified at 25 µL and 12.5 µL.

Figure 2 displays the average peak height and average peak height ratio at each DNA template amplified for 25 µL and 12.5 µL.

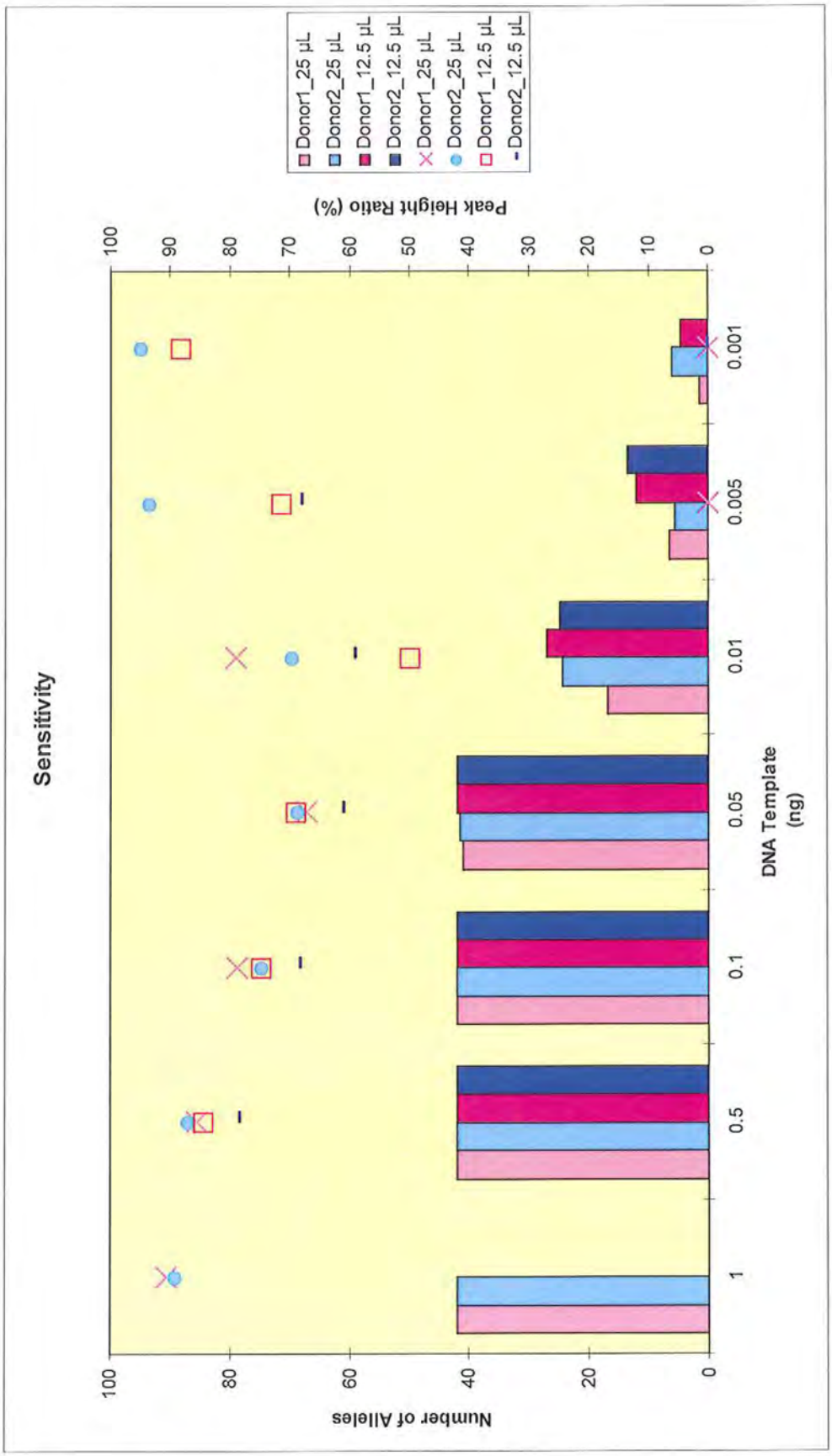

Figure 1 – Sensitivity results. The average number of alleles called (coloured bars) and average peak height ratio (coloured markers) for each donor and total PCR volume used.

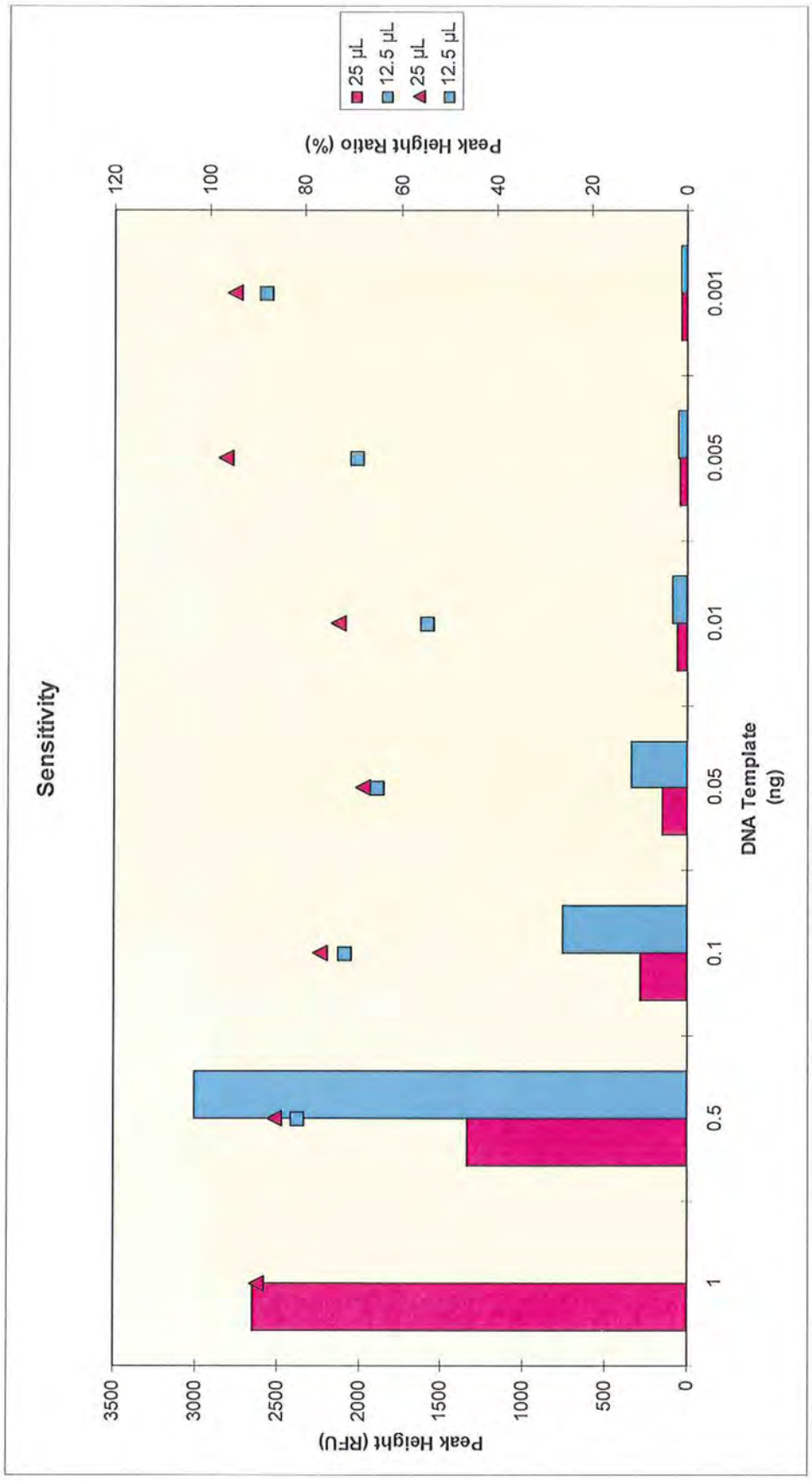

Figure 2 - Sensitivity results. The average peak height (coloured bars) and average peak height ratio (coloured markers) for each total PCR volume used.

A full complement of alleles in the PowerPlex® 21 system was obtained for both donors at total DNA template inputs of 0.5 ng and 0.1 ng when amplified at both total PCR volumes. As expected the average number of alleles decreased as the DNA template decreased.

For both total PCR volumes, as the total DNA template decreased, the peak heights also decreased. The 12.5 µL amplification gave higher peaks heights at the 0.5 ng, 0.1 ng and 50 pg DNA template inputs compared with the 25 µL amplification.

The average peak height ratio decreased as the DNA template decreased to 50 pg. Below a DNA template of 50 pg less heterozygote pairs were observed (as expected) which resulted in the peak height ratio becoming more variable and drop out being observed.

The samples from the baseline experiment ranged from template inputs of 0.5 ng to 0.025 ng. The results of these experiments are concordant with the first sensitivity experiment.

A full complement of alleles in the PowerPlex® 21 system was obtained for all samples between 0.5 ng and 0.132 ng DNA template inputs when amplified at both total PCR volumes.

The second sensitivity experiment was undertaken to enable direct comparison of the sample concentration when amplified at a total PCR volume of 25 µL and 12.5 µL rather than comparing the total DNA template input.

Figure 3 shows the results of low concentration samples amplified at 25 µL and 12.5 µL total PCR volumes with the vertical red line highlighting the limit of detection[33] (quantification) used for the AB 7500 Real Time PCR system. The numbers of alleles obtained at each concentration were counted using the LOR thresholds determined in section 6.4.

The DNA profiles exhibited increased allelic imbalance across different loci when the sample concentration dropped below 0.025 ng/µL.

Overall the PowerPlex®21 system is a very sensitive STR amplification kit capable of detecting DNA amounts below what is generally considered low copy number (LCN). The data analyses indicate that the risk of type 2 errors will increase if the DNA template is too low for both total PCR volumes.

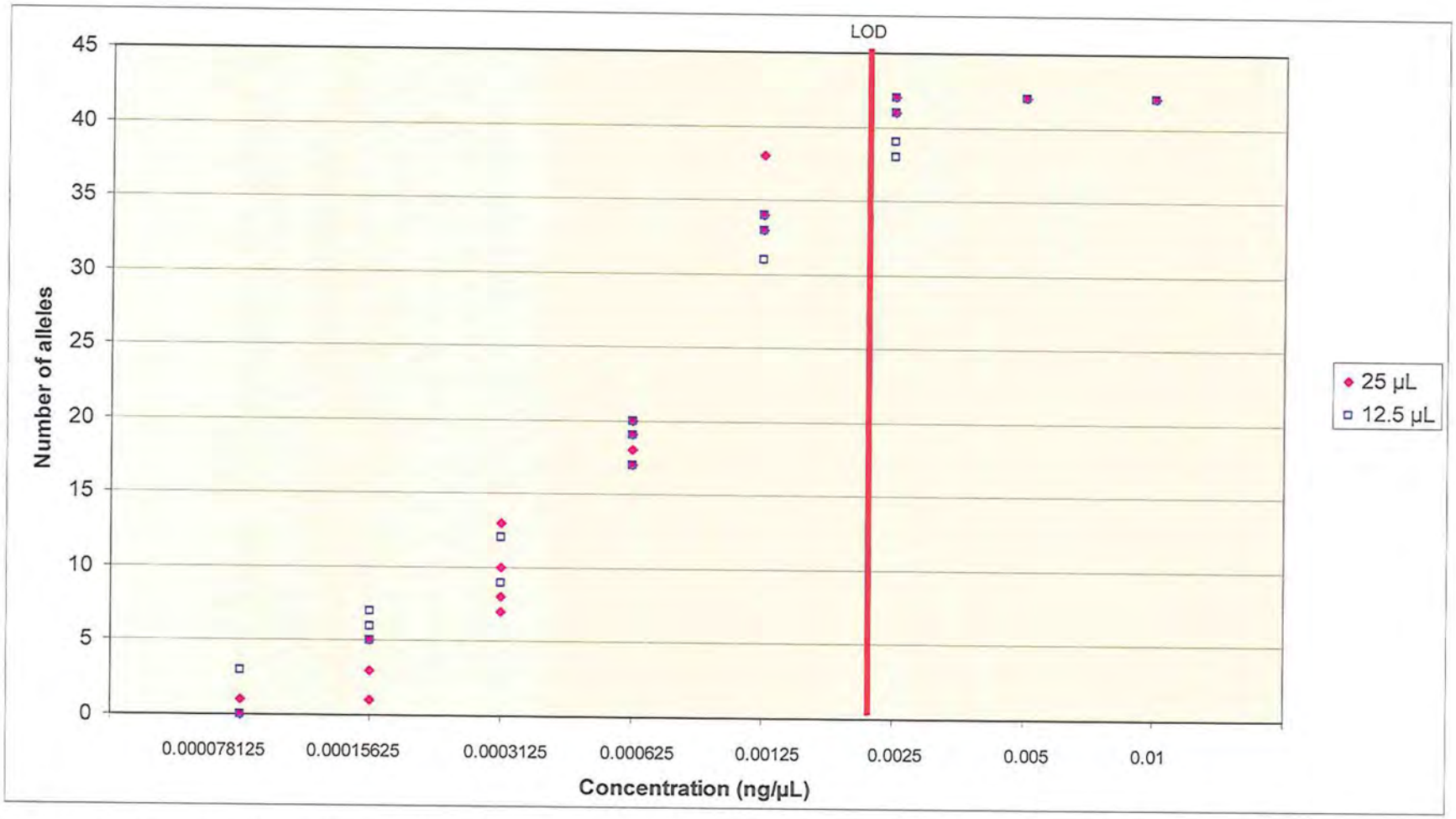

Figure 3 - Comparison of sample concentration vs allele count for 25 µL and 12.5 µL total PCR volumes. Please note the scale on the x axis is not linear.

6.5 Drop In

Allelic drop-in is due to spurious amplification products from unknown DNA, which makes allele drop-in a random event[34, 35]. The phenomenon of allelic drop-in is usually not reproducible and can be detected through testing samples multiple times[36].

For the 25 µL amplifications processed on both 3130xl instruments 3 drop in events were noted. True drop-in alleles were seen in three negative controls at D16S539 as a 7 allele at 21 RFU, D3S1358 as a 21 allele at 19 RFU and at TH01 as a 5 allele at 19 RFU.

For 12.5 µL amplifications on both 3130xl instruments no drop in events were noted.

Drop in data was sent to John Buckleton for fit to a Poisson distribution and tested. This data is required for STRmix™ validation and STRmix™ settings.

The rate of drop in events for 25µL volume amplifications (3 events in 1050 alleles above 15RFU) was calculated for STRmix™ by John Buckleton, see Figure 4.

STRmix™ uses the model for drop-in ae-bx where the values for a and b are the drop-in parameters in STRmix™. John Buckleton's calculations determined that a=b=0.393. The maximum drop-in seen at any one locus is determined in RFU; this means that if two peaks were seen at one locus the drop-in would be the total height of both peaks. Since only one drop-in peak was observed at any one locus and the highest of these events was 21 RFU, then our drop-in setting for STRmix™ would be 21 RFU. Since our LOR was determined to be 40 RFU, it seemed reasonable to set the drop-in level to 40 RFU.

Although no drop-in events were observed for half volume amplifications, the same parameters will be applied.

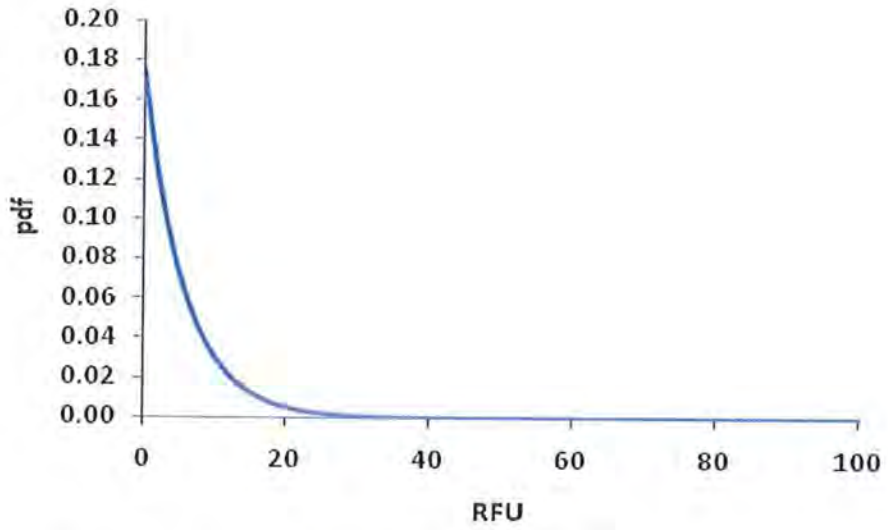

Figure 4 - Probability of Drop in for 25 µL total PCR volume.

6.6 Stutter

Stutter peaks are Polymerase Chain Reaction (PCR) artefacts commonly observed in all STR analysis[4, 37]. They are usually observed as a peak one repeat unit smaller (designated -1 repeat stutter or stutter) in size than the true allele peak [37, 38]. The slipped strand mispairing (SSM) model accounts for stutter formation via the looping out of either the template strand or the extending strand [38-40].

+1 repeat stutter (forward/over stutter) is observed as a peak one repeat unit more in size than the true allele [41, 42]. Figure 5 shows an example of -1 repeat stutter and +1 repeat stutter.

-2 repeat stutter (double back stutter) peaks are observed as a peak two repeat units less than the true allele [38, 41]. Figure 6 shows an example of -2 repeat stutter.

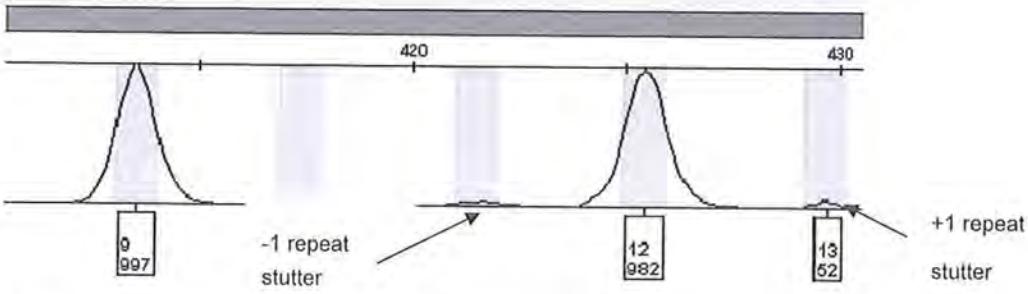

Figure 5 - Example of -1 repeat stutter and +1 repeat stutter.

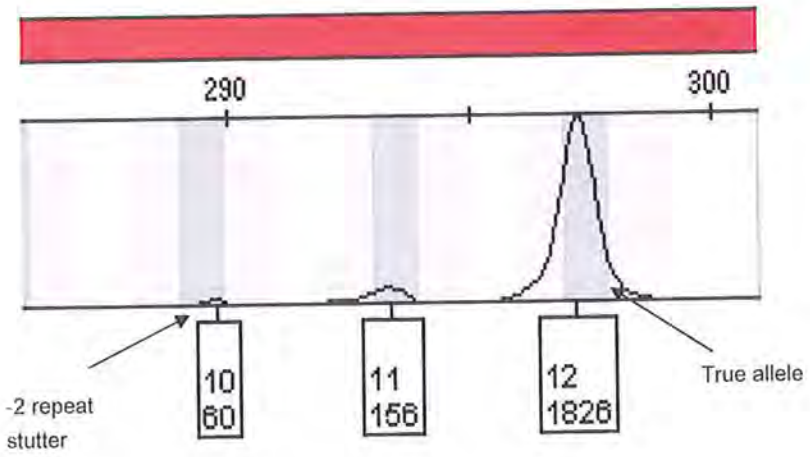

Figure 6 - Example of a -2 repeat stutter peak

The amount of stutter product formation is related to many different external factors including the type of repeat motif, the processivity of the DNA polymerase, template level and whether the allele contains interrupted repeats [38, 40, 42-44]

As evidenced by the results in Table 15 and Table 16, a different amount of stutter product formation is observed at different loci.

Promega supplied a stutter text file (using $\mu + 3\sigma$[4]) for GeneMapper ID-X v.1.1.1. We have used the same calculation as it incorporates 99.73% of the data assuming normal distribution.

The data for the observed stutter ratios (-1 repeat, +1 repeat and -2 repeat) for samples amplified at 25 µL and 12.5 µL are listed in Table 15 and Table 16 respectively.

+1 repeat stutter was observed for all loci when amplified at 25 µL and therefore a threshold was able to be calculated for each locus.

+1 repeat stutter was not observed for all loci when amplified at 12.5 µL and therefore a threshold was only able to be calculated for those loci at which +1 repeat stutter was observed. +1 repeat stutter will be continued to be monitored until enough data is obtained to review the thresholds set in this validation.

-2 repeat stutter was not observed for all loci when amplified at 12.5 µL and 25 µL, therefore a threshold was only able to be calculated at loci where at least two -2 repeat stutter peaks were observed. -2 repeat stutter will continue to be monitored until enough data is obtained to review the threshold set.

Most calculated -1 stutter thresholds were higher than the Promega supplied stutter filter file both for 25 µL and 12.5 µL as shown in Tables 15 and 16. The exceptions were D6S1043, D18D51, D2S1338, and Penta D for 25 µL and D6S1043, Penta E, D18D51, D2S1338, and Penta D for 12.5 uL.

When comparing the calculated stutter thresholds for the 25 µL and 12.5 µL total PCR volumes, they appear to be similar

Table 15 – 25 µL Calculated stutter thresholds.

Locus	$n_{SR\ -2\ repeat}$	$\mu_{SR\ -2\ repeat}$	$\sigma_{SR\ -2\ repeat}$	-2 repeat Stutter Ratio (%)	$n_{SR\ -1\ repeat}$	$\mu_{SR\ -1\ repeat}$	$\sigma_{SR\ -1\ repeat}$	-1 repeat Stutter Ratio (%)	$n_{SR\ +1\ repeat}$	$\mu_{SR\ +1\ repeat}$	$\sigma_{SR\ +1\ repeat}$	+1 repeat stutter Ratio (%)
D3S1358	147	0.0095	0.0045	2.3	310	0.0868	0.0184	14.2	60	0.0131	0.0100	4.3
D1S1656	132	0.0125	0.0102	4.3	371	0.0910	0.0269	17.2	128	0.0183	0.0163	6.7
D6S1043	33	0.0097	0.0056	2.7	366	0.0685	0.0171	12.0	84	0.0164	0.0192	7.4
D13S317	14	0.0115	0.0076	3.4	200	0.0496	0.0228	11.8	39	0.0185	0.0184	7.4
Penta E	4	0.0165	0.0016	2.1	184	0.0457	0.0203	10.7	2	0.0113	0.0018	1.7
D16S539	108	0.0088	0.0040	2.1	270	0.0686	0.0173	12.1	118	0.0133	0.0099	4.3
D18S51	133	0.0103	0.0058	2.8	422	0.0873	0.0244	16.0	119	0.0144	0.0116	4.9
D2S1338	106	0.0114	0.0058	2.9	372	0.0878	0.0203	14.9	12	0.0196	0.0150	6.5
CSF1PO	29	0.0127	0.0080	3.7	190	0.0640	0.0244	13.7	54	0.0155	0.0096	4.4
Penta D	0	0.000	N/A	N/A	86	0.0245	0.0190	8.2	8	0.0306	0.0193	8.8
TH01	39	0.0087	0.0057	2.6	243	0.0325	0.0181	8.7	22	0.0085	0.0041	2.1
vWA	54	0.0116	0.0077	3.5	278	0.0782	0.0246	15.2	52	0.0157	0.0135	5.6
D21S11	58	0.0130	0.0091	4.0	322	0.0809	0.0199	14.1	120	0.0175	0.0177	7.1
D7S820	15	0.0102	0.0078	3.4	252	0.0485	0.0218	11.4	60	0.0207	0.0124	5.8
D5S818	20	0.0116	0.0039	2.3	214	0.0595	0.0202	12.0	51	0.0165	0.0132	5.6
TPOX	2	0.0096	0.0057	2.7	164	0.0381	0.0174	9.0	4	0.0235	0.0130	6.3
D8S1179	54	0.0116	0.0048	2.6	315	0.0790	0.0177	13.2	62	0.0176	0.0123	5.5
D12S391	146	0.0111	0.0056	2.8	376	0.0948	0.0311	18.8	45	0.0146	0.0128	5.3
D19S433	32	0.0101	0.0074	3.2	210	0.0666	0.0205	12.8	8	0.0211	0.0165	7.1
FGA	48	0.0116	0.0066	3.1	280	0.0702	0.0227	13.8	40	0.0182	0.0135	5.9

Stutter thresholds higher than the recommended stutter thresholds from Promega =

μ_{SR} = mean stutter ratio, σ_{SR} = standard deviation of stutter ratio, μ_{OSR} = mean over stutter ratio, σ_{OSR} = standard deviation of over stutter ratio

Table 16 - 12.5 µL Calculated stutter thresholds.

Locus		$\mu_{SR\ -2}$ repeat	$\sigma_{SR\ -2}$ repeat	-2 repeat Stutter Ratio (%)		$\mu_{SR\ -1}$ repeat	$\sigma_{SR\ -1}$ repeat	-1 repeat Stutter Ratio (%)		$\mu_{SR\ +1}$ repeat	$\sigma_{SR\ +1}$ repeat	+1 repeat stutter Ratio (%)
D3S1358	109	0.0113	0.0042	2.4	265	0.0880	0.0194	14.6	31	0.0113	0.0067	3.2
D1S1656	115	0.0102	0.0035	2.1	348	0.0909	0.0247	16.5	83	0.0138	0.0055	3.0
D6S1043	60	0.0073	0.0027	1.5	289	0.0738	0.0153	12.0	48	0.0141	0.0088	4.0
D13S317	20	0.0096	0.0047	2.4	172	0.0544	0.0197	11.3	11	0.0148	0.0070	3.6
Penta E	2	0.0103	0.0039	2.2	152	0.0389	0.0141	8.1	5	0.0289	0.0111	6.2
D16S539	23	0.0091	0.0061	2.8	238	0.0690	0.0195	12.8	40	0.0120	0.0049	2.7
D18S51	76	0.0117	0.0044	2.5	338	0.0827	0.0258	16.0	60	0.0167	0.0125	5.4
D2S1338	67	0.0105	0.0044	2.4	310	0.0909	0.0218	15.6	5	0.0298	0.0241	10.2
CSF1PO	49	0.0077	0.0072	2.9		0.0721	0.0258	14.9	41	0.0145	0.0071	3.6
Penta D	0	N/A	N/A	N/A	32	0.0262	0.0093	5.4	2	0.0324	0.0005	3.4
TH01	3	0.0075	0.0027	1.6	176	0.0252	0.0120	6.1	1	N/A	0.0000	N/A
vWA	18	0.0079	0.0037	1.9	222	0.0836	0.0212	14.7	11	0.0149	0.0097	4.4
D21S11	77	0.0088	0.0048	2.3	302	0.0839	0.0199	14.4	43	0.0256	0.0132	6.5
D7S820	21	0.0071	0.0022	1.4	179	0.0508	0.0232	12.0	6	0.0250	0.0108	5.7
D5S818	15	0.0090	0.0029	1.8	199	0.0675	0.0230	13.7	15	0.0163	0.0139	5.8
TPOX	1	N/A	N/A	N/A	169	0.0346	0.0179	8.8	1	N/A	0.0000	N/A
D8S1179	25	0.0095	0.0039	2.1	213	0.0818	0.0208	14.4	22	0.0173	0.0125	5.5
D12S391	156	0.0118	0.0058	2.9	382	0.1026	0.0313	19.6	16	0.0135	0.0083	3.8
D19S433	70	0.0083	0.0059	2.6	236	0.0689	0.0185	12.4		0.0129	0.0032	2.2
FGA	119	0.0087	0.0031	1.8	279	0.0700	0.0218	13.5		0.0192	0.0223	8.6

Stutter thresholds higher than the recommended stutter thresholds from Promega =

μ_{SR} = mean stutter ratio, σ_{SR} = standard deviation of stutter ratio, μ_{OSR} = mean over stutter ratio, σ_{OSR} = standard deviation of over stutter ratio

6.7 Peak Balance

6.7.1 Peak Height Ratio and Allelic Imbalance Threshold

Peak height ratio (PHR) is the ratio between the two peaks in a heterozygous pair. Under optimal conditions the amplification of a pair of alleles should result in equal peak heights however, input DNA, inhibitors and quality of DNA will affect the amplification [45, 46].

The method used in Equation 4 is recommended in the SWGDAM guidelines [11]and well represented in the literature [44], although other methods have been published by Kelly et al [47].

By assigning a threshold of the mean minus three standard deviations, this incorporates 99.73% of the data, resulting in a conservative threshold. This threshold was rounded up to the nearest RFU. Use of this method to produce a threshold is a low risk to reference samples, as samples that deviate would be reprocessed.

Table 17 - Table 20 show the summary of PHR and AI_{Th} data calculated. The overall average PHR for 12.5µL- 5 s injection and 25 µL- 5 s injection total PCR volumes are 78.9% and 80.4% respectively. These values are consistent with other kits listed in the literature [12, 48]. Although the average peak height ratios are similar to those reported in the literature; given the wide standard deviation observed in our data, the calculated AI_{Th} of 31.4% for 12.5 µL (5 s injection) and 38.6% for 25 µL (5 s injection) reaction volumes are considered low.

The observed data for 3 s injection times are consistent with the 5 s injection times but slightly higher. The overall average PHR for 12.5 µL- 3s injection and 25 µL- 3 s injection total PCR volumes are 80.9% and 81.3% respectively; the calculated AI_{Th} are 39.8% and 41.5%.respectively .The differences in data is likely due to drop out of loci as the 3 s injection times have lower peak RFU.

Figure 7 - Figure 10 display the data obtained from the baseline experiments for 25 µL and 12.5 µL total PCR volumes and their respective injection times. For both total PCR volumes and both injection times, as the amount of DNA input is decreased from the recommended 0.5 ng template DNA, the average peak height ratio (μ_{PHR}) decreases and the standard deviation of the peak height ratio (σ_{PHR}) increases.

When the mean PHR are calculated for each DNA template, between 0.183 ng and 0.5 ng inputs there is no significant difference between total PCR volumes although the standard deviation is higher for the 12.5 µL total PCR volume, resulting in a much lower threshold. Refer to Tables 17 -20.

Figure 15 - Figure 33- The n of allele pairs per 0.1 PHR bin for 0.5025 ng 5 s inj. Figure 34 - The n of allele pairs per 0.1 PHR bin for 0.5025 ng 3 s inj. show observed PHR for different template DNA amounts. The PHR range is separated into 0.1 increments plotted against number of allele

pairs. Figure 15 - The n of allele pairs per 0.1 PHR bin for 0.02475 ng 5 s inj. Figure 16 - The n of allele pairs per 0.1 PHR bin for 0.02475ng 3 s inj.and Figure 15 - The n of allele pairs per 0.1 PHR bin for 0.02475 ng 5 s inj. Figure 16 - The n of allele pairs per 0.1 PHR bin for 0.02475ng 3 s inj. are the lowest template DNA amounts. This shows that at the low template DNA range, the PHR varies unpredictably for both the 25 µL (5 s inj) and 12.5 µL(5 s inj) total PCR volumes. The results for the both the 25 µL (3 s inj) and 12.5 µL(3 s inj) total PCR volumes show marked allelic drop out. As the template DNA amount increases, the PHR converges towards the ideal of 1.0.

The $\mu_{PHR\_25\_5s}$ at 25 pg input was 0.736 and at 0.5 ng input was 0.851 compared with the $\mu_{PHR\_12.5\_5\,s}$, at 25 pg input was 0.598 and at 0.5 ng was 0.832.

The $\mu_{PHR\_25\_3\,s}$ at 25 pg input was 0.971 and at 0.5 ng input was 0.842 compared with the $\mu_{PHR\_12.5\_3\,s}$, at 25 pg input was 0.735 and at 0.5 ng was 0.840. The high $\mu_{PHR\_25\_3\,s}$ at 25 pg is attributed to the extremely small sample size of 2 samples. This small sample size is too small to be reflective of the true result.

The results of our validation are consistent with previous published findings referring to low template DNA and reduced volume amplifications [13, 45, 49].

Stochastic effects were obvious in this experiment in data from templates below 0.132 ng. Stochastic effects are the result of random, uneven amplification of heterozygous allele pairs from low template samples (SWGDAM 2010 interpretation) which is displayed by low peak heights or allele/locus dropout. At 0.132 ng DNA template is approaching what is usually defined as low copy number (LCN) (~0.100 ng to 0.150 ng).

Supportive experimental data is displayed in & AI_{TH} vs input graph, which displays a rapid drop off the AI_{TH} after 0.132 ng DNA template. The calculated AI_{TH} drops below 0 for 0.02475 ng DNA template because the standard deviation is so large. The rapid drop off is likely to increase the number of type 2 errors if AI_{TH} is used calculated from the entire dataset due to the large standard deviation. Exclusion of data from templates below 0.132 ng increases the μ_{PHR} and decreases σ_{PHR}.

A multiple regression analysis was performed by Jo-Anne Bright, Duncan Taylor and John Buckleton to calculate the peak height variance for use in STRmix™[50].

The peak height ratios calculated here are for use with reference samples that have been amplified from extracted DNA and as a guideline to help determine the number of contributors for mixture interpretation as required for STRmix™ analysis.

Table 17- 25 µL 3 s inj summary

	25 µL 3 s inj All	25 µL 3 s inj 132 pg +	25 µL 3 s inj 183 pg +
µ	0.8125	0.8169	0.8213
σ	0.1325	0.1297	0.1292
AI_{Th}	41.49%	42.78%	43.38%
Th_{Hom}	193	187	184

Table 18 -25 µL 5 s inj summary

	25 µL 5 s inj All	25 µL 5 s inj 132 pg+	25 µL 5 s inj 183 pg+
µ	0.8042	0.8230	0.8298
σ	0.1393	0.1228	0.1194
AI_{Th}	38.63%	45.46%	47.17%
Th_{Hom}	207	176	170

Table 19-12.5 µL 3 s inj summary

	12.5 µL 3 s inj All	12.5 µL 3 s inj 132 pg+	12.5 µL 3 s inj 183 pg+
µ	0.8086	0.8171	0.8283
σ	0.1368	0.1291	0.1190
AI_{Th}	39.81%	42.99%	47.13%
Th_{Hom}	201	186	170

Table 20-12.5 µL 5 s inj summary

	12.5 µL 5 s inj All	12.5 µL 5 s inj 132 pg+	12.5 µL 5 s inj 183 pg+
µ	0.7894	0.8135	0.8239
σ	0.1586	0.1330	0.1240
AI_{Th}	31.36%	41.45%	45.19%
Th_{Hom}	255	193	177

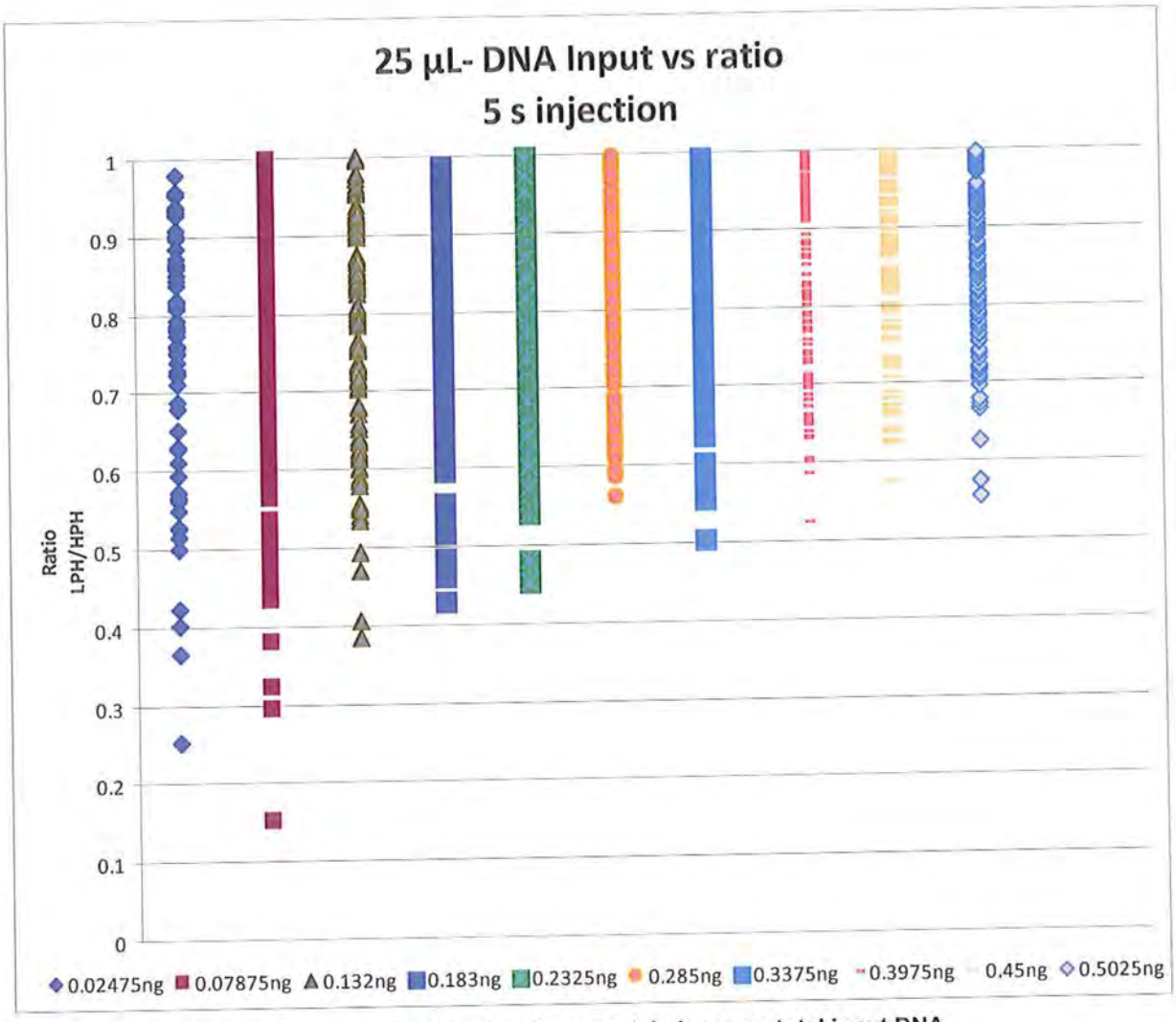

Figure 7 – 25 µL total PCR volume 5 s injection time, Peak balance vs total input DNA.

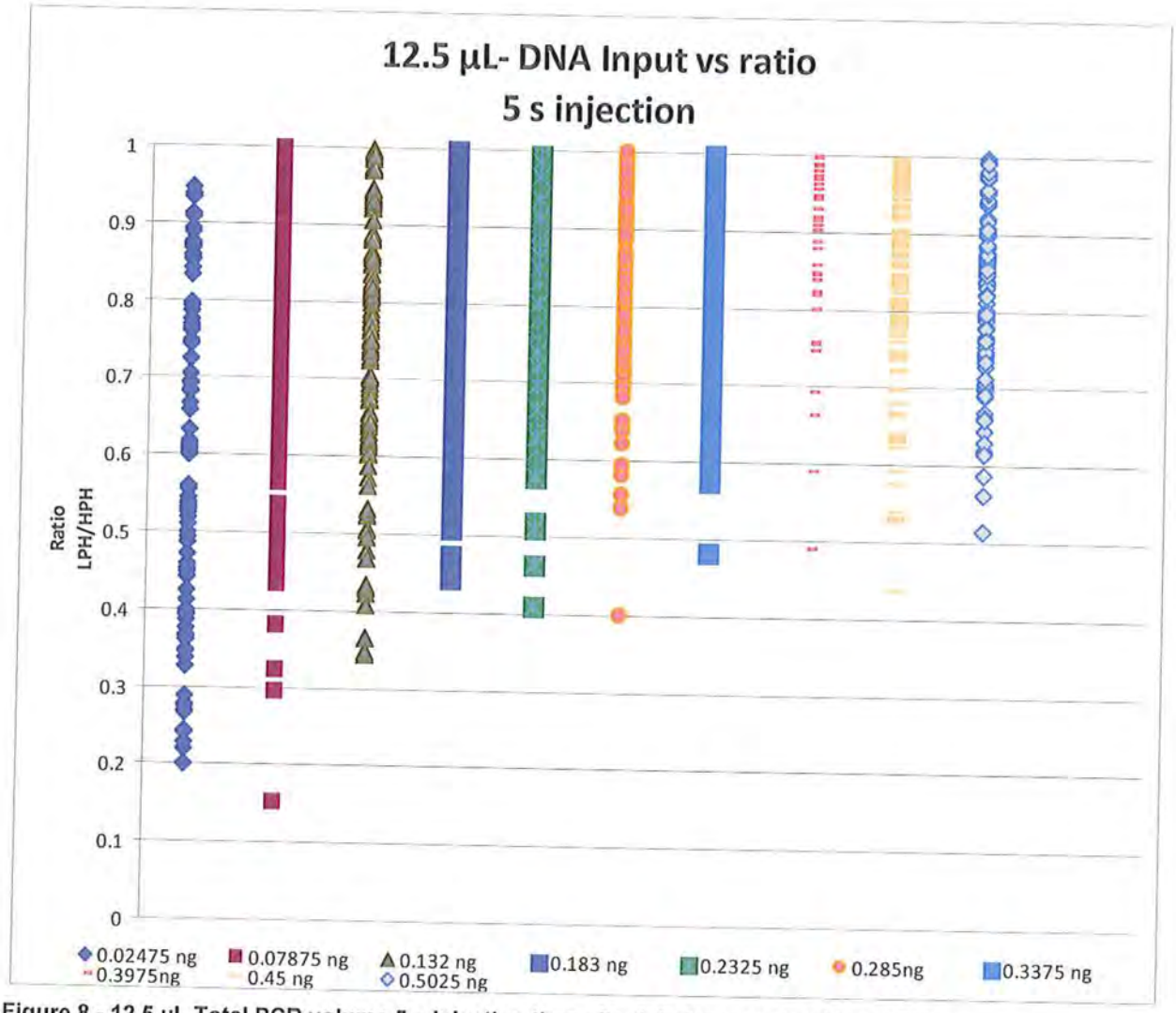

Figure 8 - 12.5 µL Total PCR volume 5 s injection time - Peak balance vs total input DNA.

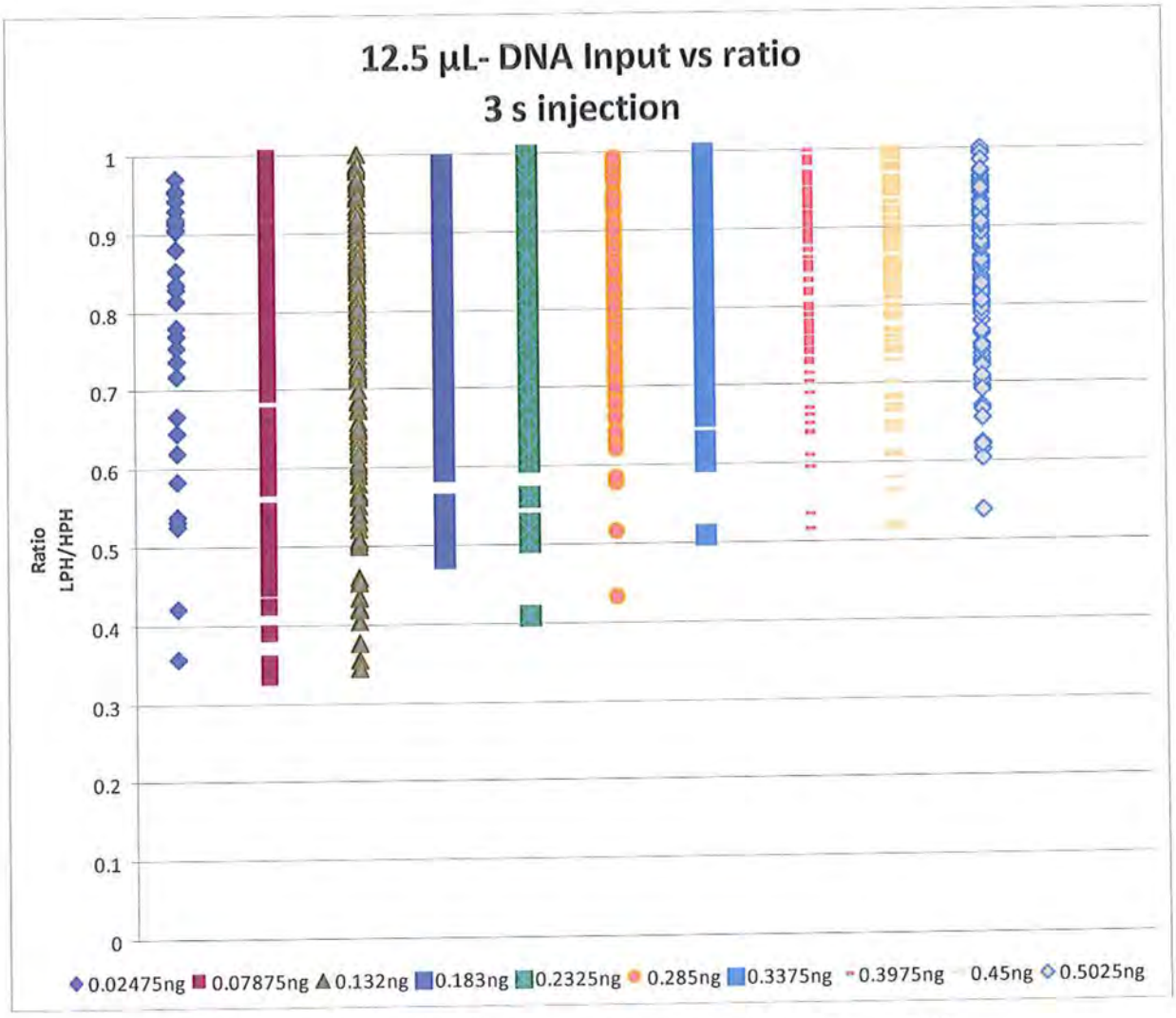

Figure 9 12.5 µL Total PCR volume 3 s injection time - Peak balance vs total input DNA.

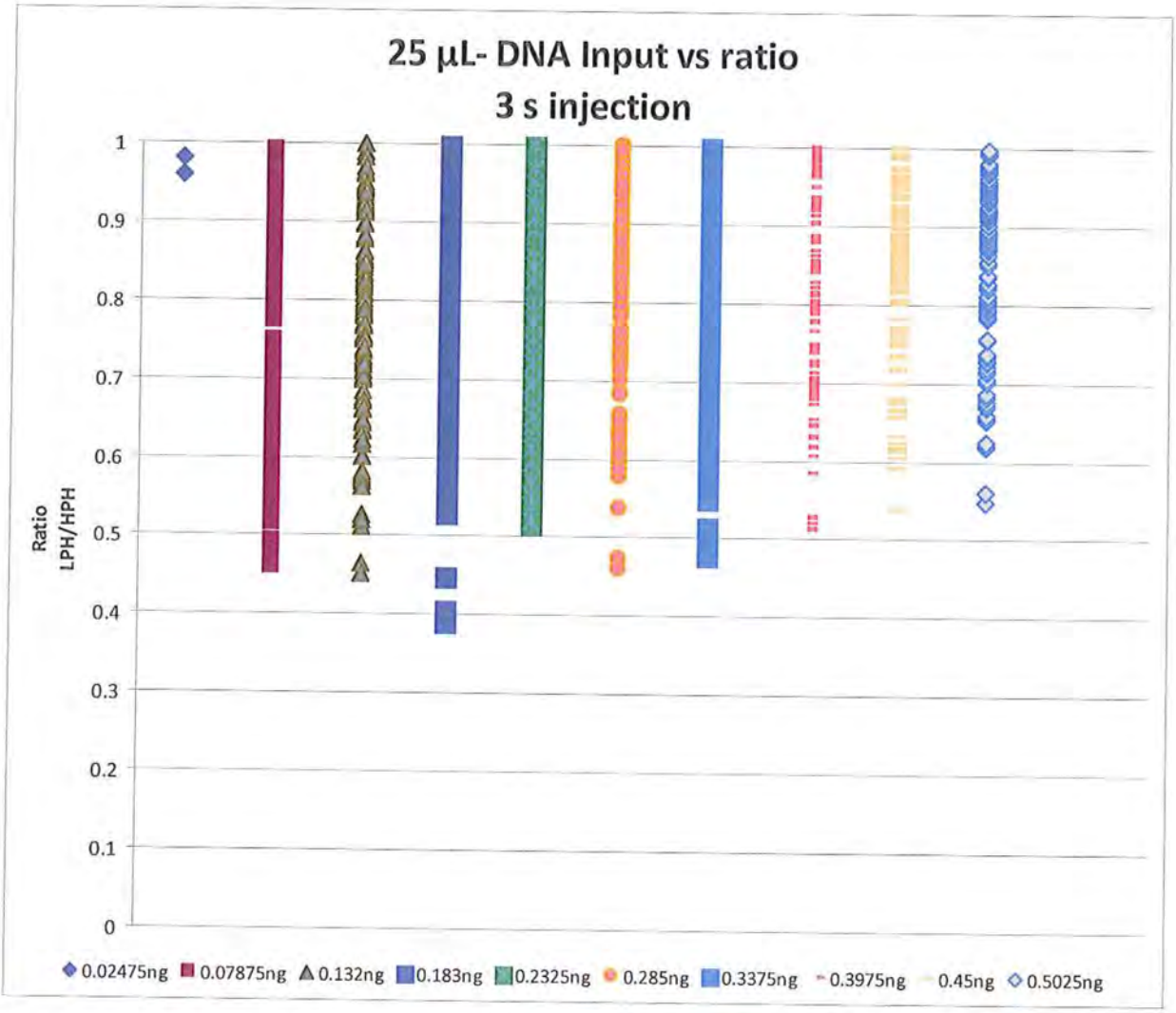

Figure 10 – 25 µL Total PCR volume 3 s injection time- Peak balance vs total input DNA.

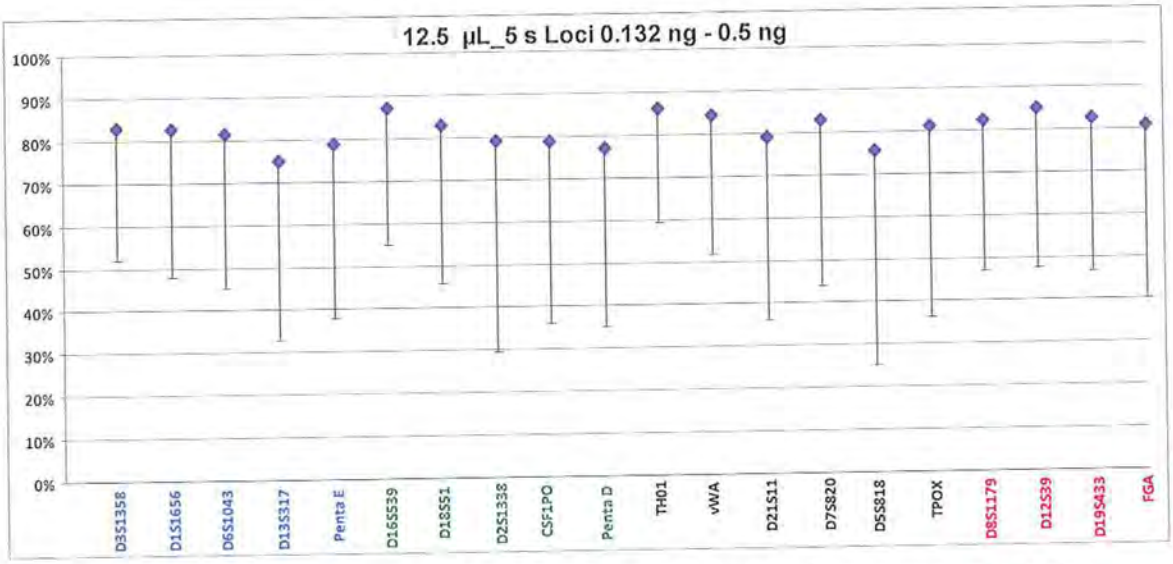

Figure 11 - 12.5 µL total PCR volume 5 s injection time µPHR per Loci. Error bars show minus 3 standard deviations

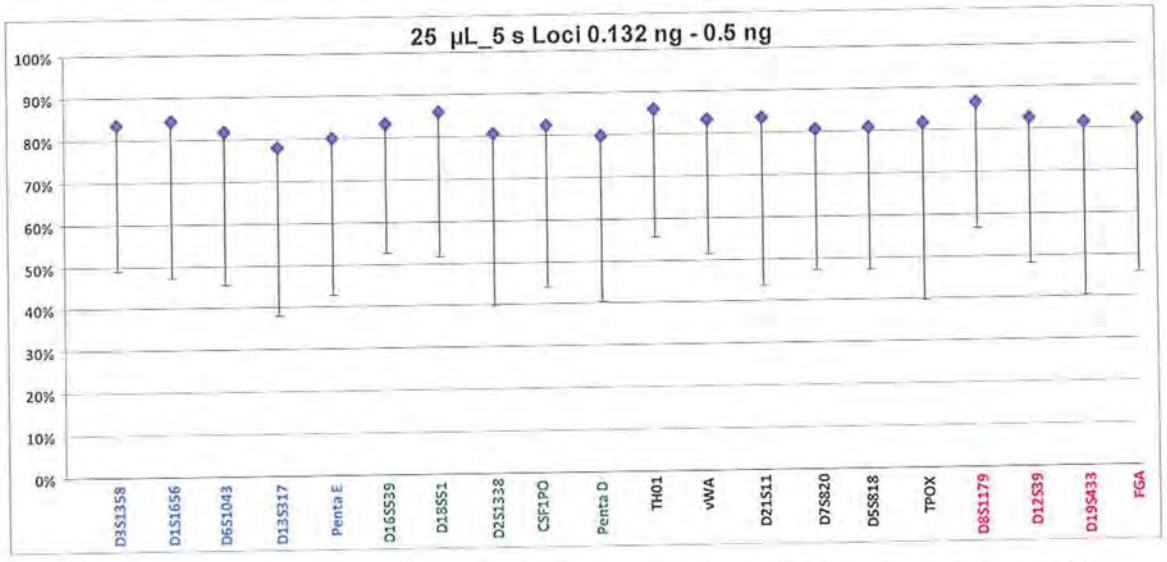

Figure 12 – 25 µL total PCR volume 5 s injection time - µPHR per Loci. Error bars show minus 3 standard deviations.

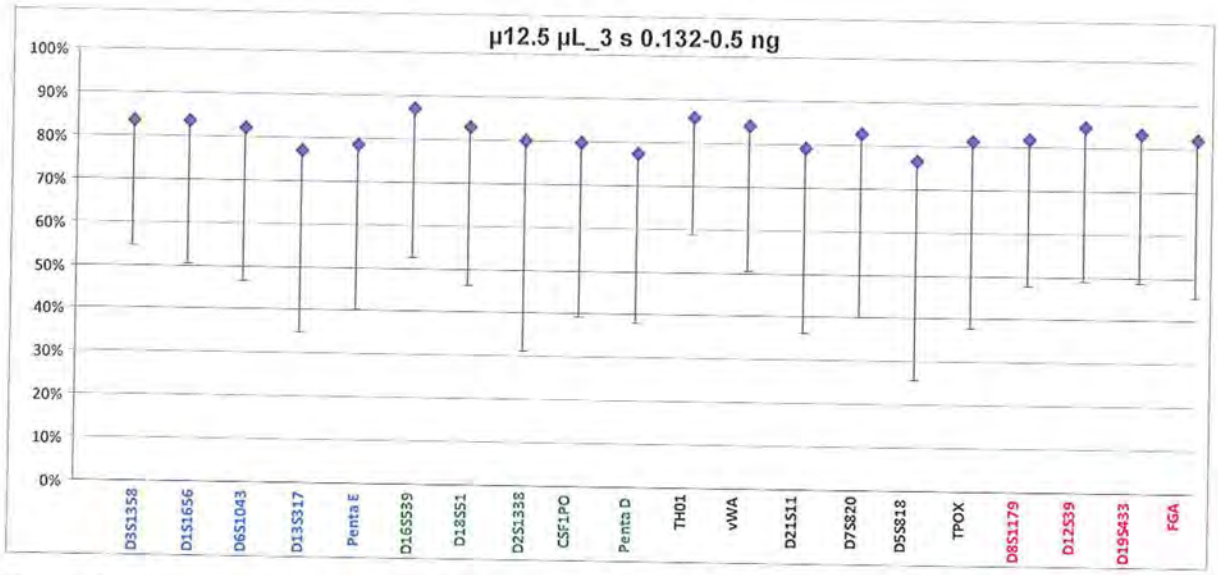

Figure 13 – 12.5 µL total PCR volume 3 s injection time - µPHR per Loci. Error bars show minus 3 standard deviations.

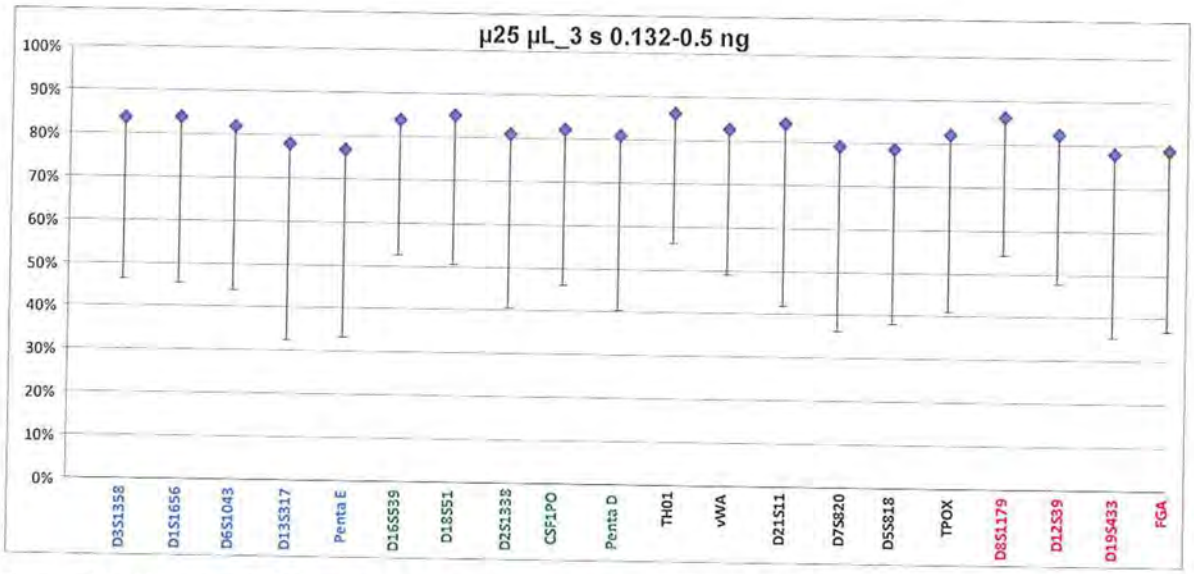

Figure 14 – 25 µL total PCR volume 3 s injection time - µPHR per Loci. Error bars show minus 3 standard deviations.

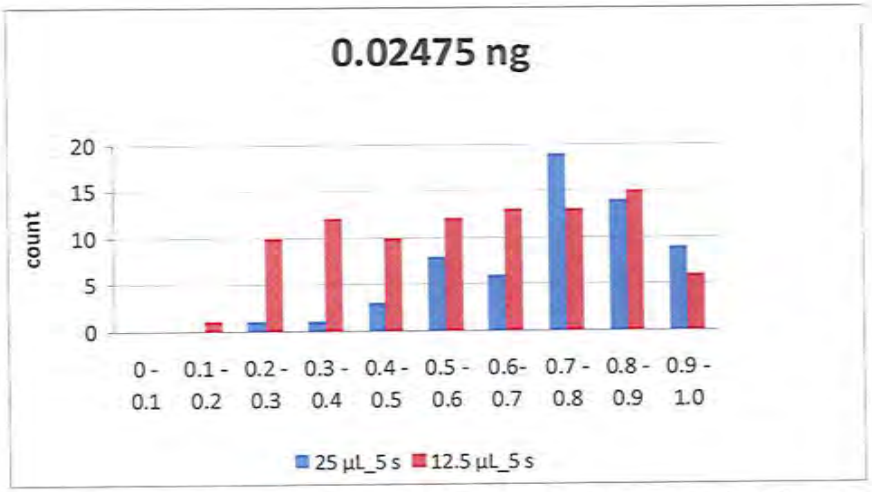

Figure 15 - The n of allele pairs per 0.1 PHR bin for 0.02475 ng 5 s inj.

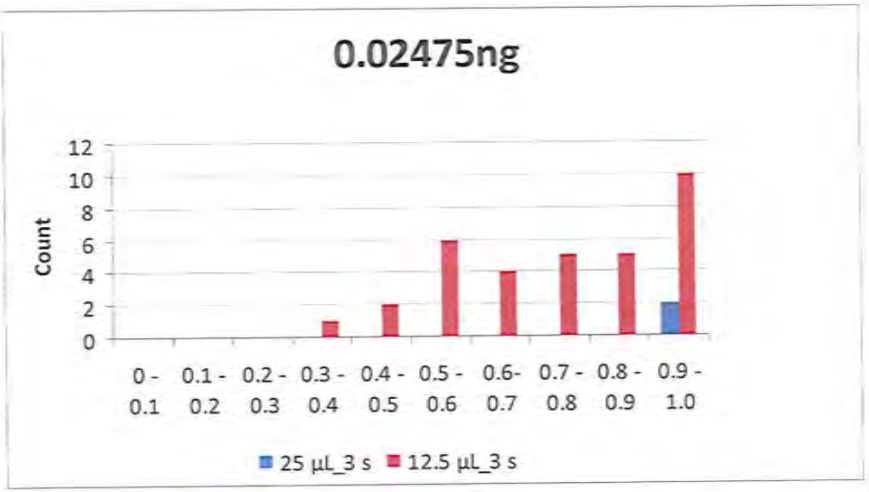

Figure 16 - The n of allele pairs per 0.1 PHR bin for 0.02475ng 3 s inj.

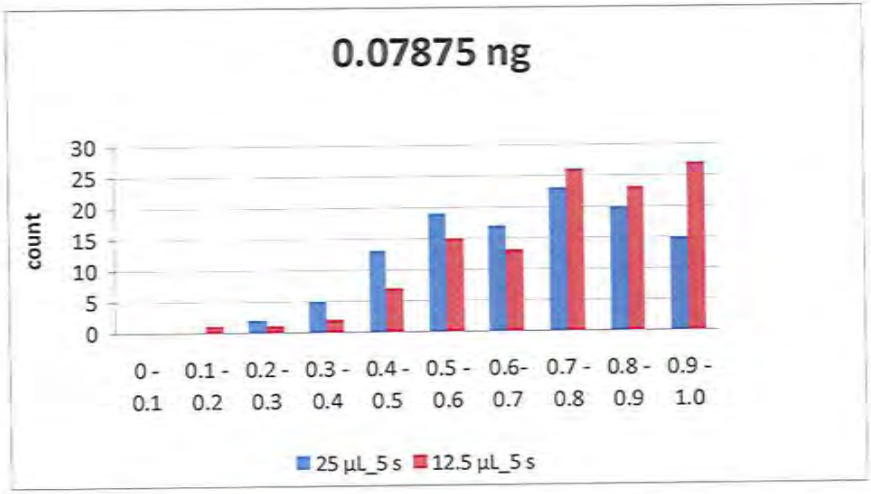

Figure 17 -The n of allele pairs per 0.1 PHR bin for 0.07875 ng 5 s inj.

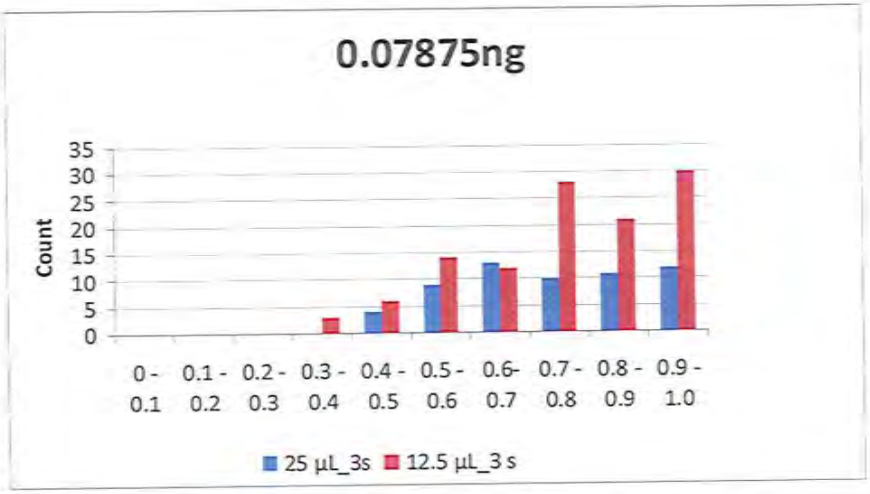

Figure 18 -The n of allele pairs per 0.1 PHR bin for 0.07875 ng 3 s inj.

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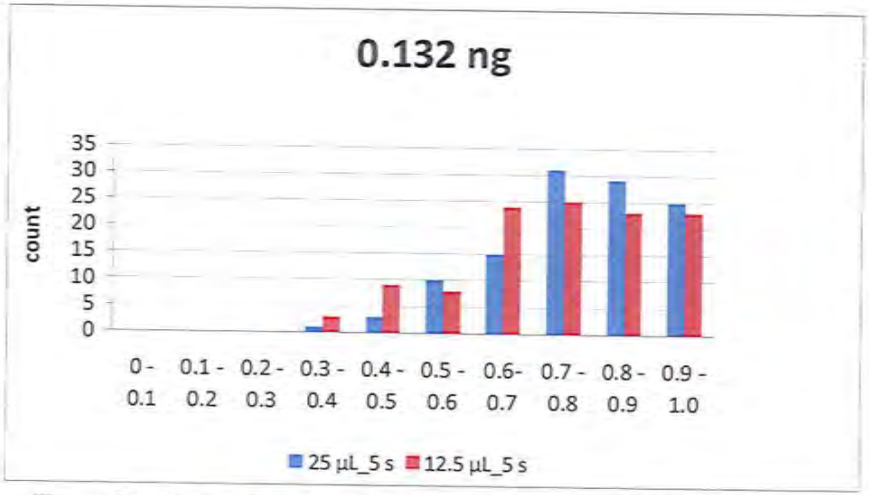

Figure 19 - The n of allele pairs per 0.1 PHR bin for 0.132 ng 5 s inj.

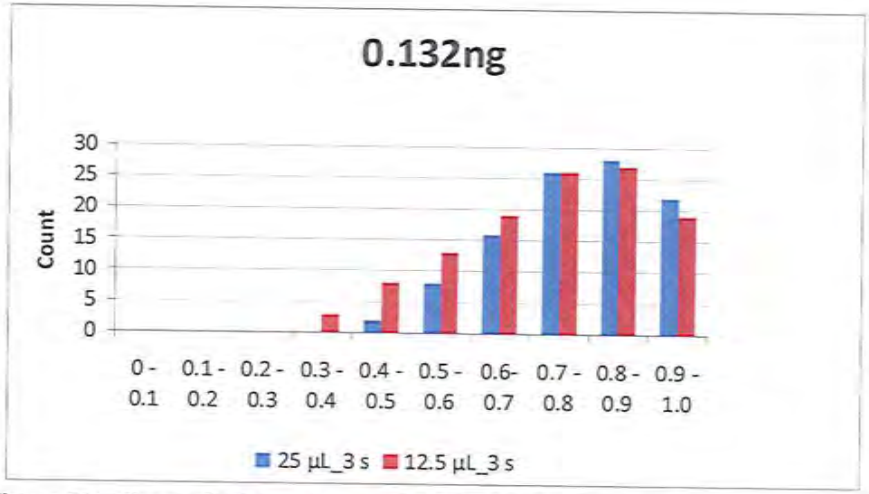

Figure 20 - The n of allele pairs per 0.1 PHR bin for 0.132 ng 3 s inj.

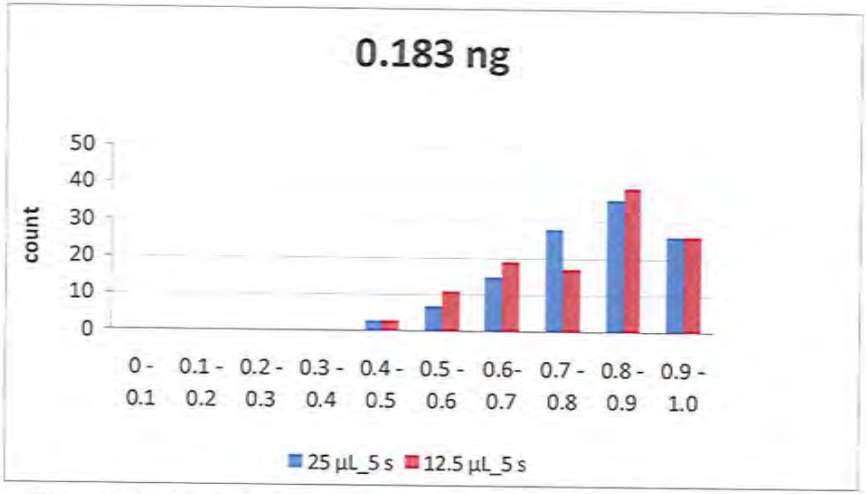

Figure 21 - The n of allele pairs per 0.1 PHR bin for 0.183 ng 5 s inj.

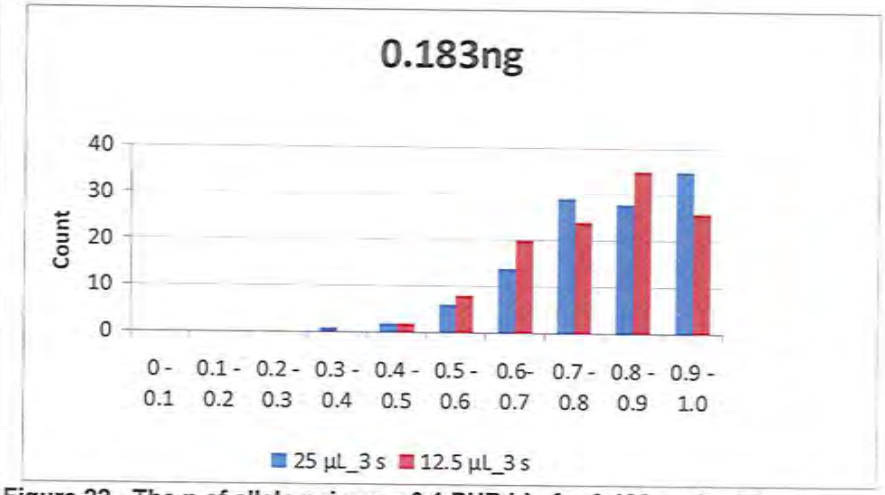

Figure 22 - The n of allele pairs per 0.1 PHR bin for 0.183 ng 3 s inj.

2875

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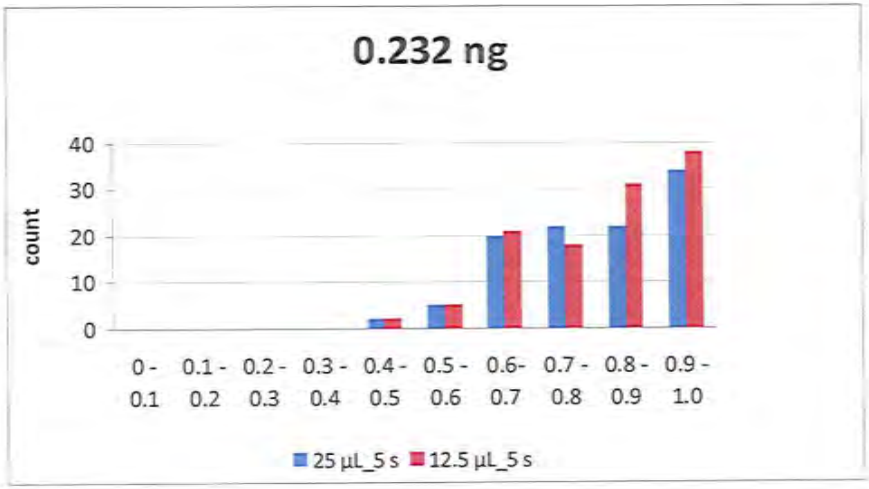

Figure 23 - The n of allele pairs per 0.1 PHR bin for 0.2.32 ng 5 s inj.

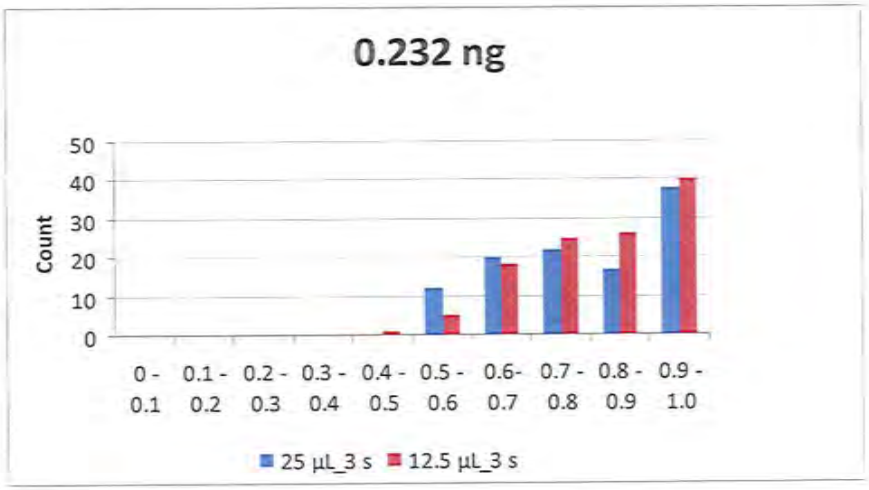

Figure 24 - The n of allele pairs per 0.1 PHR bin for 0.232 ng 3 s inj.

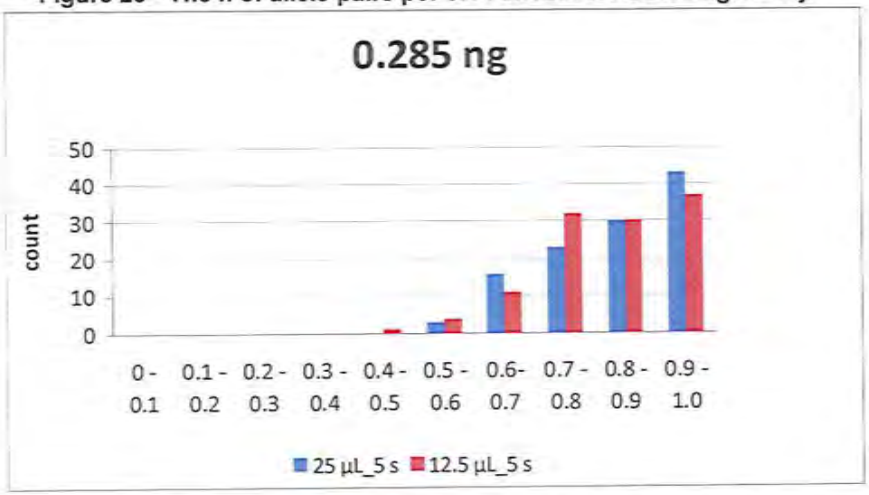

Figure 25 - The n of allele pairs per 0.1 PHR bin for 0.2.85 ng 5 s inj.

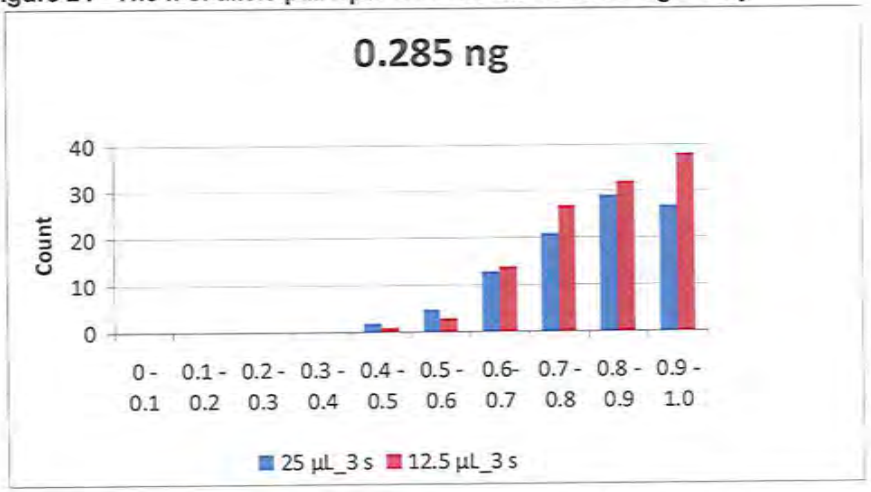

Figure 26 - The n of allele pairs per 0.1 PHR bin for 0.285 ng 3 s inj

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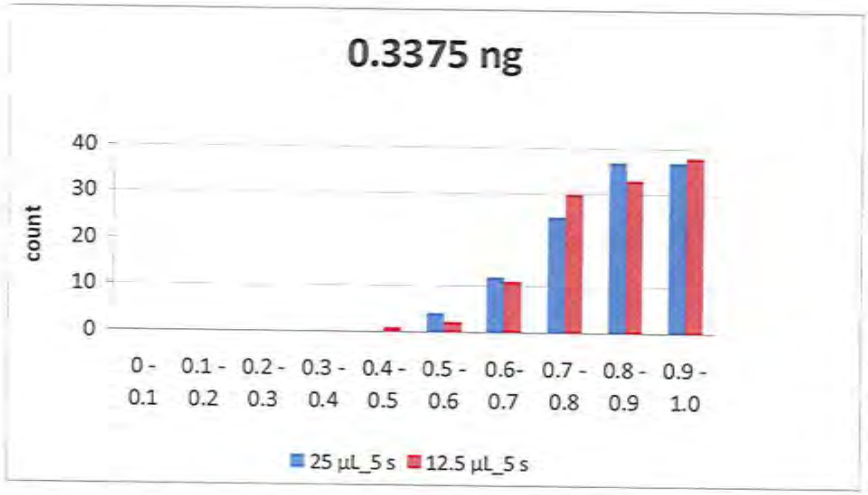

Figure 27 - The n of allele pairs per 0.1 PHR bin for 0.3375 ng 5 s inj.

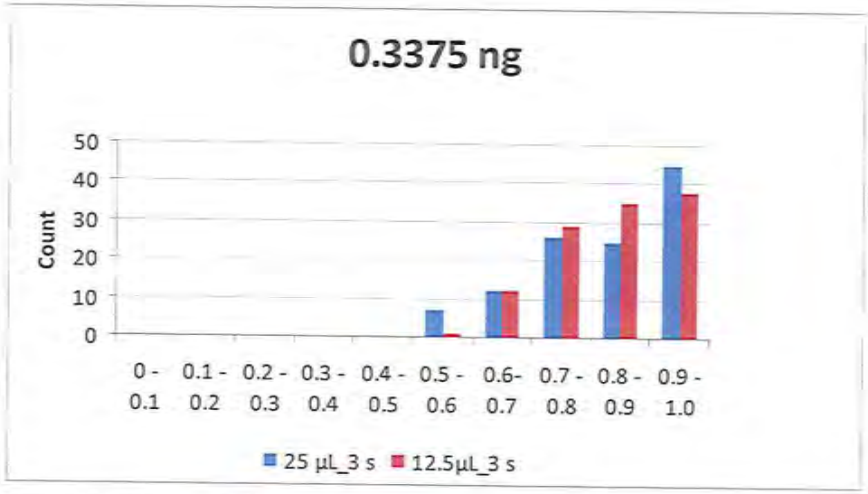

Figure 28 - The n of allele pairs per 0.1 PHR bin for 0.3375 ng 3 s inj.

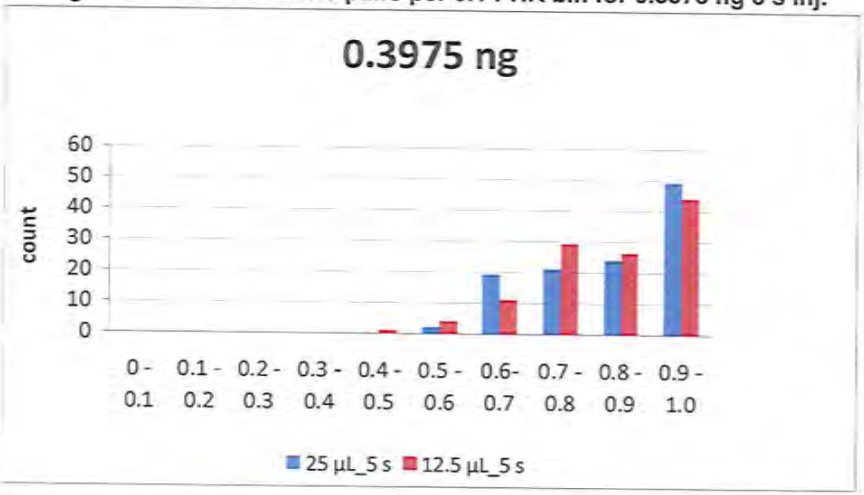

Figure 29 - The n of allele pairs per 0.1 PHR bin for 0.3975 ng 5 s inj.

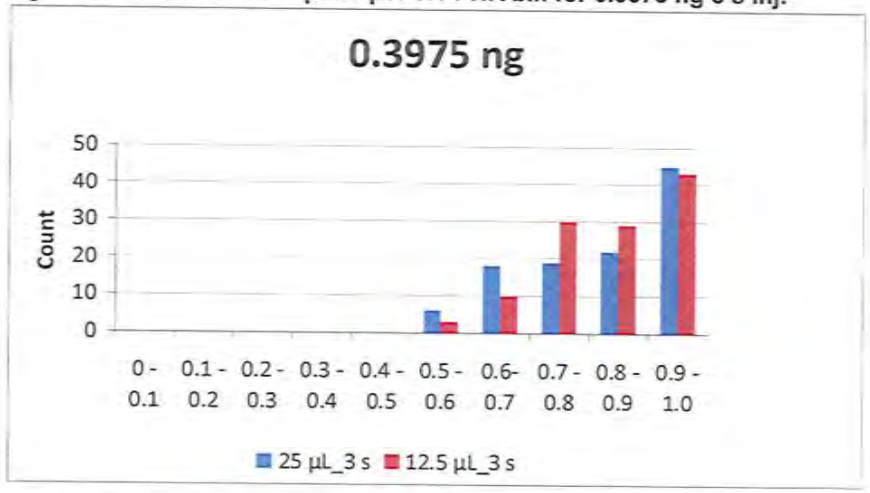

Figure 30 - The n of allele pairs per 0.1 PHR bin for 0.3975 ng 3 s inj.

28877

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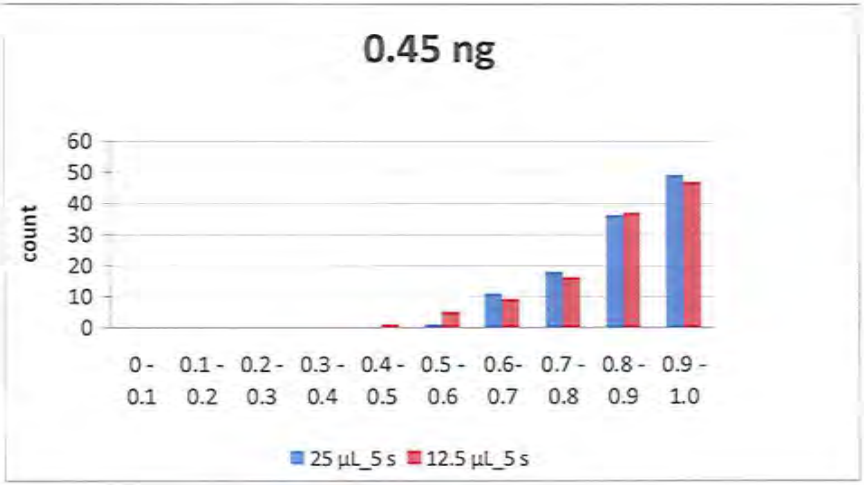

Figure 31- The n of allele pairs per 0.1 PHR bin for 0.45 ng 5 s inj.

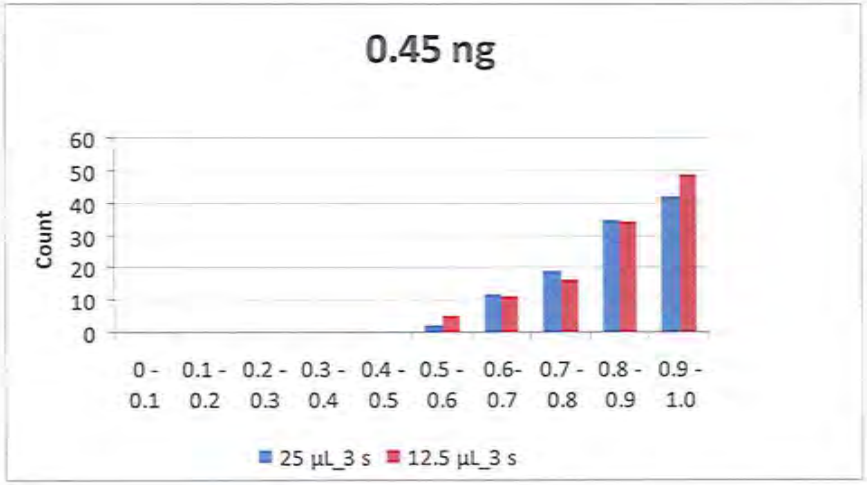

Figure 32 -The n of allele pairs per 0.1 PHR bin for 0.45 ng 3 s inj.

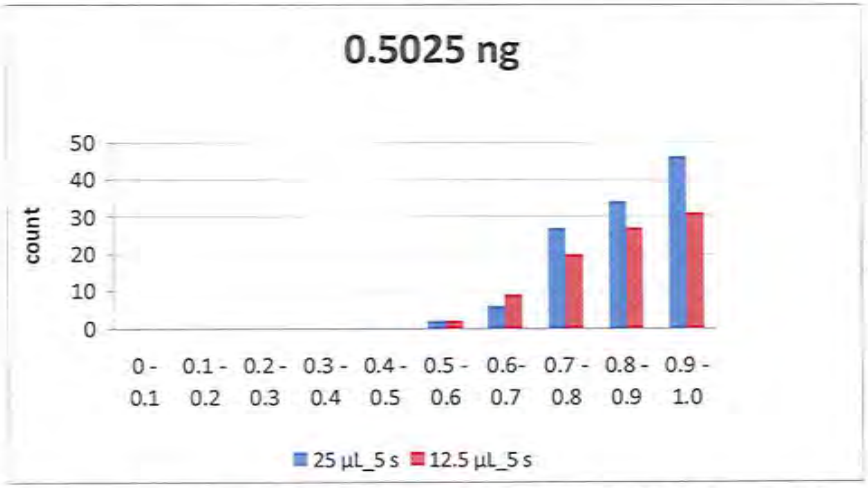

Figure 33- The n of allele pairs per 0.1 PHR bin for 0.5025 ng 5 s inj.

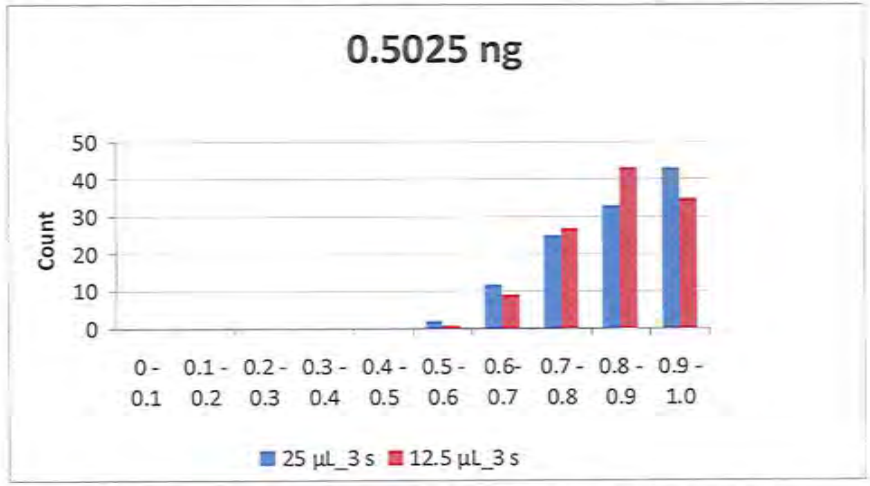

Figure 34 - The n of allele pairs per 0.1 PHR bin for 0.5025 ng 3 s inj.

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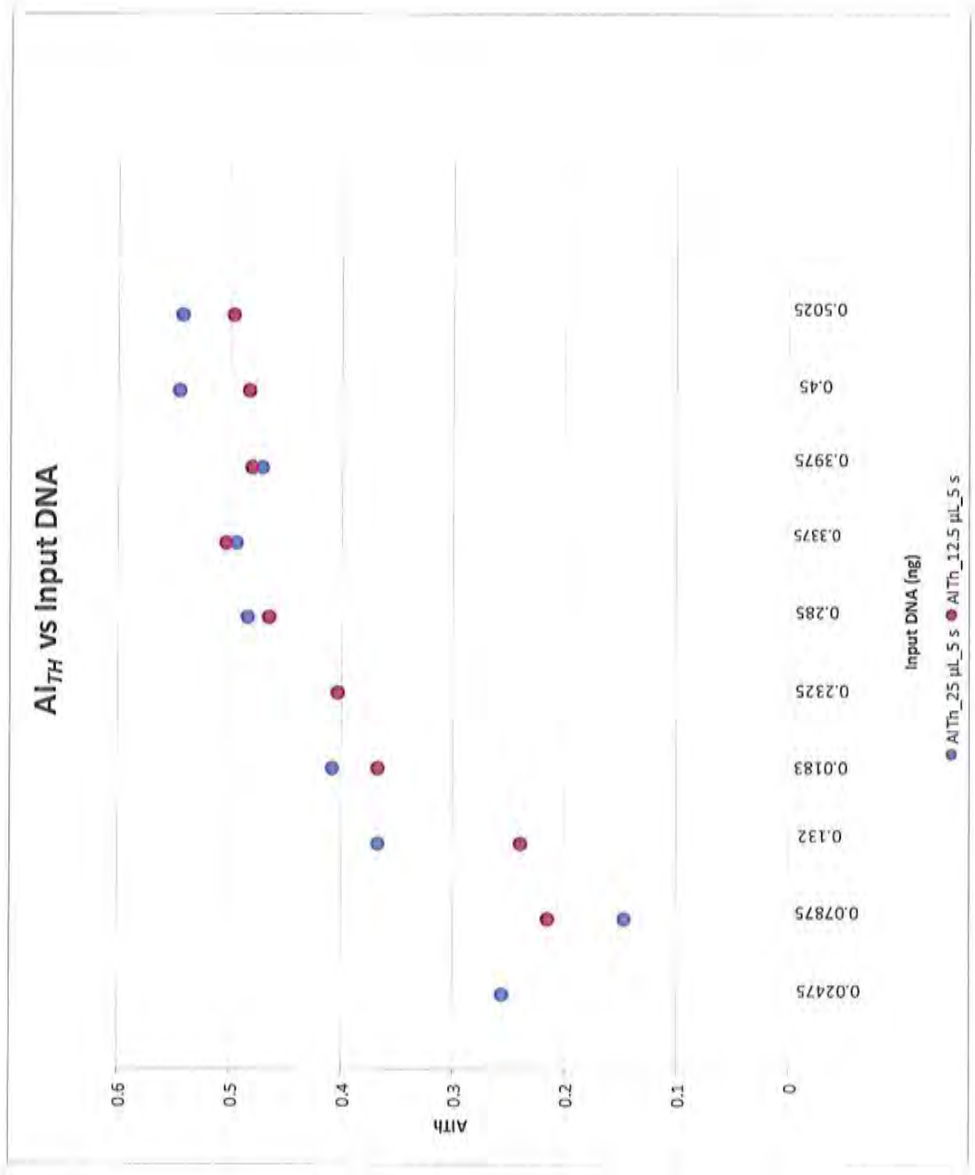

Figure 35 - Calculated AI_{TH} vs DNA template 5 s inj.

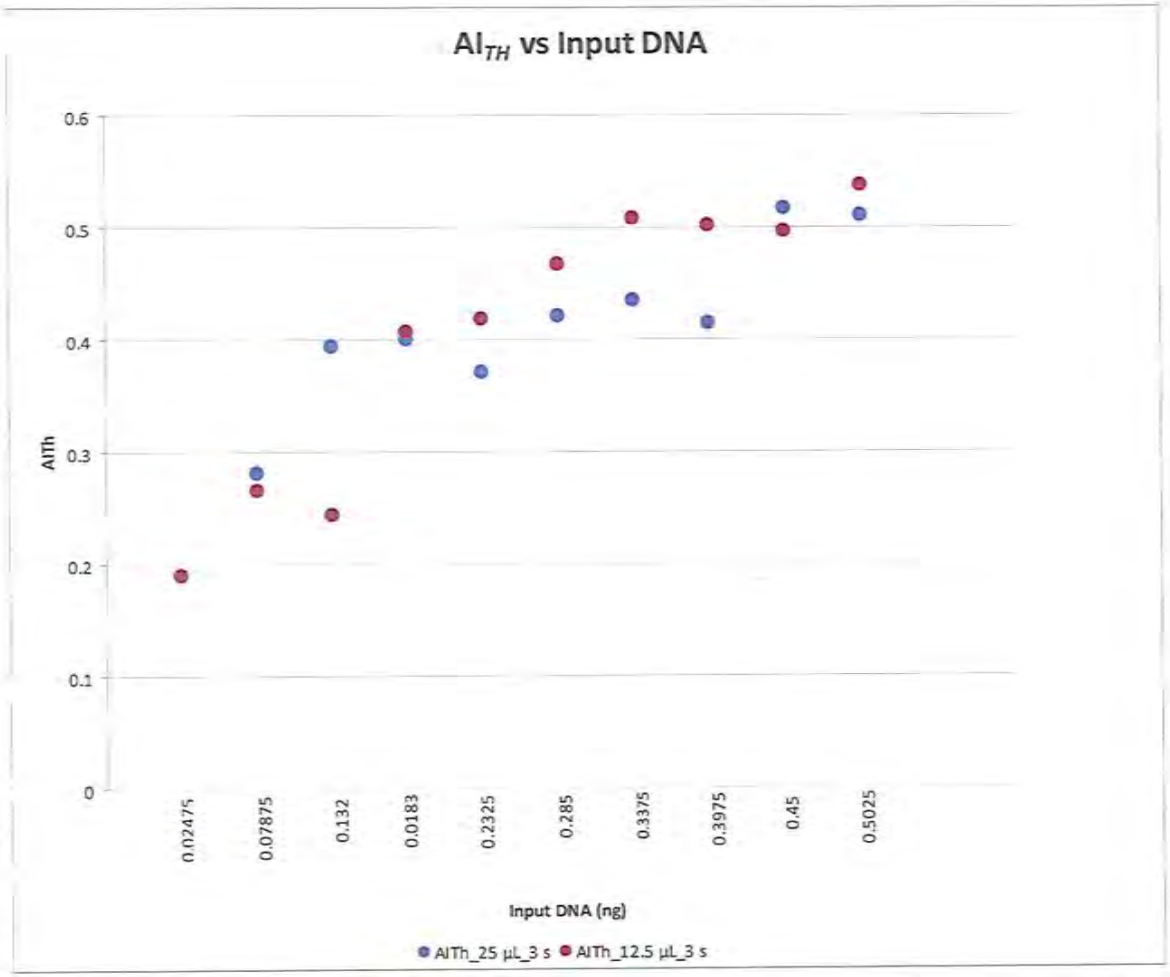

Figure 36 - Calculated AITH vs DNA template 3 s inj

6.7.2 Homozygote thresholds

The homozygote threshold is the threshold above which you can be confident that a heterozygote locus will not be incorrectly called as a homozygote locus.

Setting the homozygous threshold too high will result in excessive reworking of samples as a partial DNA profile would be called. Conversely, setting the threshold too low could result in false exclusions [1, 11, 23].

The method for determining the homozygote threshold varies in the literature. Traditionally, it had been arbitrarily designated at a particular level above the LOR. As already mentioned the risk of Type 1 and Type 2 errors should be balanced. Literature describes the setting of Th_{Hom} with respect to casework samples [21, 51, 52].

Previously in DNA Analysis, the Th_{Hom} was calculated as described in section 5.8.2 Equation 9. Using this method a result of 176 RFU for 25 µL(5 s inj), 193 RFU for 12.5 µL (5 s inj), 187 RFU for 25 µL(3 s inj), 186 RFU for 12.5 µL (3 s inj) was calculated. These thresholds have been calculated excluding data below 0.132 ng DNA template.

Another method of determining the Th_{Hom} is described in the Promega Internal Validation of STR systems reference manual[15]. This plots the peak height ratio for heterozygous loci against the lower RFU peak. The threshold is defined as the point at which peak height ratio drops off significantly. Figures 37 - 40 display the data, the average AI_{TH} calculated for the range 0.132 ng-0.5 ng in section 6.7.1 for 25 µL (5 s inj), 12.5 µL (5 s inj), 25 µL (3 s inj), 12.5 µL (3 s inj) respectively. An RFU that encompasses the majority of the data that falls below the average AI_{TH} calculated.

Unlike data reported in other publications[21, 53] there is not a rapid drop off of peak height ratios observed in the PowerPlex® 21 system, most likely due to the exclusion of the lower template data that exhibits extreme allelic imbalance. We have observed that the PowerPlex® 21 system loci tend to completely drop out completely compared to partially dropping out.

As both methods used give similar results, it is recommended the homozygote threshold be set at 200 RFU for 25 µL(both 5 s and 3 s inj) and 250 RFU for 12.5 µL(both 5 s and 3 s inj).

These methods are subjective but when considered with the observed drop out data in Figures 37 - 41, Th_{Hom} of 200RFU would result in no type 2 errors. Additionally the threshold is more than three times the LOR threshold so Type 1 errors would also be addressed.

The homozygote threshold calculated in this validation will be used for extracted reference samples as case work samples do not require a homozygote threshold for STRmix™ analysis.

To ensure all of the thresholds set for this validation are appropriate a post implementation review of the thresholds will be performed. If the

thresholds are found to be too conservative and have resulted in additional processing the review will provide an opportunity to re-adjust the thresholds based on empirical data.

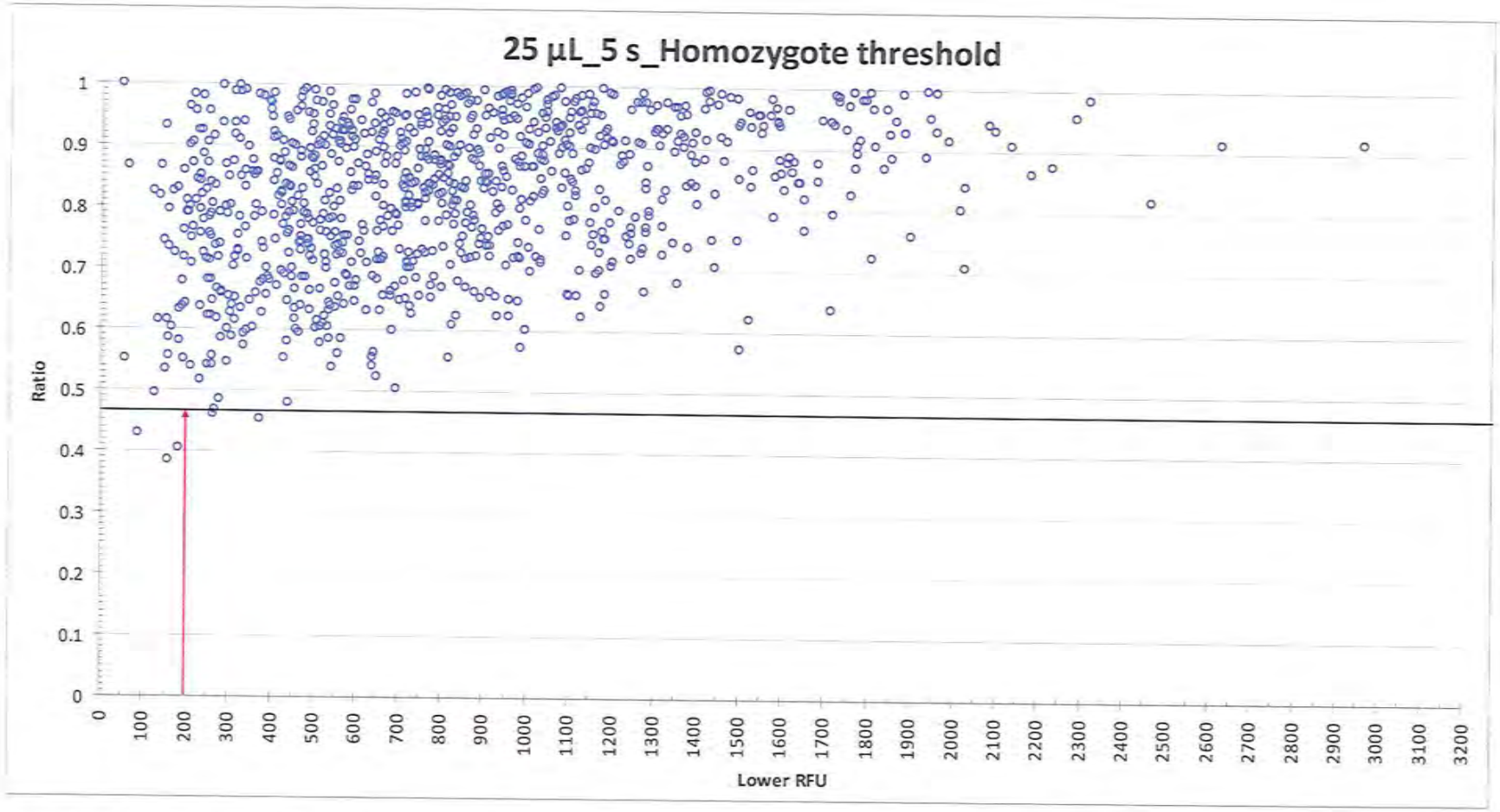

Figure 37 - Plot of the peak height ratio vs RFU of lower peak for 25 µL. The black horizontal line is the AI_{TH}. The red vertical line is set to approximately encompass the majority of points that fall below the AI_{TH}.

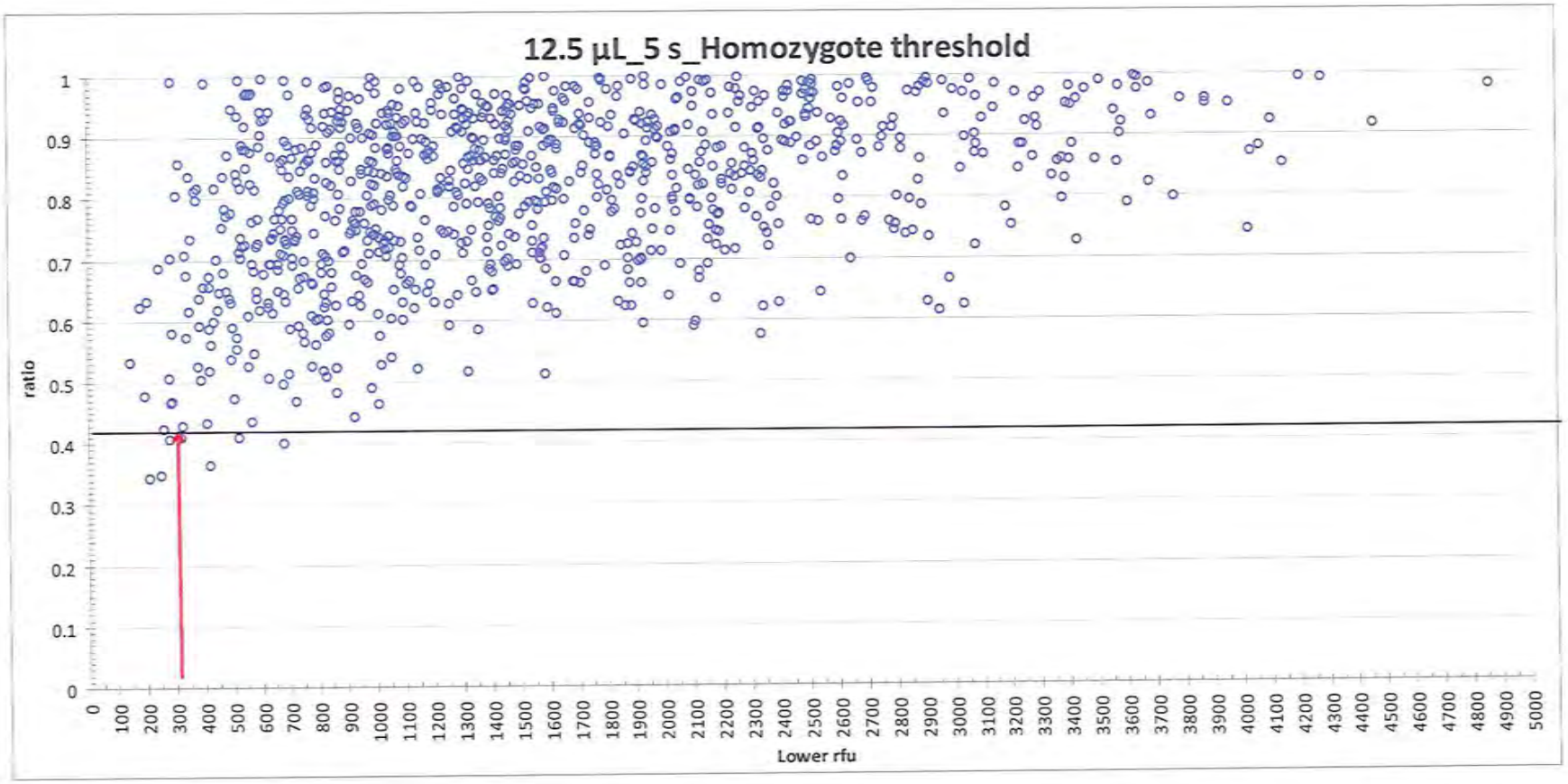

Figure 38 - Plot of the peak height ratio vs RFU of lower peak for 12.5 µL. The black horizontal line is the AITH. The red vertical line is set to approximately encompass the majority of points that fall below the AITH

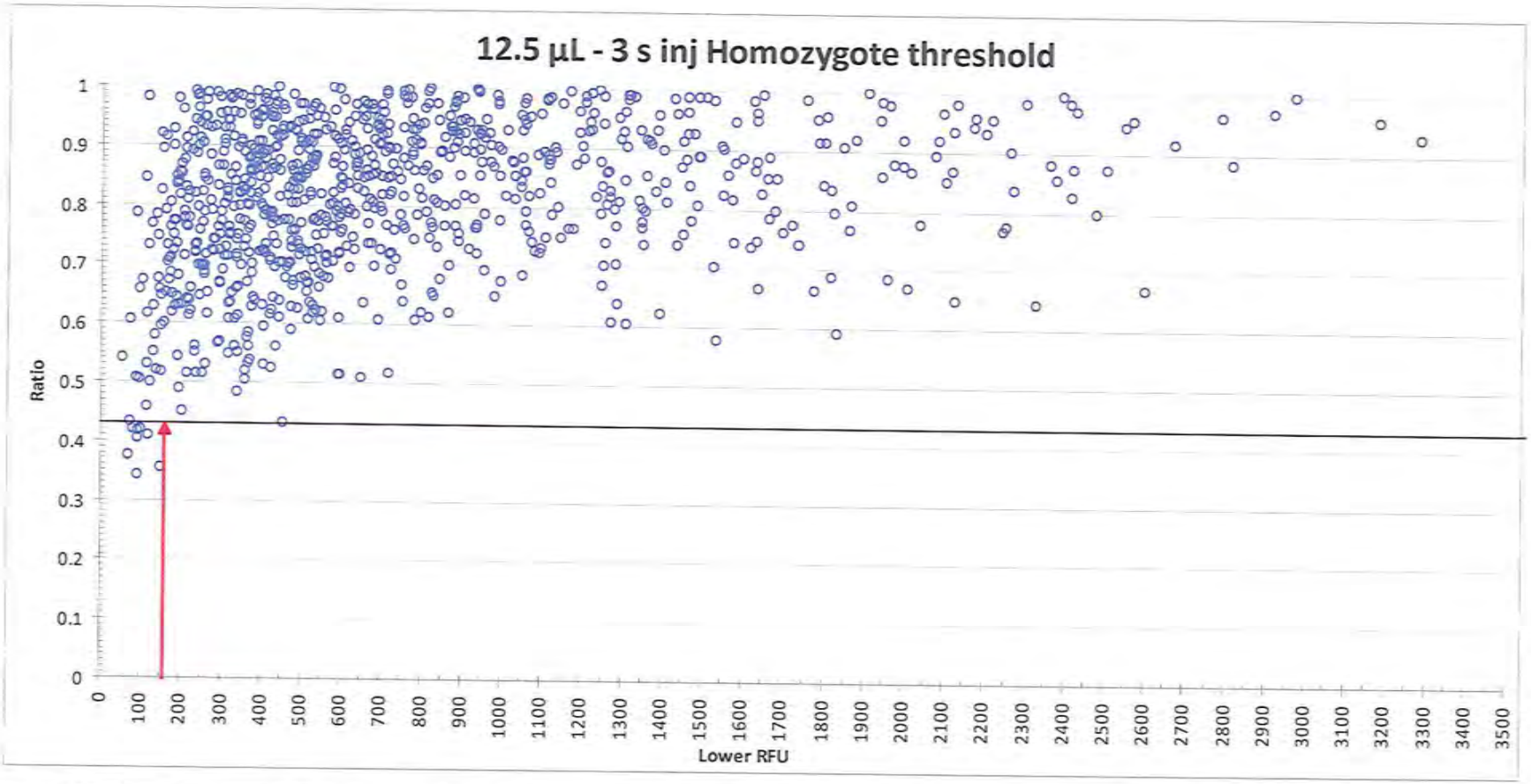

Figure 39 - Plot of the peak height ratio vs RFU of lower peak for 12.5 µL 3 s injection time. The black horizontal line is the AI_{TH}. The red vertical line is set to approximately encompass the majority of points that fall below the AI_{TH}

2885

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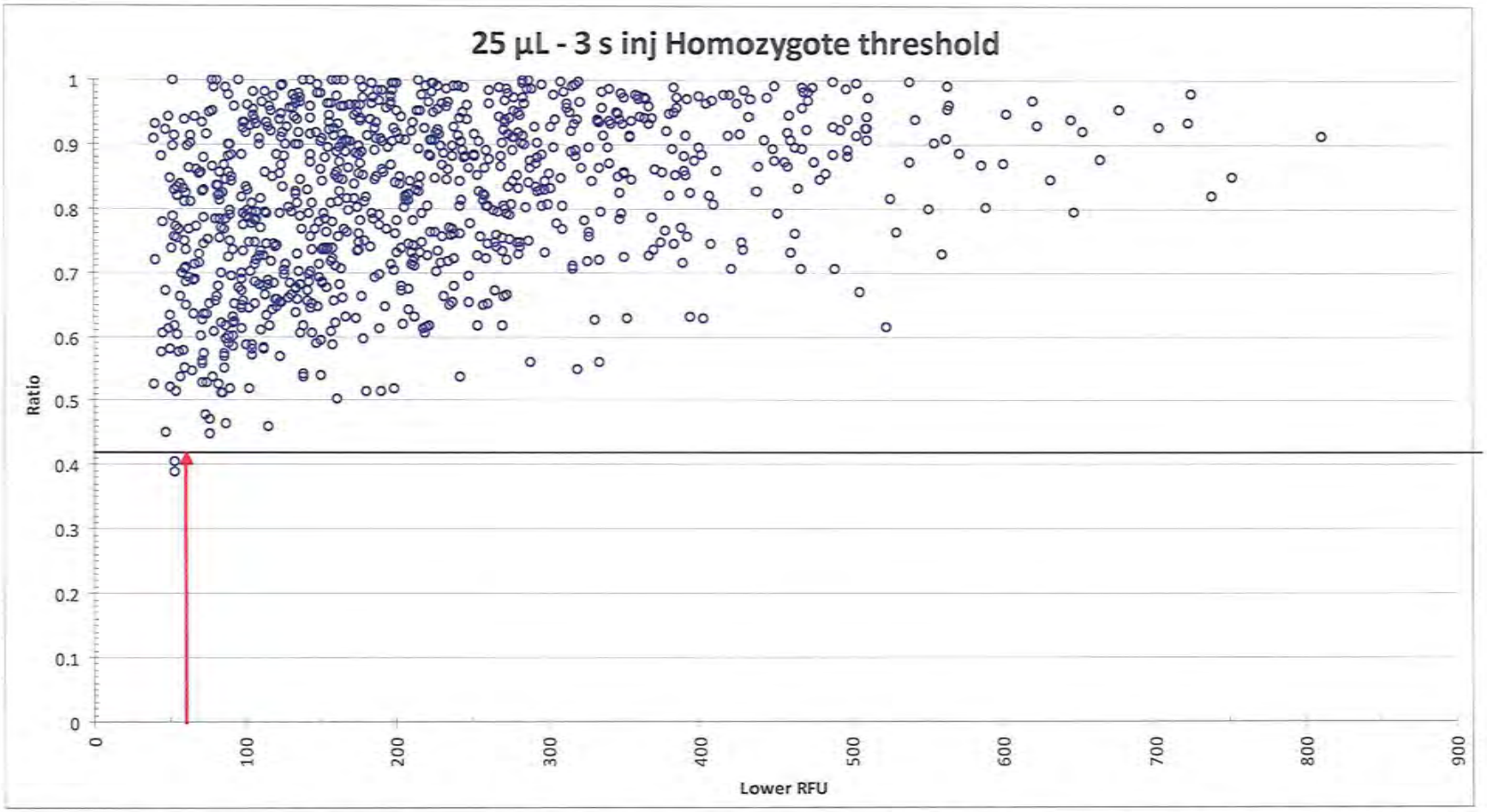

Figure 40 - Plot of the peak height ratio vs RFU of lower peak for 25 µL 3 s injection time. The black horizontal line is the AI_{TH}. The red vertical line is set to approximately encompass the majority of points that fall below the AI_{TH}

6.8 Dropout Experiments

Allelic dropout is when one allele of a heterozygous pair has not appeared or has a very low peak height[54]. One cause of dropout is one allele of a heterozygous pair is preferentially amplified thus giving the false impression of a homozygous allele at a particular locus[35].

This experiment used sensitivity 1 data of the two donors from 1 ng to 1 pg the 4 ng and 2 ng data was excluded due to the excess nature of the profiles. The heat maps shown in Figures 41 - 44 summarise the data to quickly compare the drop out events observed.

The data for the 25 µL amplification shows 62 drop out events occurred across both donors from dilutions 0.001 ng to 0.05 ng. Figures 41 and 42 show the highest peak height (RFU) where a heterozygous pair dropped out was at 160 RFU for the 0.01 ng dilution for donor 2 amplified at 25 µL total PCR volume.

The data for the 12.5 µL amplification shows 70 drop out events occurred across both donors from dilutions 0.001 ng to 0.05 ng. Figures 43 and 44 show the highest peak height (RFU) where a heterozygous pair dropped out was at 399 RFU for the 0.01 ng dilution for donor 2.



Locus dropout
Allele dropout (surviving allele RFU)
Complete heterozygous locus
Homozygous locus

	Input DNA (ng)	AMEL	D3S1358	D1S1656	D6S1043	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	D8S1179	D12S391	D19S433	FGA
Donor 1	0.001										54											
	0.001								43													
	0.005	83												50		96					69	
	0.005	41		46		61								46				54	70			
	0.01	100	76	73						58	67	49		65	51		90	103	140			
	0.01	89								47			120		41	87	42		50	40	88	63
	0.05																131					
	0.05																					
	0.1																					
	0.1																					
	0.5																					
	0.5																					
	1																					
	1																					

Figure 41 - Heat map - Donor 1 – 25 µL total PCR volume

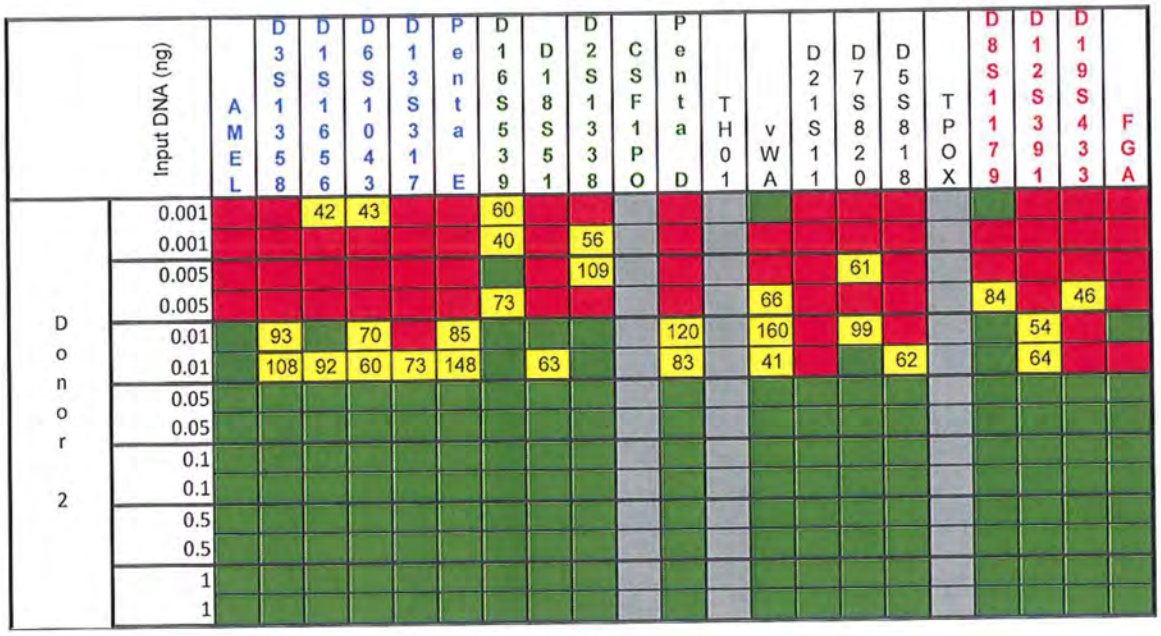

Figure 42 - Heat map - Donor 2 – 25 µL total PCR volume

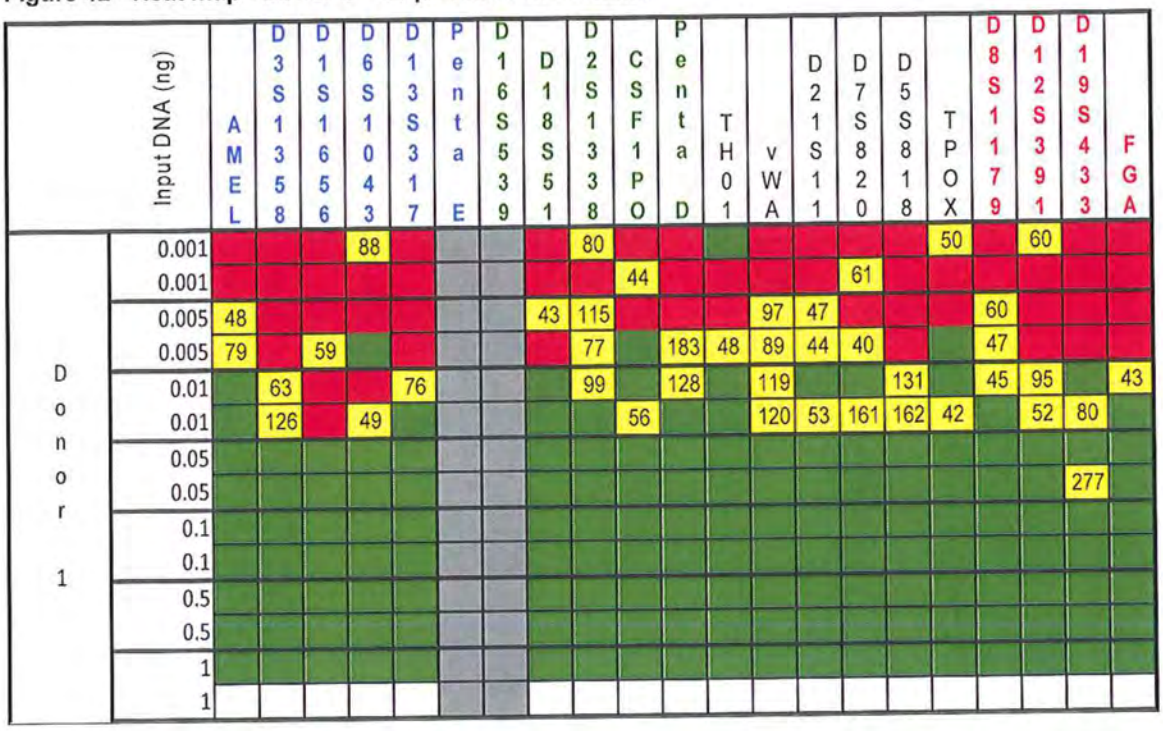

Figure 43 - Heat map - Donor 1 - 12.5 µL total PCR volume

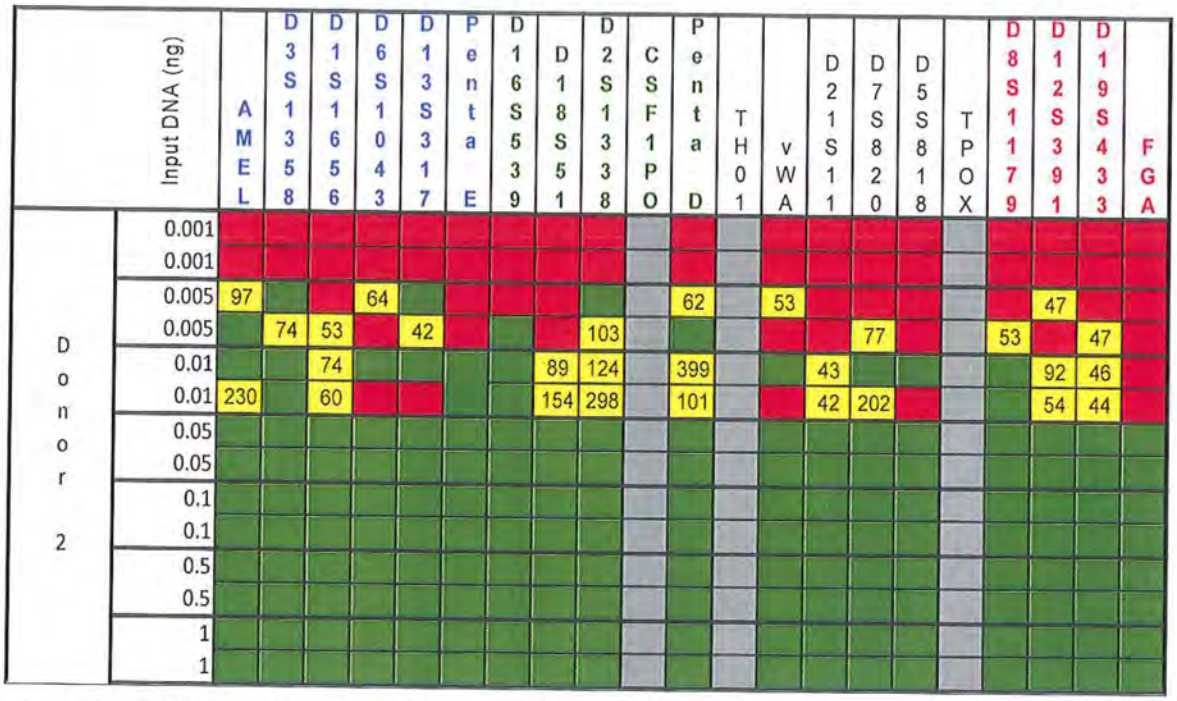

Figure 44 - Heat Map – Donor 2 - 12.5 µL total PCR volume

6.8.1 Drop out 2

Analysis for drop out 2 used the data obtain from the Aboriginal dataset and both sensitivity experiments for 25 µL total PCR volume (5 s inj), baseline experiment (3 s inj) for 25 µL total PCR volume (3 s inj), the baseline experiment, both sensitivity experiments for 12.5µL total PCR volume (5 s inj) and concordance for 12.5 µL (3 s inj). The dropout 2 results are displayed in figures 45 -48. Figure 45 shows the dropout events for all samples amplified at 25 µL total PCR volume (5 s inj). Figure 46 shows the dropout events for all samples amplified at 25 µL total PCR volume (3 s inj).

Figure 47 shows the dropout events for all samples amplified at 12.5 µL total PCR volume (5s inj). Figure 48 shows the dropout events for all samples amplified at 12.5 µL total PCR volume (3 s inj).

For both 25 µL and 12.5 µL total PCR volume amplifications and both injection times, there were more drop out events of whole loci compared with a single allele drop out events.

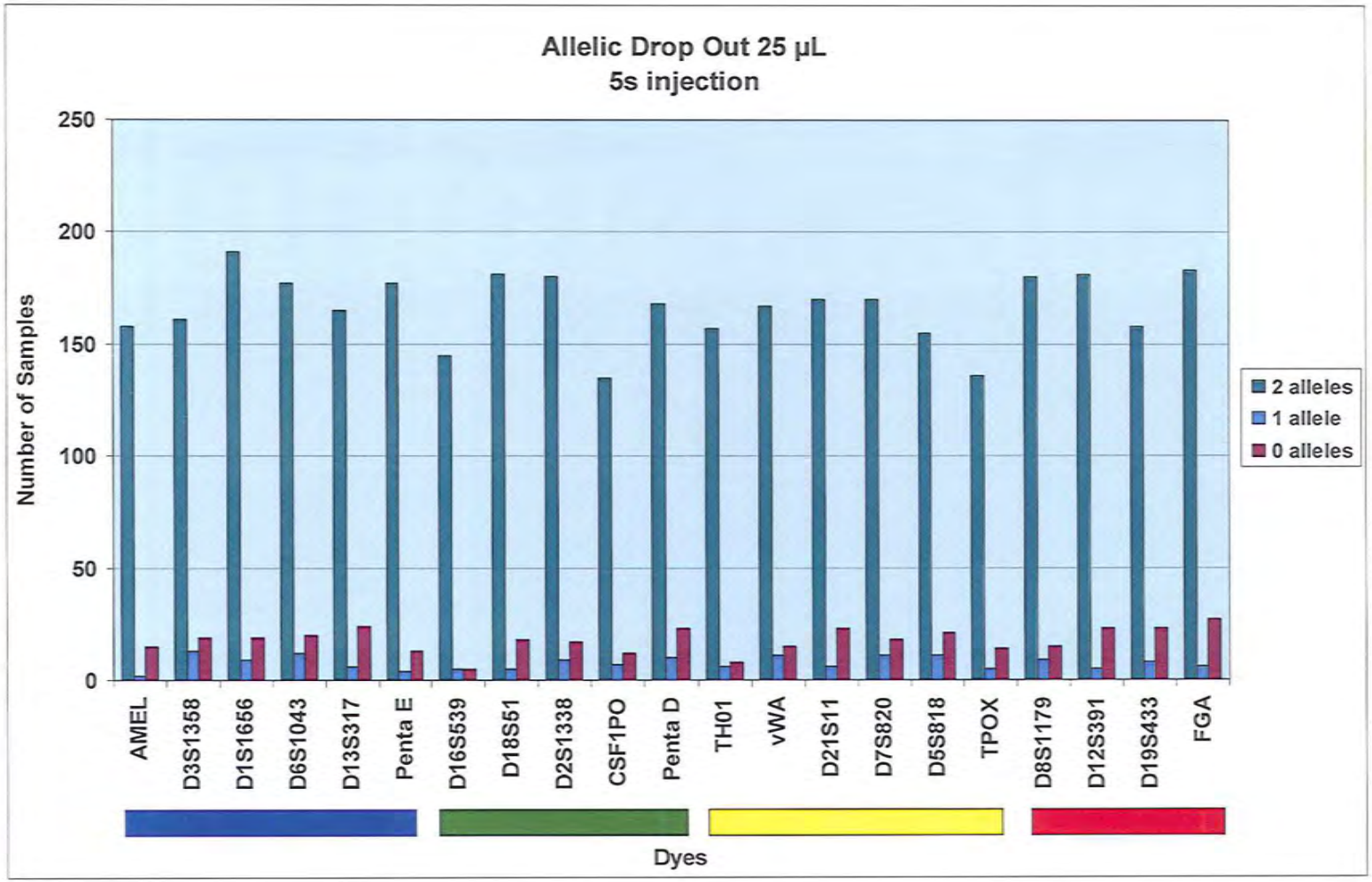

Figure 45 - Dropout events for samples amplified at 25 µL 5 s injection time.

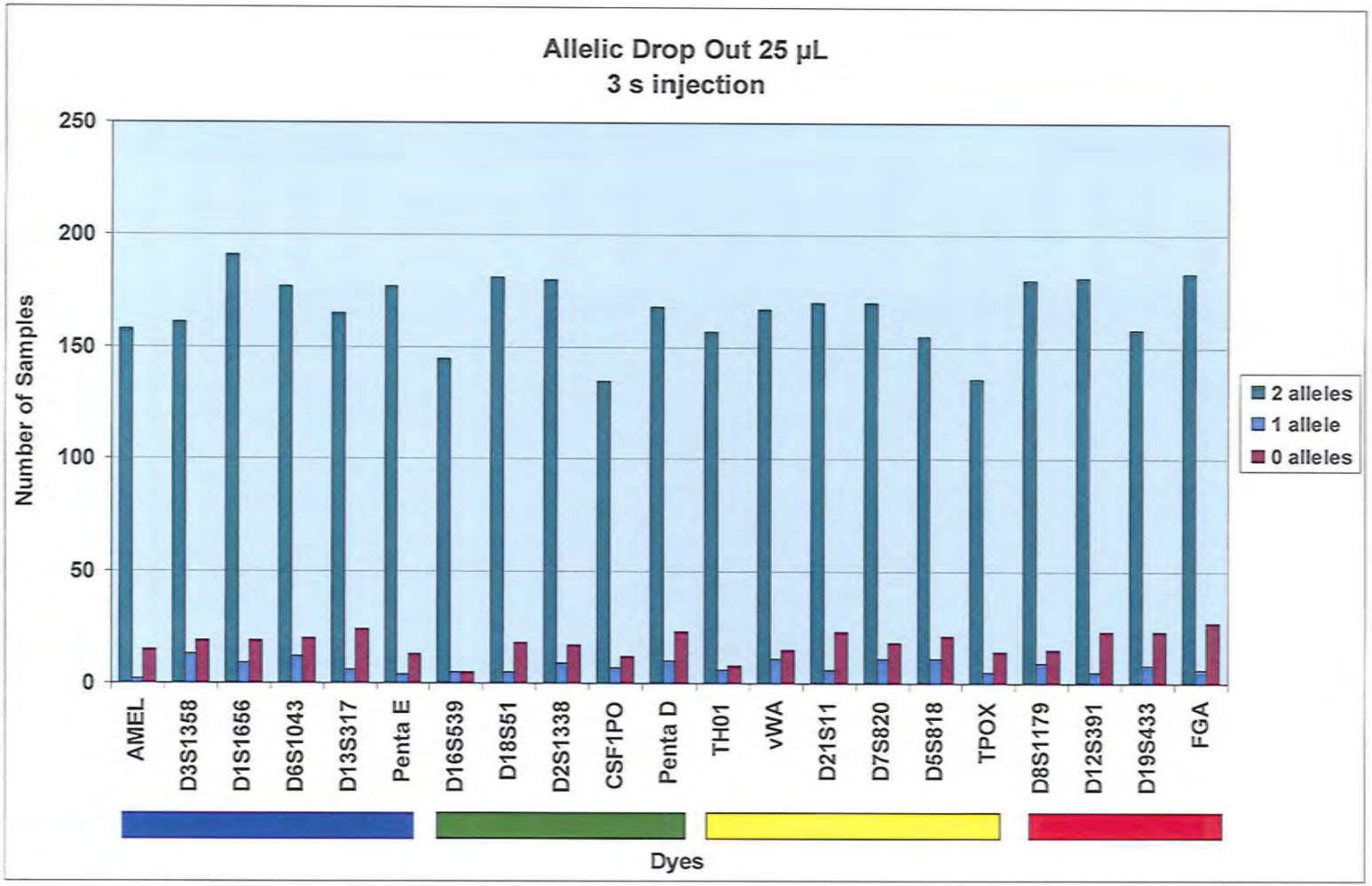

Figure 46 - Dropout events for samples amplified at 25 µL 3 s injection time.

2891

WIT.0019.0012.2965

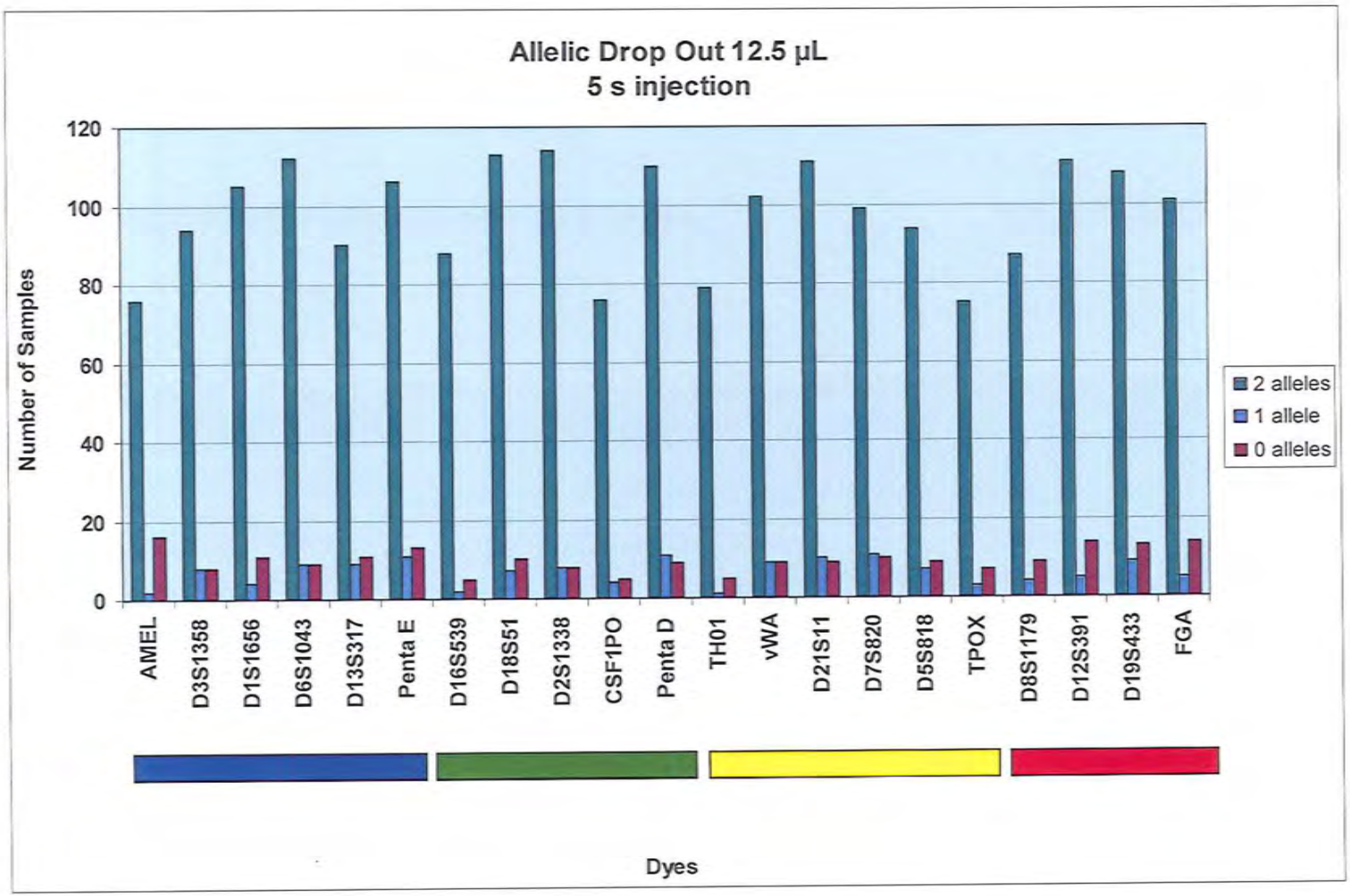

Figure 47 - Dropout events for samples amplified at 12.5 µL 5 s injection time.

2892

WIT.0019.0012.2966

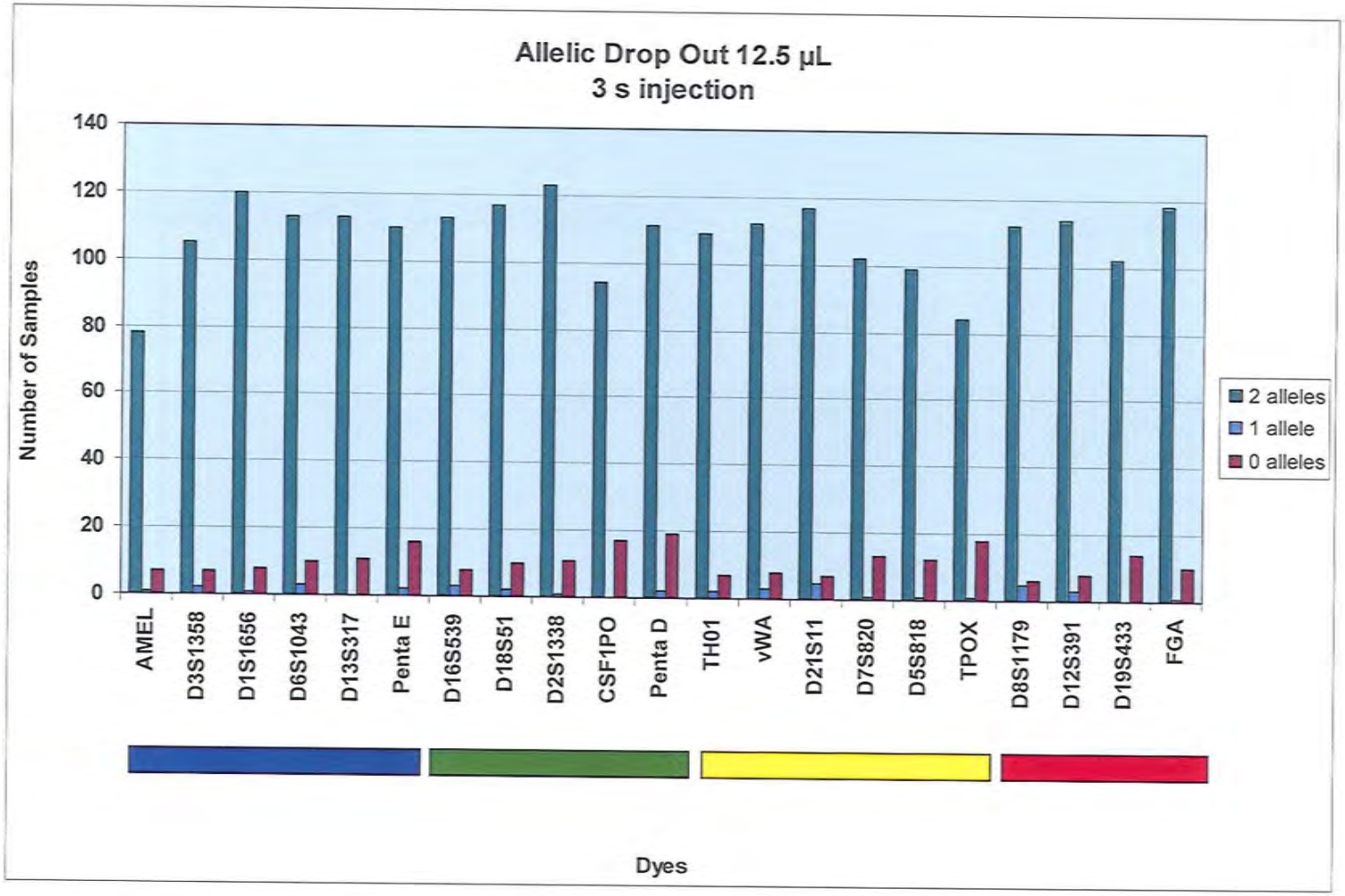

Figure 48- Dropout events for samples amplified at 12.5 µL 3 s injection time.

2893

WIT.0019.0012.2967

6.8.2 Drop out 3

Analysis for drop out 3 used the data from the baseline samples (10 x 10) and both sensitivity experiments at both 25 µL and 12.5 µL total PCR volume. There were 205 drop out events observed for the 25 µL total PCR volume compared to198 drop out events observed at 12.5 µL total PCR volume. Figure 49 shows the number of drop out events for a range of peak heights. This shows the majority of drop out events occur below 150 RFU for 25 µL total PCR volume and below 180 RFU for 12.5 µL total PCR volume.

Figures 50 - 52 show the peak heights where one of the heterozygote pairs has dropout at each DNA template. Figure 50 shows one dropout event occurred at 226 RFU for the 12.5 µL total PCR volume at a DNA template of 0.131 ng whereas no dropout events occurred at 25 µL total PCR volume at the same DNA template. The highest drop out seen for 12.5 µL total PCR volume was at 234 RFU at a DNA template of 0.025 ng and for 25 µL total PCR volume was at 193 RFU. The total number of dropout events seen for the baseline samples at 25 µL total PCR volume was 59 and 30 at 12.5 µL total PCR volume.

Figure 51 (Sensitivity 1) shows the highest drop out for 12.5 µL total PCR volume was seen at 399 RFU at a DNA template of 0.01 ng and 160 RFU at DNA template 0.01 ng for the 25 µL total PCR volume. The total number of dropout events seen for the sensitivity 1 experiment at 25 µL total PCR volume was 58 and 66 at 12.5µL total PCR volume.

Figure 52 (Sensitivity 2) shows the highest drop out for 12.5 µL total PCR volume was seen at 246 RFU at a DNA template of 0.0094 ng and 249 RFU at a DNA template of 0.0375 ng for the 25 µL total PCR volume. The total number of dropout events seen for the sensitivity 2 experiment at 25 µL total PCR volume was 89 and 102 at 12.5 µL total PCR volume.

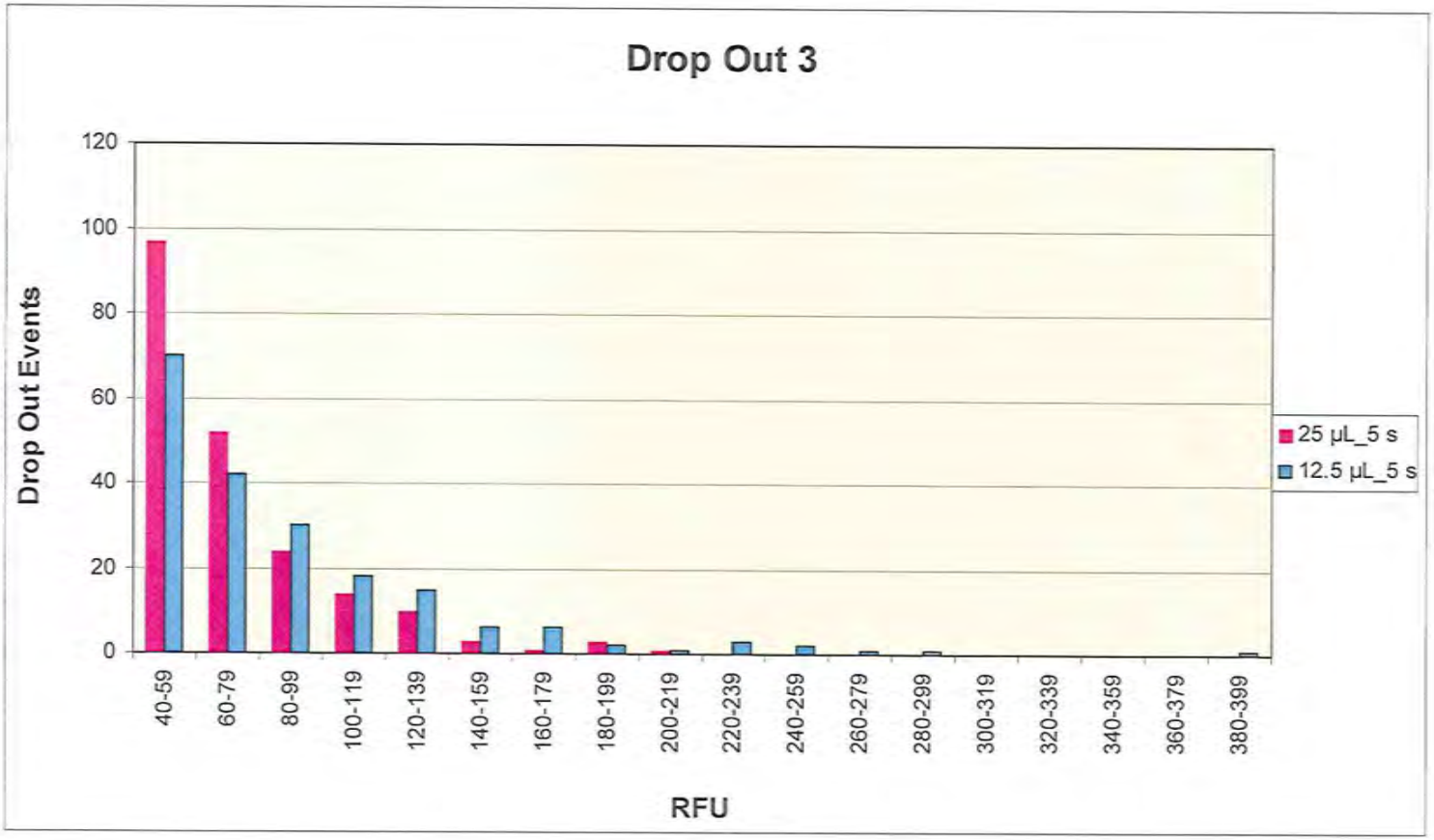

Figure 49 - Number of drop out events seen within peak height ranges at 25 µL and 12.5 µL amplifications (5 s inj)

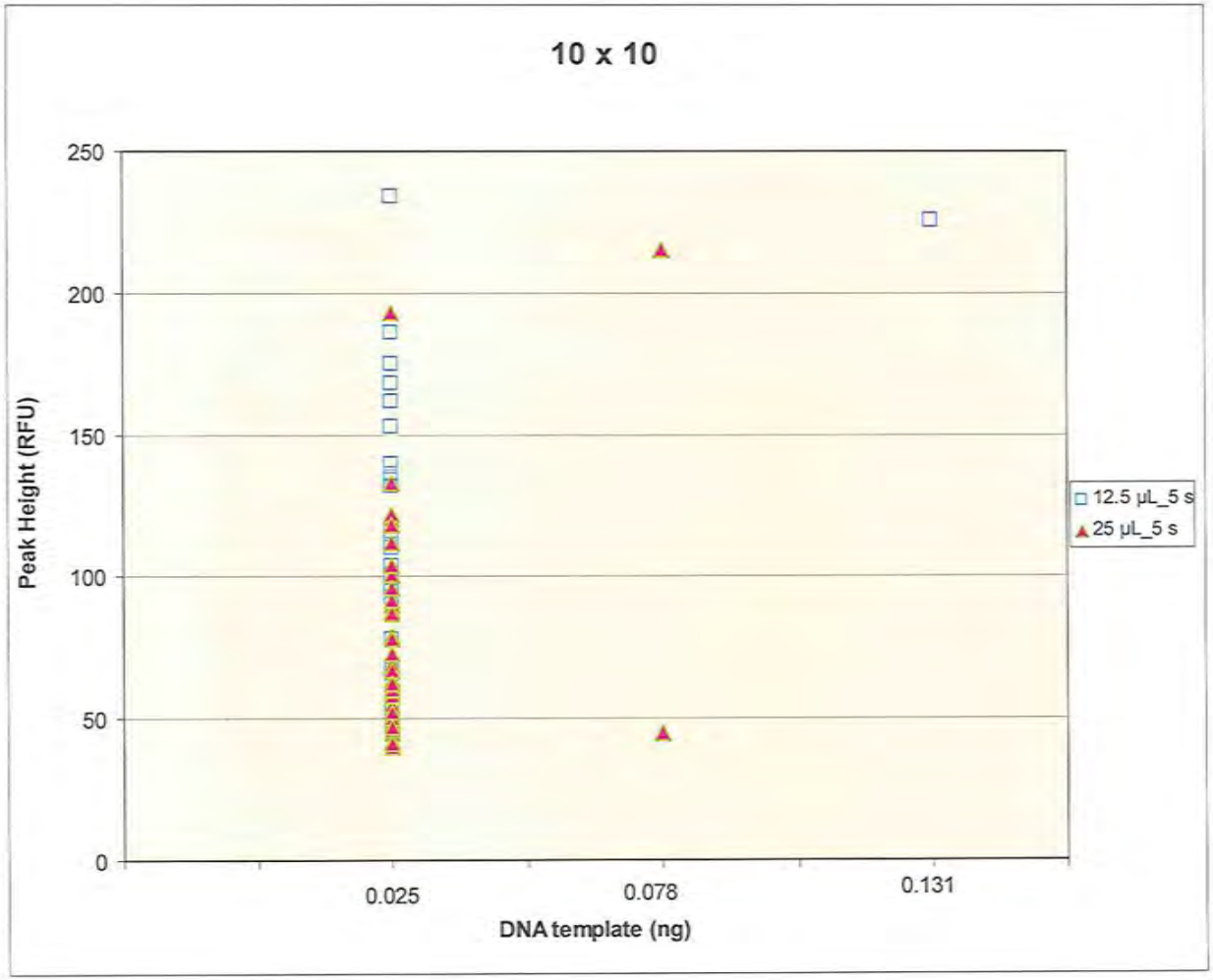

Figure 50 - Peak heights where the heterozygote pair has dropped out at different DNA templates for 12.5 µL and 25 µL using the baseline data (10 x10)

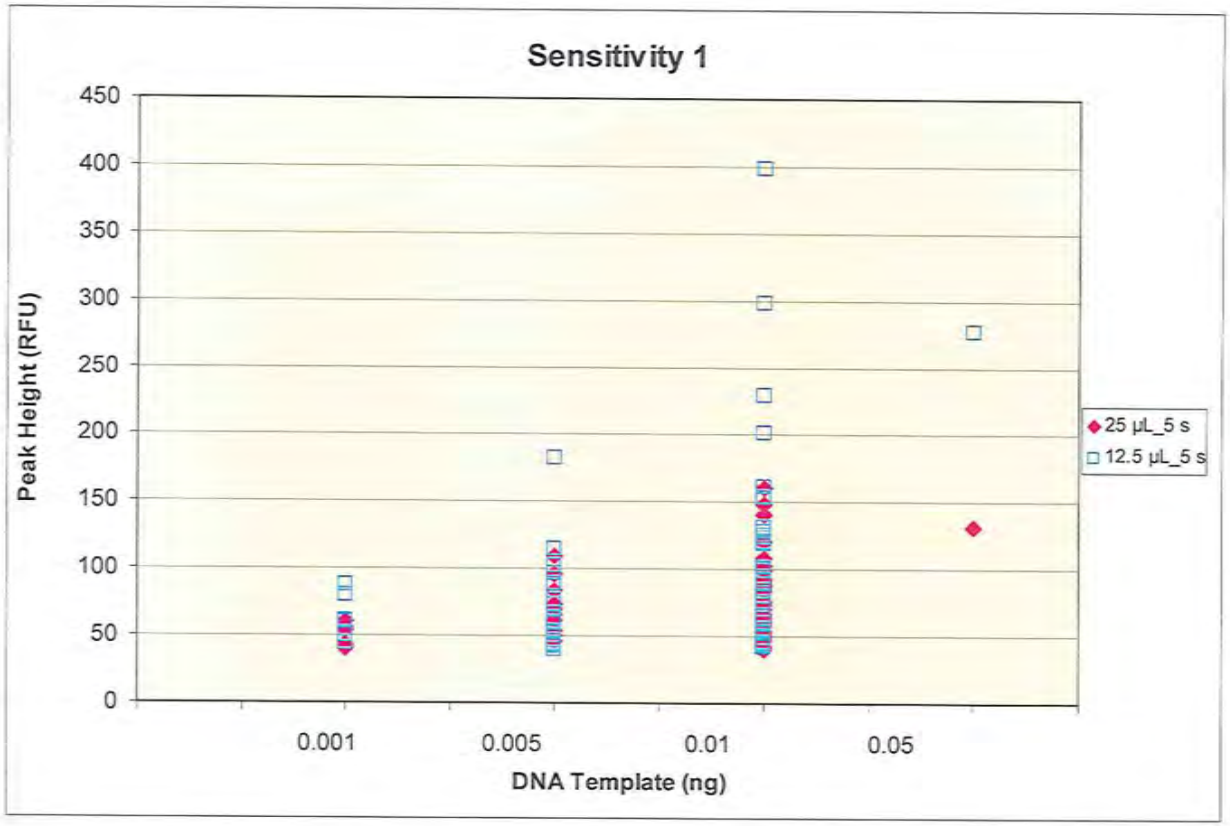

Figure 51 - Peak heights where the heterozygote pair has dropped out at different DNA templates for 12.5 µL and 25 µL using sensitivity 1 data

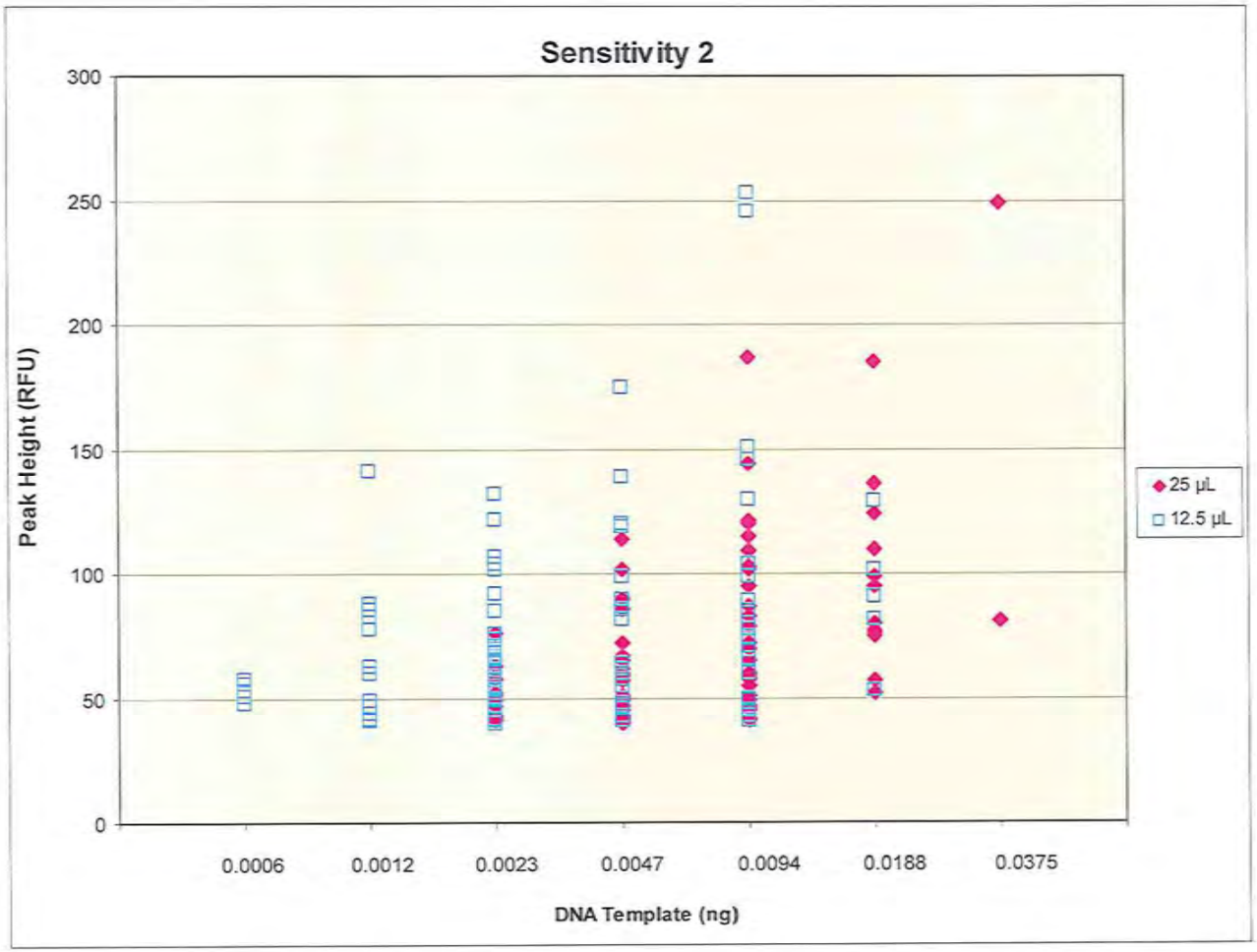

Figure 52 - Peak heights where the heterozygote pair has dropped out at different DNA templates for 12.5 µL and 25 µL using sensitivity 2 data

6.9 Mixture Studies

At a total input template of 0.5 ng, for both 25 µL and 12.5 µL, all alleles were detected for the mixtures with ratios of 1:1, 2:1 and 5:1. Any allelic imbalance was observed at a level of greater than 40%.

When the template was decreased to 0.125 ng for 5:1 mixtures, drop-out of the lower level contributor was observed for both 25 µL and 12.5 µL volumes. At this template level, allelic imbalance of down to 35% was observed for the lower level contributor at both 25 µL and 12.5 µL volumes, however, one of these peaks fell into the stutter position of the larger contributor.

When the template was decreased to 0.06 ng for 2:1 mixtures, drop-out of the lower level contributor was observed for both 25 µL and 12.5 µL volume with the partner allele being as high as 562 RFU. At this template level, allelic imbalance of down to 20% was observed for the lower level contributor and 23% for the higher level contributor.

For the remaining mixtures with ratios of 10:1, 20:1, 30:1 and 50:1 of varying template levels (maximum 0.5 ng), the lower contributors exhibited, sometimes quite marked, stochastic variation. This included drop-out with peaks up to 392 RFU and allelic imbalance as low as 20%.

The data in Table 21 and Table 22 show the approximate mixture ratio of the profile compared with the mixture ratio of the sample. For the 2 person mixtures this was averaged over all loci where there was no allele sharing between the two contributors and where the alleles did not fall into a stutter position. For the 3 person mixtures, the ratio was averaged over all loci where there was no allele sharing between the three contributors, however it was not possible to exclude loci where the alleles fell into stutter positions as there were no loci fulfilling this criteria. It was not possible to accurately calculate mixture ratios for the four person mixtures.

The data shows that the mixture ratio after DNA amplification is approximately equal to the mixture ratio of the initial sample for both 25 µL and 12.5 µL volumes at all ratios. The mixture ratio deviates more as the ratio increases most likely due to the stochastic effects of the lower contributor. The mixture ratios for the 25 µL volume amp appear to be slightly lower than for the12.5 µL volume amp.

Although mixture ratios have not been calculated for the four person mixtures, the alleles obtained are consistent with expected profiles.

Table 21 - 12.5 µL total PCR volume mixture studies

Mixture Ratio of Sample	Total Input Template (ng)	Approximate Mixture Ratio of Profile
2 Person Mixtures		
1:1	0.500	1.2:1
2:1	0.500	2.2:1
	0.060	2.9:1
5:1	0.500	6.1:1
	0.125	6.1:1
10:1	0.500	12:1
	0.125	11:1
20:1	0.500	24:1
	0.250	16:1
	0.125	19:1
30:1	0.500	21:1
50:1	0.500	35:1
	0.250	49:1
	0.125	Unable to calculate
3 Person Mixtures		
5:2:1	0.500	4.2:1.3:1
	0.125	Unable to calculate
10:5:1	0.500	13:9.1:1
20:10:1	0.500	10:5.7:1
	0.125	Unable to calculate
4 Person Mixtures		
5:3:2:1	0.500	Unable to calculate
	0.125	Unable to calculate

Table 22 – 25 µL total PCR mixture studies

Mixture Ratio of Sample	Total Input Template (ng)	Approximate Mixture Ratio of Profile
2 Person Mixtures		
1:1	0.500	1.2:1
2:1	0.500	1.8:1
	0.060	1.7:1
5:1	0.500	4.1:1
	0.125	4.8:1
10:1	0.500	8.5:1
	0.125	6.3:1
20:1	0.500	22:1
	0.250	17:1
	0.125	10:1
30:1	0.500	15:1
50:1	0.500	26:1
	0.250	9.2:1
	0.125	6.7:1
3 Person Mixtures		
5:2:1	0.500	2.9:1.5:1
	0.125	2.7:1.1:1
10:5:1	0.500	7.4:5.4:1
20:10:1	0.500	10:6.4:1
	0.125	10:4.7:1
4 Person Mixtures		
5:3:2:1	0.500	Unable to calculate
	0.125	Unable to calculate

7 Conclusion

The results from this validation support that Promega's PowerPlex®21 System is suitable for analysis of STRs.

Despite slight differences observed between the two 3130xl analysers, the use of single LOD and LOR of 16 RFU and 40 RFU is more practical for use in DNA Analysis.

The PowerPlex21® System displays full concordance with all alleles observed in testing being concordant.

The three national population datasets (Caucasian, Aboriginal and SE Asian) created collaboratively within Australia, have been externally validated and will be implemented in conjunction with STRmix™ for statistical interpretation.

12.5 µL total PCR volumes gave higher peak heights than their 25 µL counterparts at the same DNA template.

The PowerPlex®21 system is a very sensitive amplification kit when used at either the standard amplification volume (25 µL) or reduced volume amplification (12.5 µL); however the increased sensitivity does not necessarily result in more reliable information.

The two sensitivity experiments explored the range on DNA template inputs from very large inputs (4 ng) to very small inputs (0.00059 ng). Within this validation complete PowerPlex® 21 DNA profiles were obtained with as little as 0.01875 ng of template DNA. However, the PHR data indicate that as the amount of template DNA decreases the μ_{PHR} decreases and σ_{PHR} increases. The risk of type 2 errors is greatly increased from template DNA amounts of less than 0.132 ng for both 25 µL and 12.5 µL total PCR volumes, which is supported by the experimental drop out data.

The data presented within this report indicates that input templates less than 0.132 ng total DNA (concentrations 0.0176 ng/µL if using 12.5 µL total PCR volume or 0.0088 ng/µL for 25 µL total PCR volume) may result in increased stochastic effects.

As previously documented in DNA Analysis[55, 56], the Quantifiler™ Human DNA Quantification kit gives an estimate of the DNA concentration. Careful consideration of the DNA profile is required before reporting because the precision within a quantification method and between different quantification methods may vary.

For the range of DNA templates specified above, significant differences between 12.5 µL and 25 µL total PCR volumes was not observed. The use of 12.5 µL total amplification volume as the default protocol with DNA Analysis is indicated. The disadvantage of the 12.5 µL total PCR volume are the physical constraints of the process i.e. a maximum of 7.5 µL of sample can be used compared with 15 µL for the 25 µL total PCR volume. However, higher peak heights and the cost savings associated with

reduced volume amplifications even with additional processes to increase the sample concentration, mitigate the disadvantage.

The implementation of PowerPlex® 21 for amplification of DNA extracts will coincide with the implementation of STRmix™. The combination of the two processes will apply a continuous biological model rather than a binary model to DNA interpretation. STRmix™ models stutter, drop out, heterozygote balance and homozygote threshold for case work samples.

The rate of drop in events has been calculated for both total PCR volumes and will be implemented in conjunction with STRmix™.

At a total input template of 0.5 ng, for 25 µL and 12.5 µL total PCR volumes, all alleles were detected for the mixtures with ratios of 1:1, 2:1 and 5:1.

For the remaining mixtures with ratios of 10:1, 20:1, 30:1 and 50:1 of varying template levels (maximum 0.5 ng), the lower contributors exhibited, sometimes quite marked, stochastic variation.

Mixture interpretation is beyond the scope of this validation and will be dealt with in the STRmix™ validation report.

8 Recommendations

1. A common LOD/LOR (16 RFU/40 RFU) will be used for both 3130*x*/ instruments as outline in section 6.4.
2. The default total PCR volume will be 12.5 µL. Samples can also be amplified at 25 µL total PCR volume.
3. Initially samples with concentrations below 0.01 ng/µL will not be routinely processed in the first instance. If necessary, these samples may undergo post extraction concentration via centrifugal filter concentration procedure to increase the concentration or re-amplify at 25 µL total PCR volume.
4. Initially samples with concentrations between 0.01 ng/µL and 0.0176 ng/µL will not be routinely amplified. These samples are considered as candidates for post extraction concentration via centrifugal filter concentration procedure to increase the concentration to the point that stochastic effects are minimized.
5. Initially samples with concentrations between 0.0176 ng/µL and 0.0244 ng/µL will be amplified and assessed for stochastic effects during case management to ensure the suitability of these DNA profiles for reporting.
6. Samples with concentrations above 0.0244 ng/µL will be routinely amplified.
7. AI_{TH} to be set at 40% and Hom_{TH} 250 RFU for extracted reference, environmental and quality control samples amplified at 12.5 µL total PCR volume.

8. AI_{TH} to be set at 45% and Hom_{TH} 200 RFU for extracted reference, environmental and quality control samples amplified at 25 µL total PCR volume.
9. Adoption of the national Caucasian, Asian and Aboriginal sub-population datasets that DNA Analysis contributed to as part of this validation for use within statistical calculations.
10. Adoption of the locus specific stutter filter as per results section.
11. Thresholds listed in 7 and 8 are to be used as a guidelines when assessing the number of contributors in a mixture.
12. A post implementation review must be performed to review the appropriateness of points 3 – 8. The review will at minimum examine the outcomes of samples amplified within 0.0176 ng/µL and 0.0244 ng/µL concentration range. Similarly, all of the extracted reference samples will be reviewed with regards to the AI_{TH} and homozygote threshold.
13. A default injection time of 5 s is to be used.

9 Notes on this version

The initial version of the validation published results that had been obtained from multiple capillary electrophoresis injection times (5 s or 3 s injection times). The amount of DNA injected into the capillary during capillary electrophoresis is affected by a number of factors including injection time [57]. A reduction in the injection time will decrease the amount of DNA injected (relative to a longer injection time) and therefore the peak height RFU will be decreased.

As the injection time was the only factor that varied, it is assumed that a reduction in peak height RFU is the only effect on the results.

Appendix A below is a summary of each experiment and the injection time used. A decision was made by the Forensic DNA Analysis Management Team not to re-analyse experiments where the peak height RFU were not significant or did not impact the final results. These experiments were:

1. Population Datasets (Experiment 5.1). The allele calls are not affected by the time of injection.
2. Concordance (Experiment 5.2). As with the Population datasets, the allele calls are not affected by the time of injection.
3. Stutter (Experiment 5.7). The amount of stutter product generated is proportional to the allele peak height.

The original data published for the experiments below was a mix of results obtained from 5 s and 3 s injection times. Re-analysis was required to separate these data. As the net effect of a reduced injection time is lower peak height RFU; combination of these data would be expected to skew results slightly for lower template inputs. This is because if the sample is

close to the limit of reporting when injected for 5 s, the sample is likely to partially or fully drop out when injected for 3 s. The experiments that were re-analysed were:

1. Drop out 2.
2. Drop out 3

The original data published for the experiments relating to Peak Balance was restricted to data obtained for 5 s injection times. Re-Analysis was performed on data already obtained at 3 s injection time but not previously analysed.

1. Peak Balance, additional results are published for 3 s injection times. (See section 6.7)

New experiments performed:

1. Baseline, additional baseline experiments on 3130xlB at 5 s injection time was performed and results are published in the summary report[25].

This version of the validation report also incorporates updated stutter thresholds to incorporate the -2 repeat thresholds.

Additional Reference

After this internal validation was initially published, a developmental validation for the PowerPlex 21 system kit was published [58]. This developmental validation covered a wider spectrum than was required of our internal validation including species specificity, polymerase titration, Mastermix concentration, magnesium concentration, primer concentration. The most relevant to our internal validation are discussed below.

Cycle number:

The authors of this study varied the cycle number. For extracted DNA they examined cycle numbers from 28 – 32 cycles. Higher cycle number with higher concentrations of sample may cause poor balance due to preferential amplification. The results we present here are consistent with these results.

While this validation did not examine the variation in results if the PCR cycle number was varied, the observation of poor balance and preferential amplification at high template amounts was observed in our validation.

Reaction volume:

Unlike our validation, which was designed to validate multiple reaction volumes; this developmental validation only amplified the same DNA concentration (e.g. 500 pg / 25 µL, 250 pg/ 12.5µL and 125 pg / 6.25µL). The article presents results consistent to our results; reduced volume amplification is possible with this kit but increased stochastic effects and inhibitor concentration should be considered.

Stutter:

The authors conducted stutter calculations from 568 CTS samples but only included stutter with peak heights greater than 200 RFU to prevent artificially inflating the stutter thresholds (Personal communication from author). The results they have published are similar to our results although some of our stutter thresholds are much higher presumably because of the limited data and inclusion on stutter peak heights less than 200 RFU. This will not greatly impact on our thresholds as the stutter file used in STRmix was made from all Australian Laboratories data. However, the -2 repeat and +1 repeat thresholds are also used for providing information regarding the number of contributors in a sample for STRmix and consideration of the limited data is essential.

Artefacts:

Author observed similar artefacts to what we have observed and is listed in the technical manual.

Sensitivity:

Within the developmental validation, templates from 50 pg to 500 pg were amplified in triplicate with more than 95% alleles called with the lowest template. They also confirmed that as the amount of template decreased the peak height ratios also decreased and the variation was greater.

We performed several sensitivity studies and had similar results.

Mixture Study:

The authors performed mixture studies at several ratios and found that up to a 1:5 mixture ratio 99% of unique alleles were called. We found similar results up to the same ratio, at the 1:5 ratio 100% of alleles were detected.

Concordance:

In this study they examined 32 382 alleles and found two discordant calls (one @D7S820 8,9.3 that should have been 8,11, and one @Amel Y,Y that should have been X,Y). We did not observe any discordant allele calls within our experiments although the total number of alleles compared was much lower (.4644 alleles in our study).

Final notes:

Although data was re-analysed for completeness and accuracy, the application of this data is for use in reference samples and determination of number of contributors to a mixture. Model maker is used to determine parameters for STRmix analysis.

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Appendix A - Index to Supplementary data

The summary of experiment is documented in: **PowerPlex 21 summary of experiments v2.0.xls**

Reference	Description	Project	Version 1	Version 2
5.1.1	Aboriginal & Torres Strait Islander dataset	101	Aboriginal-Torres Straits Results.xls	Project 107 - 5.1 v2.0.xls
5.1.2				
5.1.3	Caucasian dataset		Caucasian results.xls	
5.1.4	South East Asian dataset		PP21_SEAsian_Population data.xls	
5.2	Concordance	104	PowerPlex_21 to CTS manufacturer results comparison.xls	Project 107 - 5.2 v2.0.xls
			Powerplex21_Concordance_Allele Table_PowerPlex_21_IDX_v1.0.xls	
5.3	Baseline determination	102	Baseline_3130xlA-original.xlsx	Project 107 - 5.3 v2.0.xls
			Baseline_3130xlA.xlsx	
			Baseline 3130xl A_rerun.xls	
			Baseline_3130xlB - original.xlsx	
			Baseline_3130xlB.xlsx	
			Baseline 3130xl B_rerun.xls	
			Baseline 3130xl A Half.xls	
			Baseline 3130xl B Half.xls	
5.4	Sensitivity 1	100	DA for PowerPlex21_Exp1_Exp3_40RFUs	Project 107 - 5.4 v2.0.xls
5.5	Sensitivity 2		Low quant values.xls	Project 107 - 5.5 v2.0.xls
5.6	Drop in	105	Baseline_3130xlA-original.xlsx	Project 107 - 5.6 v2.0.xls
			Baseline_3130xlA.xlsx	
			Baseline 3130xl A_rerun.xls	
			Baseline_3130xlB - original.xlsx	
			Baseline_3130xlB.xlsx	
			Baseline 3130xl B_rerun.xls	
			Baseline 3130xl A Half.xls	
			Baseline 3130xl B Half.xls	
5.7	Stutter	102	10x10 CW data full volume - stutter data	Project 107 - 5.7 v2.0.xls
			12.5uL n-1_n+1 Summary	
5.8	Peak Balance	102	Alth_Homoth_summary.xls	Project 107 - 5.8 v2.0.xls

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			Pk balance_both_final.xls	
			Alt_Homozygote_b_20130719.xls	
			PP21_10x10_half_B_20130722_Results Table_PowerPlex_21_IDX_v1.1.1.xlsx	
5.9.1	Drop out 1	102	Dropout1_heat maps.xls	Project 107 - 5.9 v2.0.xls
5.9.2	Drop out 2	102	Allelic drop out_full20130718.xls	
			Allelic drop out_half20130717.xls	
5.9.3	Drop out 3	102	Drop out20130718.xls	
5.10	Mixture studies	103	Mixtures_val_2012.xls	Project 107 - 5.10 v2.0.xls

WIT.0019.0012.2985

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Or by telephone [redacted]

Opportunity for Quality Improvement (OQI) Management Procedure (HSSA)

1 PURPOSE

Continuous improvement is the underlying principle of the HSSA quality program. This procedure describes the management of an "Opportunity for Quality Improvement" (OQI) arising within the organisation. The appropriate Standard clauses are ISO 9001 (clause 8.5) ISO 17025 (clauses 4.11, 4.12) and ISO 15189 (clauses 4.10, 4.11).

2 Scope

This document covers creation, investigation, action, follow-up and approval of OQIs. This procedure applies to all HSSA employees.

3 DEFINITIONS

Actioner The person responsible for investigating and actioning the OQI.
Approver The person responsible for approving the OQI (normally the Actioners Line Manager)
BTS Biomedical Technology Services
Creator The person responsible for raising the OQI
FSS Forensic and Scientific Services
HR Human Resources
HSSA Health Services Support Agency
IMS Incident Management System
Issue Register – List of issues or situations requiring resolution. Registers are maintained at a low level (eg team/laboratory), and pose negligible/low risk
LISS Laboratory Information Systems and Solutions
NATA National Association of Testing Authorities
NCSI NATA Certification Services International
OQI Opportunity for Quality Improvement
Participant A person whose name is specified in a particular field in an OQI
Path Qld Pathology Queensland
PRIME Clinical Incident Management System
Private Viewer – A person appointed when there is a security risk if the information is made generally available. If a Private Viewer is nominated, only they and the OQI participants can view the OQI.
QH Queensland Health
QIS Quality Information System
Quality Administrator – The person who can perform all functions in the OQI module
Task Assignee – The person who receives and completes a task
TAT Turn around time
WH&S Workplace Health and Safety

Not Current

4. ACTIONS

4.1 General Information

This procedure does not cover the in-depth instructions for recording OQIs in QIS. That information is contained in document 26209http://qis.health.qld.gov.au/DocumentManagement/Default.aspx?DocumentID=10001 – QIS^2 Users Manual – Opportunity for Quality Improvement (OQI).

OQIs are process and system focused. They are about making permanent improvements to the way we do things. They shall not be used to blame or confront people and do not replace good communication, management, process and policy. They do not replace the QH grievance procedures and should not be used to advise managers and supervisors of HR issues with other staff members.

Instances that present themselves as opportunities to improve processes and systems arise from many sources. An indication of what should and shouldn't be managed as an OQI is described below.

Some OQIs must also be reported in official Queensland Health Reporting systems such as PRIME (clinical incidents), IMS (Workplace Health and Safety Incidents), Consumer Complaints and QHRisk Management. As these systems and the associated policies are implemented, the Health Services Support Agency is developing business rules around how our processes and QIS interact.

All staff may raise an OQI and where ever possible have access to the records in QIS; however a degree of judgment needs to be exercised in deciding what resources to expend on corrective and preventive action and associated record keeping. Examples of what should be classified as an OQI are detailed below.

An OQI **must** be raised for:

- Complaints from external clients (external to HSSA) – if a client or external party expresses displeasure, irritation or anger over an issue where accepted service levels, or behaviour have, or are perceived to have been breached. This does not include general enquiries about completion dates if agreed TATs have not been exceeded.

- Conditions identified during external audits/assessments/quality assurance processes by NATA/NCSI or other Regulatory Authorities (TGA) e.g. major or Minor non-conformances, or a material, product or service that fails to meet one or more of the applicable specifications (Audit – External Assessment for HSSA, 27329)

- When continuity of evidence has been significantly compromised

- Where there is a significant deviation from the documented process

An OQI **can** be raised for:

- Problems that occur internally (within HSSA). For example:
  - Breakdowns in communication that lead to errors or a reduced level of service
  - Incorrect results or reports
  - Problem with specimen referral between laboratories or service delivery problems between teams or work units.

- Issues arising from an audit (non-compliances or recommendations);

No Current

- Work Place Health and Safety improvements.
- Compliments or praise received from clients external to the work unit.
- Suggestions for improvements from staff members
- Actions from specific improvement initiatives such as the Staff Survey strategies.
- Problems and complaints with suppliers of goods and services to HSSA –these may be directed to the Procurement Manager who will use the information in both addressing the issue and as an information source in any future negotiations. In these instances, the Supplier should be provided with a copy of the OQI details in order for them to have the right of reply. Their response can then be added to the OQI for completeness.
- EQAP, collaborative or external proficiency trial where outliers or problems/trends with test methods have been identified.
- Unintended Human Error (non-cognitive error) – an example in a laboratory setting is a scientist who enters "positive" instead of "negative" as a laboratory result because of distraction or fatigue. This is an unintended, non-cognitive error or slip. (Refer Laboratory and Patient Safety, E.A Wagar, S Yuan, Clinics in Laboratory Medicine 27, 2007)
- Environment – this is often used as a cause and effect category. An example could be where the air-conditioner breaks down and the resulting increase in temperature causes the biochemistry analyzer to malfunction or break down.
- Mitigation of risk – when things might go wrong

Issues registers can be used at the team/laboratory level for negligible and low risk issues where an OQI does not need to be created. Issues registers shall be reviewed on a regular basis (eg at each team/lab meeting) and if any systematic issues are detected, an OQI shall be raised. The use of issues registers can be used for recording the circumstances listed above, and may assist with determining when an OQI should be raised.

OQIs should **not** be used for:

- Routine maintenance issues with equipment **UNTIL** the problem becomes systemic, calamitous or a regular occurrence that requires a root cause analysis.
- Minor methodology or QC errors **UNTIL** the problem becomes systemic, calamitous or a regular occurrence that requires a root cause analysis.
- Ministerials **UNLESS** systematic issues are detected. Ministerials are managed and recorded at the Office of the Chief Executive. In most cases Ministerials are not systematic errors but are "show cause" issues that require names and personal details to be documented. If systematic issues are detected that require investigation and action, these shall be logged as OQIs as internal problems by the person managing the Ministerial process.
- Grievances regarding other staff. These should be lodged according to standard HR process.

Not Current

- Software problem reporting. For the reporting of these problems, use the relevant systems – e.g. QIS feedback [redacted], LISS feedback ([redacted]
- Complaints received by the Animal Ethics Committee (AEC). These are dealt with according to AEC complaints grievance procedure 23782.

With very sensitive or confidential issues or where there is a need to name individuals, it is possible to limit access of the OQI details via the use of 'private viewers' functionality in QIS (See QIS^2 User Manual – Opportunities for Quality Improvement 26209).

Although the primary purpose of the OQI system is to record information on situations that require changes to systems or processes, the OQI database can also be used as an information resource. When a problem is encountered, such as an instrument malfunction that is difficult to overcome, details of the nature of the problem, the root cause and the solution can form the basis of an OQI. Staff encountering similar difficulties at a later date can benefit from the previous work that was done.

Personal Information

Please note: staff, patient, client or offender/complainant/suspect names must not be recorded in the OQI module on QIS. Recording personal information in this manner does not meet the requirements of the Privacy Principles contained in Information Standard 42A (IS42A) that sets out the privacy regime for the Queensland Health. Furthermore, revealing the identity of a person who has received a public sector health service contravenes Section 63 of the Health Services Act 1991. However, staff names can be used in Compliment OQIs.

When identifying, investigating and actioning OQIs that relate to laboratory results, de-identified information such as Auslab or laboratory numbers shall be used to provide traceability.

4.2 Initiating or Creating an OQI

When creating an OQI in QIS, important points to note are:

- Title and a description of the OQI – keep it simple, brief and to the point but ensure that the whole issue can be understood.
- The source of the OQI - For example an external complaint, an internal problem, as the result of an audit, a suggestion, a WH&S issue or positive feedback from a client or external organisation.
- An attempt made to classify what needs fixing/changing
- Your location details
- The person who you believe is responsible for taking appropriate action, known as the 'actioner'. It is important to ensure that this person is in a position in which they have the authority or knowledge to progress the issue.
- You may also add Private Viewers and Notifiees, however these fields are not mandatory. It is suggested that the creator's line manager be added as a Notifiee, if the creator's line manager and the actioner's line manager are not the same person.

Private Viewer: Please note that the use of private viewers should be discretionary, as populating this field limits the view of the OQI to the creator, actioner, actioner's line manager and private viewer only. If other staff are required to be kept abreast of the OQI's progress, please use the notifiees field instead.

It is a common courtesy to communicate with the person to whom you will be assigning the OQI. In this way, issues are bought to their attention sooner, any misunderstandings can be talked through and the OQI can be assigned to the appropriate person if the original actioner feels that it is beyond their control.

4.3 Assignment Acceptance/Rejection

Once an OQI is created, it is sent to the 'actioner' who can either accept or reject the OQI assignment. If the 'actioner' accepts the assignment then the 'actioner' takes responsibility for the investigation and action stages of the OQI. If the 'actioner' rejects the assignment, a comment is mandatory to inform the creator of the reasons for the rejection. The comment should also nominate an alternate 'actioner'.

4.4 Edit an OQI

If an OQI assignment is rejected by an 'actioner', the creator can change the name of the 'actioner' and resubmit the OQI to the Assignment stage.

If an OQI is rejected by the 'actioner' as being unnecessary (as per details listed in Section 4.1), then the 'creator' can delete the OQI.

If an OQI is rejected by the 'actioner' as being unnecessary, but the 'creator' would prefer the issue be recorded, the 'creator' can:

- escalate the OQI to the actioner's line manager
- escalate the OQI to the branch quality advisor if applicable
- raise the OQI to themselves as 'actioner'

4.5 Investigating an OQI

When investigating the reasons why an OQI has arisen it is essential to determine the real "Root Cause". For example, it may be tempting to attribute the cause to a one off mistake; however, it is more probable that the real cause is due to:

- inappropriate or inadequate training,
- problems with communication,
- inadequate or incorrect documentation, or
- an ambiguous, confusing or ineffective process

Unless the real cause is dealt with, there is every chance there will be a recurrence of the situation.

Some OQIs can take an extended period of time to determine the root cause. Dated notes should be added as progress reports to the investigation text field until finalized. This will indicate that things are still ongoing and that the OQI is not being ignored.

4.6 Actioning an OQI

When taking action in response to an OQI it is often necessary to take corrective action immediately, e.g. recall and replace a report or update a record. However, it is essential to address the root cause of the problem (as identified in the investigation phase) and make permanent changes to systems and processes, e.g. change methodology, train/retrain staff or revise a form to ensure ease of use. This is "preventive action" and aims to stop the same situation arising in the future.

Not Current

Some OQIs require various tasks to be completed as part of the action process. It is the responsibility of the actioner to assign tasks to relevant staff, and to ensure that tasks are completed in a timely manner. If tasks have been assigned, an OQI cannot be finalized until all tasks have been completed.

If an OQI has been raised because of an external complaint, feedback must be provided to the complainant prior to the OQI being closed, and this should be documented as part of the OQI action.

For OQIs that turn out to be complex or resource intensive, a business case and project management process might be required. In this case it is acceptable to advise that this avenue has been pursued to progress the OQI and an audit scheduled for a suitable time to follow up on the effectiveness of the action.

In all other cases, the action shall be carried out before the entry is made in the action text box. In this way it stays on the events of the person who still has a responsibility to do something with it. **Promises are not actions.**

4.7 Following up and Accepting an OQI

Once the OQI has been actioned, the OQI returns to the person who created it. This communicates that:

- the issue has been resolved in some manner and
- creates an obligation to follow up to ensure that the actions been appropriate and effective.

It is possible at this stage that the OQI creator does not believe the action is enough/correct and may explain their reasons for rejecting the action and send it back to the actioner.

It is not enough to accept promises of action unless real progress has been made in implementation.

4.8 Approving an OQI

After acceptance, the OQI will divert to the line manager of the person who has actioned it. Approving an OQI involves a 2 stage process. The first stage is "Approval Status", and it is here where an OQI can be rejected and returned to the actioner for further investigation and/or action. Therefore a decision needs to be made from a management perspective whether the action has been effective. If effective action has been taken, the OQI can be accepted and closed as Approved. In some cases it may be impossible to take effective action, for example, due to insufficient resources or legislative reasons. In this case the OQI may be accepted with comment and closed as Rejected or Abandoned. It may be necessary to begin a new OQI process from the outcome of the current OQI, and in this case the OQI is accepted and closed as New. When the new OQI is created, cross-referencing occurs between the OQIs.

4.9 Create an Audit from an OQI

An audit can be scheduled from an OQI to ensure that the solution is effective over time. The creator and the actioner both have the ability to create an audit from the findings of an OQI, by using the New Audit action button on the OQI.

Not Current

4.10 Timeframes for Addressing OQIs

There is no definitive timeframe for progressing an OQI from investigation to action to follow-up. However, the following guidelines shall apply:

- An entry to the investigation field shall be made no longer than one week from the creation date to at least explain the approach that will be taken to address the issue. The investigation field of the OQI can be updated as progress is made in addressing the issue. Once an investigation is complete, the OQI moves to the action stage.
- When the issue is finalised, and all tasks and actions have been taken, the action can be completed. This will move the OQI back to the creator for follow-up, and should occur within 30 days of the creation of the OQI.
- Follow-up shall occur at a time that will be able to verify the success of the implementation of the action. This might be immediately or might require weeks or a few months to ensure effectiveness. Provided there is an adequate record of intentions, and the follow-up is expedited as soon as possible, there is no need to rush the close out of the OQI.

4.11 Management Review

The Management Review module allows the status of OQIs to be obtained at all levels of the organisation. Managers at all levels shall monitor issues within their own area and follow up on issues that appear to be stalled. They can then make decisions on resourcing, priorities and responsibilities to ensure the best possible outcome for the organisation.

Where OQIs are open more than 30 days, a status report must be escalated by the unit manager to the next management level. They should communicate intended actions and expected timeframes. Where these undertakings are not delivered, the next level of management shall decide on appropriate actions and record these as part of the management meeting minutes.

The designated responsible officer within each Group Laboratory/Department/BTS Site/FSS team/Branch shall analyse the OQIs on a monthly basis and report any critical issues and the proposed or completed actions at least monthly. Critical issues would be those that could or have affected the safety of staff, the integrity of reported results or have major (>$5000) resource ramifications. These issues shall be reported to the next level of management via the most efficient means e.g. Management meetings. These in turn will be escalated to the service executive meetings or HSSA executive by the chair of the committee, if deemed appropriate.

4.12 Roles and Responsibilities of the Quality Administrator

The role of the Quality Administrator is to help Line Mangers and others in their work area to manage events, and to assist in the management of OQIs, audits, and reminders within their scoped Organisational Unit.
The responsibilities of the Quality Administrator include complying with the requirements of the standards and relevant HSSA procedures, and obtaining appropriate authorization to perform various functions.

5 RECORDS

OQI records in QIS
Meeting minutes where issues have been escalated and actions assigned.

6 ASSOCIATED DOCUMENTATION

QIS^2 User Manual – Opportunities for Quality Improvement	26209
Opportunity for Quality Improvement (OQI) Presentation	25919

Opportunity for Quality Improvement Manual Form	19132
Opportunity for Quality Improvement Definitions	19133
Pathology Queensland Procedures for External Assessments	12661

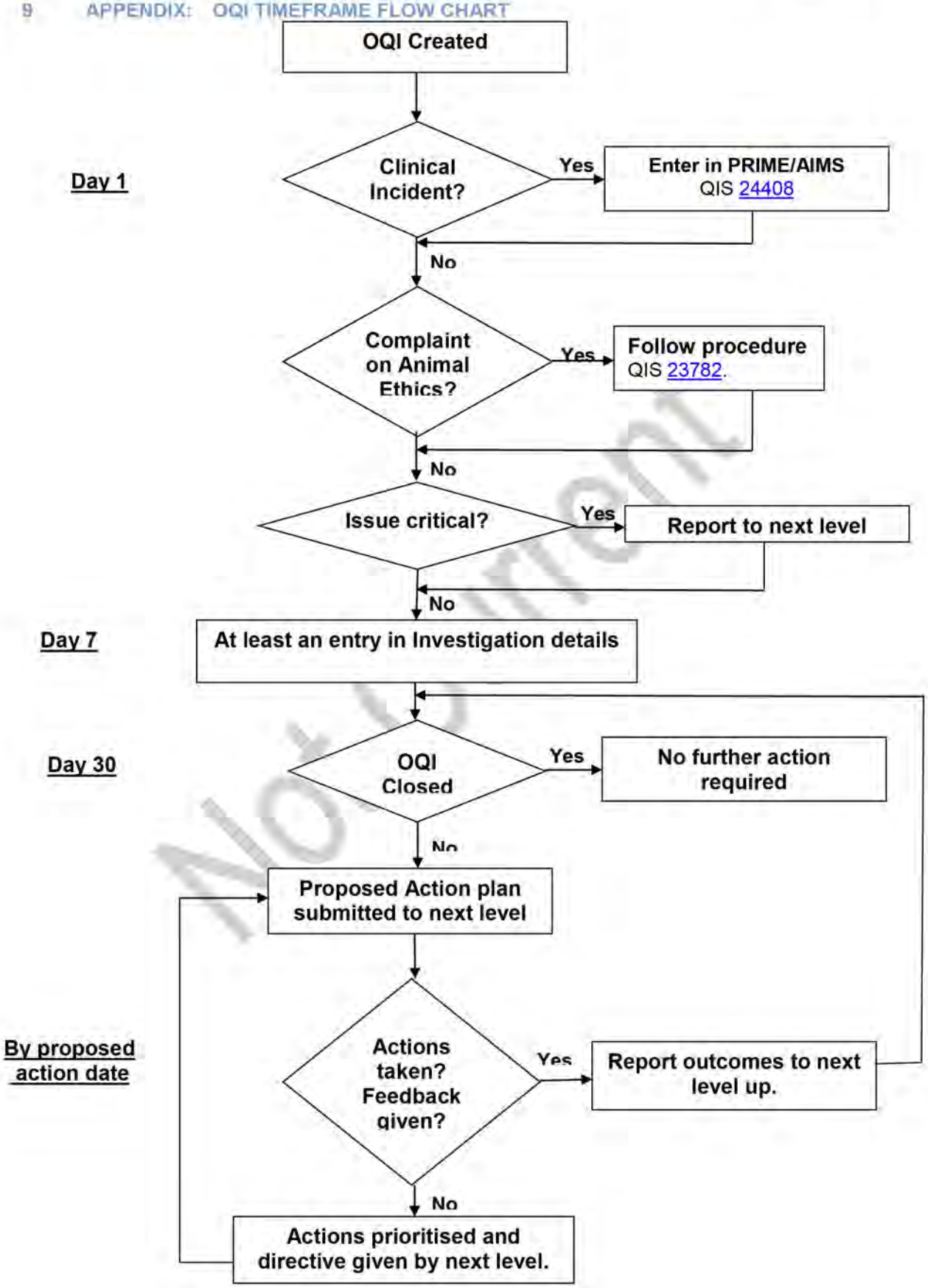
7 REFERENCES

8 AMENDMENT HISTORY

Version	Date	Author/s	Amendment
0	Sep 1998	N Douglas	New format. Deletion of specific keywords. Requirement to monitor effectiveness of OQI's
1	Dec 2001	S.Nilsen S.Anderson	Conversion to QHPSS-wide document & QIS references
2	Feb 2003	S.Nilsen	Addition to scope-Problems and complaints with suppliers of goods and services to QHPSS; Addition to 4.1 Problems and complaints regarding suppliers to QHPSS may also be directed to the Materials Manager who will use the information in both addressing the issue and then in any future contract negotiations.
3	May 2004	S.Nilsen	Addition to scope re. logging conditions from NATA/NCSI audits & privacy issues wrt names in OQI's
4	Jan 2007	S.Nilsen	Almost a total rewrite. Addition of a more rigorous governance and management review process, timeframes for action and examples and responsibility matrix. Change over to Cass.
5	Apr 2009	C. Della	Amended to reflect QIS^2 functionality.
6	July 2010	C. Della	Update Standards, what OQI can be used for, new committee names
7	Oct 2011	C Della	Minor changes to Section 4.1; additional information to Sections 4.3 and 4.4; All CaSS branches added to 9.1; clinical incident process added to 9.3
8	Nov 2011	C Della	Additional information to Section 4.1
9	Sept 2012	H Gregg	Inclusion of Issues Registers to Section 4.1, update to include HSSA, remove Appendix A,B

Not Cla

9 APPENDIX: OQI TIMEFRAME FLOW CHART



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CA-129

Queensland Government

29 July 2019

Health Support Queensland

Department of
Health

Deputy Commissioner Gollschewski
Crime, Counter-Terrorism and Specialist Operations
Queensland Police Service
GPO Box 1440
BRISBANE QLD 4001

Dear Deputy Commissioner Gollschewski

I am writing regarding the recent 'Delivering forensic services' audit conducted by the Queensland Audit Office and the recommendations that the Queensland Police Service (QPS), Department of Justice and Attorney-General and Queensland Health have accepted.

Recommendation 1 from that Audit Report refers to the need to have an enhanced governance process for managing cases between our agencies. Several months ago I met with Assistant Commissioner McCarthy and discussed the development of an Memorandum of Understanding (MOU) that would facilitate collaboration between our agencies and provide a mechanism to jointly govern the effective provision of analytical services provided by Queensland Health to the QPS.

Queensland Health has engaged Crown Law to draft the MOU which will comprise a head agreement supported by a number of services schedules that specifically relate to testing services undertaken by Forensic and Scientific Services (FSS). The schedules would include services such as roadside drug testing, DNA analysis of crime scene and person items, and the analysis of items seized as illicit drugs and clandestine laboratories. In light of the recent audit, we have given initial priority to the DNA Schedule.

As a working draft is now well underway, I would like to take the opportunity to meet with you to discuss the proposed MOU and the appropriate contact points within QPS who can assist with further drafting of the MOU and the service schedules.

If you require any further details, our contact at FSS is Executive Director John Doherty, who can be contacted on [redacted]

Yours sincerely

Michel Lok
General Manager
Strategy, Community and Scientific Support

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Prepared by:	Cathie Allen Managing Scientist Police services Stream [redacted] 3 July 2019
Cleared by:	John Doherty Executive Director FSS [redacted] 4 July 2019

CA-130

Queensland Health

HealthSupport Queensland

Forensic and Scientific Services

QAO Audit Action Plan – Police Services Stream (as of 13 September 2019)

Task	Specific Action	Assigned To	Measurable KPI	Target Date	Date Completed	Status and comment
1. Implement a governance structure to effectively coordinate and provide accountability for managing forensic services across agencies						
Implement a governance structure	Work with the QPS on a Governance structure - specifically establish a MOU for each service offering with measurable KPIs and mechanisms for feedback and collaboration. MOU to comprise: • Header agreement: • Forensic DNA schedule • Illicit Drug schedule • Chemical Testing schedule • Toxicology schedule • Clinical forensic medicine schedule	John Doherty, Cathie Allen Deborah Whelan Dr Adam Griffin	Recruitment completed with start date nominated.	Phased with header agreement and Forensic DNA schedule by 31 October 2019 Other schedules to be finalised by 30 June 2020.		In progress Draft header agreement and Forensic DNA schedule prepared. Awaiting response from the QPS regarding key contacts for collaboration

Task	Specific Action	Assigned To	Measurable KPI	Target Date	Date Completed	Status and comment
2. Implement a process to coordinate and manage collecting, transport, prioritising and destroying illicit drugs. The revised process should reduce the risks to security, occupational health and safety and the cost of unnecessary handling						
Assist the QPS with a process to prioritise and destroy illicit drugs.	Request the QPS review all illicit drug cases held at FSS to ensure all cases are required to be tested	John Doherty & Cathie Allen	Return of completed spreadsheet	31 Oct 2019		Ongoing - Spreadsheet provided to the QPS 9th Sept 2019
	Prepare Brief for additional resources to clear the cases once the total number of outstanding cases is advised by the QPS	Cathie Allen	Approved Brief			
	Upon approval of a Brief for additional resources, recruit additional staff, devise training plans	John Doherty & Cathie Allen	Recruitment completed, Training plans drafted			
	Work with the QPS to devise a prioritisation structure based on crime class code (similar to Forensic DNA Analysis)	Cathie Allen & QPS representative	Prioritisation of cases agreed upon			
	Request enhancements within the Forensic Register to automatically set the prioritisation	Cathie Allen	Automatic prioritisation of cases included within Forensic Register			
3. Improve the prioritisation and timely sharing of case information between agencies. This should include establishing systems and processes to ensure there is real-time notification of changes in priority or status.						
Work with DJAG and the QPS regarding electronic advice for cases	Request enhancements within the Forensic Register to advice the outcome of testing.	John Doherty & Cathie Allen	Enhancements updated within Forensic Register			

CA-131

Nicole Watt

From: Michel Lok
Sent: Friday, 1 November 2019 4:23 PM
To: [redacted]
Cc: John Doherty [redacted]
Subject: Draft MOU - Forensic Services
Attachments: 19.11.01 Draft MOU.doc

Good afternoon Shane and Bruce,

As discussed on Wednesday, I have enclosed a draft of the MOU prepared by Crown Law earlier this year which we had started prior to Alan's illness.

Very much want to treat this as a 'good start' and welcome your thoughts and views on the scope, content and coverage.

I would like to maintain some momentum on this and would suggest we regroup in a month's time, allowing you some scope to comsider and consult with your legal department.

Regards

Michel

Michel Lok GAICD, CPA
General Manager

Community and Scientific Services
Health Support Queensland, Queensland Health

[redacted]
a Level 5, 41 O'Connell Terrace, Bowen Hills QLD 4006
[redacted]u w Health Support Queensland

CA-132

Delivering Forensic Services Implementation Update

Current as at 06 July 2020

Legend - status		
Green	Amber	Red
Implementation is in progress	Implementation is on hold or actual timeframes are dependent on decisions/actions from other stakeholders	Implementation is stalled with key risks that need to be addressed

RECOMMENDATION	UPDATE	RESPONSIBLE AGENCIES	RISKS/ISSUES	TIMEFRAME
We recommend that the Queensland Police Service and Queensland Health: **1.** implement a governance structure to effectively coordinate and provide accountability for managing forensic services across agencies The terms of reference should include: • identifying current and future demand and the required resources for forensic services • establishing processes to capture the extent and impact of delays from forensic services, including the impact on courts • implementing a performance framework to measure and report on the effectiveness and efficiency of forensic services. This should include ensuring each agency has appropriate performance targets • ongoing consultation with the Department of Justice and Attorney-General about the delivery of forensic services and impact on the justice system. (Chapters 2 and 3)	Jun-19 Agencies acknowledge long history of collaboration and agree to develop an MOU Jul-19 Letter from QH to QPS (DC Gollshcewski) initiating MOU discussion Oct-19 Liaison meeting – MOU proposal Nov-19 Draft MOU drafted outlining: • An MOU Committee and scope of role • Cooperation and Scientific collaboration • Performance of Services and Fees • Services Schedules July-20 Liaison meeting – QAO implementation	Queensland Police Service and Queensland Health	▲ MOU drafted, though progress delayed by COVID-19 pandemic response priorities.	**December 2019**
We recommend that the Queensland Police Service and Queensland Health: **2.** implement a process to coordinate and manage collecting, transporting, prioritising, and destroying illicit drugs. The revised process should reduce the risks to security, occupational health and safety, and the cost of unnecessary handling (Chapter 2).		Queensland Police Service and Queensland Health	▲ Progress delayed by COVID-19 pandemic response priorities.	**December 2020**
We recommend that the Queensland Police Service: **3.** improves its quality assurance processes and practices to ensure all police property facilities conduct an annual audit of all property and exhibits. These audits should be standardised and		Queensland Police Service		**Third Quarter 2020**

RECOMMENDATION	UPDATE	RESPONSIBLE AGENCIES	RISKS/ISSUES	TIMEFRAME
documented, with findings reported to senior management (Chapter 3).				
The Department of Health, in collaboration with the Queensland Police Service and all hospital and health services: **4.** continues to develop and deliver reforms to forensic medical examinations to improve services to victims, including: • implementing service agreements to deliver forensic medical examinations • developing strategies to recruit and retain appropriately trained physicians and nurses for forensic medical examinations across the state • implementing a range of reporting pathways and supporting processes for all victims requiring forensic medical examinations • improving clinician's awareness of reporting options for victims of sexual assault • improving the availability of, and access to, paediatric services for child victims of sexual assault • establishing local interagency support services which better integrate clinicians, police and non-government services (Chapter 2).	Agreements - HHS Service Agreements for 2019-22 were amended to include responsibility to provide forensic medical examinations. Health Service Directive *Caring for people disclosing sexual assault* effective from 22 July 2019. Medical officer professional education sessions schedule delivered to HHS doctors. Sexual Assault Nurse Examiner training program launched in September 2019 in collaboration with Central Queensland University. Resource material published to QH Intranet site. Pathways developed for victims of sexual assault to offer informed choice of just-in-case examination without immediate reporting to police as well as ensuring victims are aware of alternate reporting options (police website). Patient referral to support service is part of the pathway. Post-acute counselling support services supplemented with telephone-based service through the RBWH sexual assault response team. Information resources on sexual assault pathways included in clinician professional education and available on QH Intranet site. The Health Service Directive and pathway require each HHS to establish a pathway for child victims of sexual assault. Examinations must be conducted by a Paediatrician. Support and assistance is available through the state-wide Child Protection and Forensic Medical Service based at Queensland Childrens Hospital. HHS and police commands have been encouraged to establish local interagency groups and consult with local support agencies regarding the effectiveness of sexual assault responses. It is expected the revised interagency Guidelines on Responding to People who have Experienced Sexual Assault will further promote the establishment of local sexual assault networks.	Department of Health Queensland Police Service Hospital and Health Services	Completed	**December 2019**
We recommend that the Queensland Police Service, Queensland Health and the Department of Justice and Attorney-General: **5.** improve the prioritisation and timely sharing of case information between agencies. This should include establishing systems and processes (and where possible automation) to ensure there is real-time notification of changes in priority or status to avoid unnecessary analysis (Chapter 3).		Queensland Health Queensland Police Service Department of Justice and Attorney-General		**December 2020**

CA-133

Forensic Services Liaison Meeting

1:00pm - 2:00pm, Wednesday 29 July 2020 [redacted]

Attendees:

Brian Connors, A/g Assistant Commissioner, Operational Support Command, QPS
Bruce McNab, Superintendent, Forensics Services Group, QPS
Michel Lok, General Manager, Community and Scientific Services, HSQ
Joh Doherty, Executive Director, Forensic and Scientific Services, HSQ

Agenda

Item	Topic	Lead
1	Welcome and Introduction • Establishment of regular liaison meetings	Chair
2	Business Outlook • COVID pandemic • 2020-21 Budgets and resourcing • Emergent priorities	
3.	Business Items	
	3.1 QAO Performance Audit Report No 21 2018-19: Delivering Forensic Services - Recommendation 1 – Governance Structure - Recommendation 2 – Illicit Drugs - Recommendation 4 – Sexual assault response - Recommendation 5 – Sharing case information	 HSQ QPS HSQ
	3.2 Proposal to undertake Y-STR testing	HSQ
	3.3 Options for collecting sexual assault reference samples	HSQ
	3.4 Commercialisation of Forensic Register	QPS
4	Other Business	
5	Meeting finalisation - actions	Chair

CA-134

Delivering Forensic Services Implementation Update

Current as at 30 September 2020

Legend - status		
Green	Amber	Red
Implementation is in progress	Implementation is on hold or actual timeframes are dependent on decisions/actions from other stakeholders	Implementation is stalled with key risks that need to be addressed

RECOMMENDATION	UPDATE	RESPONSIBLE AGENCIES	RISKS/ISSUES	TIMEFRAME
We recommend that the Queensland Police Service and Queensland Health: **1.** implement a governance structure to effectively coordinate and provide accountability for managing forensic services across agencies The terms of reference should include: • identifying current and future demand and the required resources for forensic services • establishing processes to capture the extent and impact of delays from forensic services, including the impact on courts • implementing a performance framework to measure and report on the effectiveness and efficiency of forensic services. This should include ensuring each agency has appropriate performance targets • ongoing consultation with the Department of Justice and Attorney-General about the delivery of forensic services and impact on the justice system. (Chapters 2 and 3)	Jun-19 Agencies acknowledge long history of collaboration and agree to develop an MOU Jul-19 Letter from QH to QPS (DC Gollshcewski) initiating MOU discussion Oct-19 Liaison meeting – MOU proposal Nov-19 Draft MOU drafted outlining: • An MOU Committee and scope of role • Cooperation and Scientific collaboration • Performance of Services and Fees • Services Schedules July-20 Liaison meeting – postponed Nov-20 Liaison meeting	Queensland Police Service and Queensland Health	MOU drafted, though progress delayed by COVID-19 pandemic response priorities.	December 2019
We recommend that the Queensland Police Service and Queensland Health: **2.** implement a process to coordinate and manage collecting, transporting, prioritising, and destroying illicit drugs. The revised process should reduce the risks to security, occupational health and safety, and the cost of unnecessary handling (Chapter 2).	Sep-20 Service alignment program commenced. CIB is leading optimisation of internal processes.	Queensland Police Service and Queensland Health	Progress delayed by COVID-19 pandemic response priorities.	December 2020
We recommend that the Queensland Police Service: **3.** improves its quality assurance processes and practices to ensure all police property facilities conduct an annual audit of all property and exhibits. These audits should be standardised and	Sep-20 A service-wide High Risk property Audit was finalised Dec-19, implementation date on 4 recommendations extended to Dec-20. Property dashboard redeveloped on a Power BI platform and trialled, but not yet distributed for use.	Queensland Police Service	Progress delayed by COVID-19 pandemic response priorities.	Third Quarter 2020

RECOMMENDATION	UPDATE		RESPONSIBLE AGENCIES	RISKS/ISSUES	TIMEFRAME
documented, with findings reported to senior management (Chapter 3).					
The Department of Health, in collaboration with the Queensland Police Service and all hospital and health services: **4.** continues to develop and deliver reforms to forensic medical examinations to improve services to victims, including: • implementing service agreements to deliver forensic medical examinations • developing strategies to recruit and retain appropriately trained physicians and nurses for forensic medical examinations across the state • implementing a range of reporting pathways and supporting processes for all victims requiring forensic medical examinations • improving clinician's awareness of reporting options for victims of sexual assault • improving the availability of, and access to, paediatric services for child victims of sexual assault • establishing local interagency support services which better integrate clinicians, police and non-government services (Chapter 2).	Sep-20	HHS Service Agreements 2019-22 amended to include responsibility to provide forensic medical examinations. Health Service Directive Caring for people disclosing sexual assault effective from 22 July 2019. QH Medical officer professional education sessions schedule delivered. Sexual Assault Nurse Examiner training program launched in September 2019 in collaboration with Central Queensland University. Resource material published to QH Intranet site. QPS victim centred training package developed. Pathways developed for victims of sexual assault to offer informed choice. QH launched just-in-case examination option. QPS introduced online sexual assault reporting in Aug-20 to supplement alternate reporting options, with Police Link alerting urgent reports.). Patient referral to support service is part of the pathway. Post-acute counselling support services supplemented with telephone-based service through the RBWH sexual assault response team. Information resources on sexual assault pathways included in clinician professional education and available on QH Intranet site. The Health Service Directive and pathway require each HHS to establish a pathway for child victims of sexual assault. Examinations must be conducted by a Paediatrician. Support and assistance is available through the state-wide Child Protection and Forensic Medical Service based at Queensland Childrens Hospital. HHS and police commands have been encouraged to establish local interagency groups and consult with local support agencies regarding the effectiveness of sexual assault responses. It is expected the revised interagency Guidelines on Responding to People who have Experienced Sexual Assault will further promote the establishment of local sexual assault networks.	Department of Health Queensland Police Service Hospital and Health Services	Completed	**December 2019**
We recommend that the Queensland Police Service, Queensland Health and the Department of Justice and Attorney-General: **5.** improve the prioritisation and timely sharing of case information between agencies. This should include establishing systems and processes (and where possible automation) to ensure there is real-time notification of changes in priority or status to avoid unnecessary analysis (Chapter 3).	Sep-20	Coronial service working group is exploring options to share information and data across IT platforms of the agencies. Opportunity to leverage. Meeting planned in oct-20 with Chief Justice	Queensland Health Queensland Police Service Department of Justice and Attorney-General	MOU drafted, though progress delayed by COVID-19 pandemic response priorities.	**December 2020**

CA-135

Forensic Services Liaison Group

11:00am - 12:00pm, Monday 26 October 2020
By Teams

Attendees:

Brian Connors, A/g Assistant Commissioner, Operational Support Command, QPS
Bruce McNab, Superintendent, Forensics Services Group, QPS
Todd Fuller, Office of the Director of Public Prosecutions, DJAG
Michel Lok, General Manager, Community and Scientific Services, HSQ
John Doherty, Executive Director, Forensic and Scientific Services, HSQ

Agenda

Item	Topic	Lead
1	Welcome and Introduction • Establishment of regular liaison meetings	Chair
2	Business Outlook • COVID pandemic • 2020-21 Budgets and resourcing • Emergent priorities	All
3.	Business Items	
	3.1 QAO Performance Audit Report No 21 2018-19: Delivering Forensic Services - Recommendation 1 – Governance Structure - Recommendation 2 – Illicit Drugs - Recommendation 4 – Sexual assault response - Recommendation 5 – Sharing case information Legislative Affairs and Community Safety Committee Inquiry https://www.parliament.qld.gov.au/Documents/TableOffice/TabledPapers/2020/5620T1832.pdf	HSQ QPS HSQ All
	3.2 Proposal to undertake Y-STR testing	HSQ
	3.3 Options for collecting sexual assault reference samples	HSQ
	3.4 Commercialisation of Forensic Register	QPS
4	Other Business	
5	Meeting finalisation - actions	Chair

Delivering Forensic Services Implementation Update

Current as at 30 September 2020

Legend - status		
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RECOMMENDATION	UPDATE	RESPONSIBLE AGENCIES	RISKS/ISSUES	TIMEFRAME
We recommend that the Queensland Police Service and Queensland Health: **1.** implement a governance structure to effectively coordinate and provide accountability for managing forensic services across agencies The terms of reference should include: • identifying current and future demand and the required resources for forensic services • establishing processes to capture the extent and impact of delays from forensic services, including the impact on courts • implementing a performance framework to measure and report on the effectiveness and efficiency of forensic services. This should include ensuring each agency has appropriate performance targets • ongoing consultation with the Department of Justice and Attorney-General about the delivery of forensic services and impact on the justice system. (Chapters 2 and 3)	Jun-19 Agencies acknowledge long history of collaboration and agree to develop an MOU Jul-19 Letter from QH to QPS (DC Gollshcewski) initiating MOU discussion Oct-19 Liaison meeting – MOU proposal Nov-19 Draft MOU drafted outlining: • An MOU Committee and scope of role • Cooperation and Scientific collaboration • Performance of Services and Fees • Services Schedules July-20 Liaison meeting – postponed Nov-20 Liaison meeting	Queensland Police Service and Queensland Health	MOU drafted, though progress delayed by COVID-19 pandemic response priorities.	**December 2019**
We recommend that the Queensland Police Service and Queensland Health: **2.** implement a process to coordinate and manage collecting, transporting, prioritising, and destroying illicit drugs. The revised process should reduce the risks to security, occupational health and safety, and the cost of unnecessary handling (Chapter 2).	Sep-20 Service alignment program commenced. CIB is leading optimisation of internal processes.	Queensland Police Service and Queensland Health	Progress delayed by COVID-19 pandemic response priorities.	**December 2020**
We recommend that the Queensland Police Service: **3.** improves its quality assurance processes and practices to ensure all police property facilities conduct an annual audit of all property and exhibits. These audits should be standardised and	Sep-20 A service-wide High Risk property Audit was finalised Dec-19, implementation date on 4 recommendations extended to Dec-20. Property dashboard redeveloped on a Power BI platform and trialled, but not yet distributed for use.	Queensland Police Service	Progress delayed by COVID-19 pandemic response priorities.	**Third Quarter 2020**

RECOMMENDATION	UPDATE		RESPONSIBLE AGENCIES	RISKS/ISSUES	TIMEFRAME
documented, with findings reported to senior management (Chapter 3).					
The Department of Health, in collaboration with the Queensland Police Service and all hospital and health services: **4.** continues to develop and deliver reforms to forensic medical examinations to improve services to victims, including: • implementing service agreements to deliver forensic medical examinations • developing strategies to recruit and retain appropriately trained physicians and nurses for forensic medical examinations across the state • implementing a range of reporting pathways and supporting processes for all victims requiring forensic medical examinations • improving clinician's awareness of reporting options for victims of sexual assault • improving the availability of, and access to, paediatric services for child victims of sexual assault • establishing local interagency support services which better integrate clinicians, police and non-government services (Chapter 2).	Sep-20	HHS Service Agreements 2019-22 amended to include responsibility to provide forensic medical examinations. Health Service Directive Caring for people disclosing sexual assault effective from 22 July 2019. QH Medical officer professional education sessions schedule delivered. Sexual Assault Nurse Examiner training program launched in September 2019 in collaboration with Central Queensland University. Resource material published to QH Intranet site. QPS victim centred training package developed. Pathways developed for victims of sexual assault to offer informed choice. QH launched just-in-case examination option. QPS introduced online sexual assault reporting in Aug-20 to supplement alternate reporting options, with Police Link alerting urgent reports.). Patient referral to support service is part of the pathway. Post-acute counselling support services supplemented with telephone-based service through the RBWH sexual assault response team. Information resources on sexual assault pathways included in clinician professional education and available on QH Intranet site. The Health Service Directive and pathway require each HHS to establish a pathway for child victims of sexual assault. Examinations must be conducted by a Paediatrician. Support and assistance is available through the state-wide Child Protection and Forensic Medical Service based at Queensland Childrens Hospital. HHS and police commands have been encouraged to establish local interagency groups and consult with local support agencies regarding the effectiveness of sexual assault responses. It is expected the revised interagency Guidelines on Responding to People who have Experienced Sexual Assault will further promote the establishment of local sexual assault networks.	Department of Health Queensland Police Service Hospital and Health Services	Completed	**December 2019**
We recommend that the Queensland Police Service, Queensland Health and the Department of Justice and Attorney-General: **5.** improve the prioritisation and timely sharing of case information between agencies. This should include establishing systems and processes (and where possible automation) to ensure there is real-time notification of changes in priority or status to avoid unnecessary analysis (Chapter 3).	Sep-20	Coronial service working group is exploring options to share information and data across IT platforms of the agencies. Opportunity to leverage. Meeting planned in oct-20 with Chief Justice	Queensland Health Queensland Police Service Department of Justice and Attorney-General	MOU drafted, though progress delayed by COVID-19 pandemic response priorities.	**December 2020**

HealthSupport
Queensland
Forensic and Scientific Services

Agenda Item 3:2

Reference Samples taken from Complainants and Suspects

Recommendation:

That agencies note the options and implications associated with changing reference sampling processes.

Issue(s):

The Queensland Police Service (QPS) have previously made enquiries regarding changes to the process of collecting reference samples from complainants of alleged sexual assault with a view to avoiding re-traumatising victims and improving operational efficiency (locating complainants and collecting samples).

There are several ways this could be achieved.

(i) *Police officers collect a buccal cell sample when a complaint is made or immediately prior to a forensic examination*

Part 2, Section 454 of the PPRA requires a police officer to undertake several aspects to capture a person's informed consent, prior to a forensic examination being undertaken. Whilst a police officer is undertaking the process of consent, this may be the opportune time to also take a reference FTA sample, thereby negating the need to follow-up with them.

The exception for this would be if the allegation involved oral assault and the taking of a reference FTA sample would need to be delayed.

(ii) *Clinicians collecting a buccal cell or blood sample during the forensic examination.*

Currently buccal cell samples transferred onto FTA cards are submitted by the QPS for profiling from complainants and suspects. The workflow for processing these items has been created for maximum efficiency.

Buccal cell sampling is the preferred form of reference testing. Forensic and Scientific Services (FSS) has found that processing of a blood FTA card, there is a high likelihood of cross contamination on instruments within the laboratory, due to the high amounts of DNA found in blood. Investigation of laboratory cross contamination is both resource and labour intensive. Usually, the only blood FTA cards that the FSS laboratory receives are from the FSS Mortuary, and these samples are manually examined and sampled prior to DNA profiling. This process can be sustained due to the low numbers that are submitted from the FSS Mortuary. Larger numbers of reference blood FTAs being submitted would result in the creation of a new workflow, which could mean a longer turnaround time for results.

If collected by the clinician, the reference FTA may be included inside the SAIK. However, FSS recommends that reference samples on FTA and crime scene samples continue to be submitted in a different time and space, as this is best practice.

A number of other matters need to be considered if a change in process is to be undertaken:

- Whilst FSS is budgeted to undertake DNA profiling of samples in a SAIK, the QPS pays a fee for service for testing the additional reference samples (the QPS are operationally funded for taking reference FTA samples). Funding for reference samples will need to be preserved if samples are returned to the FSS laboratory associated with the SAIK.

- Current training for forensic examinations does not cover taking a reference FTA sample.

- The FSS DNA Elimination Database would need to be extended to include all clinicians performing forensic examinations, in case of inadvertent contamination of the sample from the person sampling the complainant. Whilst there may be a low risk of cross contamination, investigation into the root cause would be resource and labour intensive. The risk may be mitigated with appropriate training.

- There is the potential for incorrectly recording the complainant's details, leading to data quality issues if a medical officer was to obtain the reference samples, rather than a police officer. Quality assurances steps regarding the legality of the reference sample would still be required to be undertaken prior to the sample being subjected to DNA profiling. The QPS have set up the DNA Sample Management Group to review all data relating to reference samples prior to their submission to FSS. A mechanism would need to be developed regarding notification to proceed with testing as quality checks had been completed.

- Consistency of sample on an FTA card is the key to obtaining a DNA profile. Given the QPS' experience in this area, it is unlikely that medical officers will be able to obtain samples at the same standard in the first instance. Initially, there could be an increase in costs for reference samples due to poor sample collection, which would be borne by the QPS.

- The QPS would no longer have oversight of all reference samples submitted to FSS and subsequently included on an invoice. A mechanism would need to be developed that provides quality assurance, approval for testing and details regarding the category for the sample for the NCIDD purpose. This may be mitigated if a SAIK is only registered on the Forensic Register (FR) by a Scenes of Crime Officer (SOCO) if a reference sample has been taken. If one hasn't been taken, this would prompt the Investigating Officer to obtain one.

Background:

Queensland legislation, which became the Police Powers and Responsibilities Act (PPRA) was introduced in 2000 which deemed the taking of a buccal cell sample from a person to be a 'non-intimate' sample. This means a trained QPS officer can take a reference sample (sometimes called person samples) from complainants and suspects.

In 2001, the QPS undertook a program which saw the sampling of all prisoners using the Flinders Technology Associates (FTA) card, as per Part 3 of the PPRA. Both the QPS and the FSS laboratory have invested in automated processes to rapidly obtain and process these reference samples and place DNA profiles on the National Criminal Investigation DNA Database (NCIDD). In addition, the FSS laboratory has invested in automated equipment to assist with processing these samples which reduces the risk of cross contamination between FTAs being processed at the same time. A Memorandum of Understanding between the QPS and FSS regarding the testing of FTA samples and their costing was signed at this time.

In 2002, a review called 'Forensics under the Microscope: Challenges in Providing Forensic Science Services in Queensland' was undertaken due to the miscarriage of justice of Mr Button in a sexual assault case. The QPS and FSS implemented recommendations made by the review, with one of those being reference samples from suspects and complainants were to be received in a 'different time and space' from exhibits within the case. The ability to collect reference blood samples was removed from the Sexual Assault Investigation Kit (SAIK) to ensure that a buccal cell FTA sample was taken. This enabled the QPS to register the reference sample (FTA) on QPRIME, allowing the electronic flow of information to the Forensic Register and AUSLAB (a laboratory information system used by FSS at that time). During the registration of the FTA, the QPS select the appropriate category to be applied to the reference samples, based on their knowledge of the consent process under which the FTA was taken and the case, which in turn ensures that a profile from an FTA is or isn't uploaded to the NCIDD. Prior to submission for testing at FSS, the QPS DNA Sample Management Group undertake quality assurance steps to ensure that only FTAs that have met the required legal criteria are submitting for a DNA profiling.

Each month, FSS issues an invoice to the QPS for the reference samples that have been profiled. Prior to the implementation of the QPS Forensic Register (FR) at FSS, the QPS required a list of the barcodes invoiced so that checks could be made to ensure accuracy. This is no longer required as FSS uses the FR for their processes. FSS processes approximately 16,500 FTA samples per year.

In 2019, amendments were made to caring for people affected by sexual assault. These changes include Hospital and Health Service medical staff undertaking the examination to recover evidence. This involved new training to be implemented and delivered to medical staff that are not managed by Health Support Queensland or FSS.

HealthSupport Queensland
Forensic and Scientific Services

Agenda Item 3.3

Additional DNA Testing Capability offered at Forensic & Scientific Services

Recommendation:

That the Queensland Police Service confirm interest in progressing new testing services:

- Y-STR testing targets the male portion of a sample when routine DNA testing doesn't provide a useful profile for a case (or alternatively, a profile can be loaded and searched on the National Criminal Investigation DNA Database in a no suspect case).
- Massively Parallel Sequencing (MPS) provide information about the ancestry and external visible characteristics (eg hair and eye colour) of a potential suspect.

Issues:

Two new services are currently being investigated and would provide useful investigative information to the QPS.

Currently, FSS receives funding from Queensland Health for autosomal testing of major crime samples. Each year, there is about a 10% increase in the number of Sexual Assault Investigation Kits (SAIKs) received. In 2019, 402 SAIKs were received and analysed. Y-STR testing uses existing consumables and instruments, however an additional profiling kit and reagents are required for this type of testing. As the technique for Y-STR testing would be in addition to routine autosomal testing, a fee for service model would need to be developed for its use, noting that no charge would be made if the Y-STR test was in place of the routine autosomal testing. The Y-STR profiling kit and the autosomal profiling kits are comparable in cost. If it is assumed that at least 1 sample from a SAIK is tested using the Y-STR profiling kit, then about 440 crime scene samples and 440 reference samples would be tested by this technology in one year (this excludes Cold Case testing).

Legal advice is required prior to implementation, due to the paternal lineage aspect of this testing. Queensland Health Legal have been engaged, however given the complexity of the request, it has been referred to Crown Law. This request is on hold, pending a decision from the QPS regarding use of the service.

It is anticipated that the MPS technique will also require a fee for service model to be developed as it is a new technique offered, additional to current techniques. Currently, other laboratories advise that the MPS technique takes approximately 2 weeks to obtain results so is more suitable in the first instance for cases with a prolonged period of no suspect or Cold Cases.

The MPS technique still requires validation and training before it is able to be offered, thereby allowing the QPS to build a budget for this technique in the financial year 2021 – 2022. Upon completion of validation, cost per unit would be able to be determined.

Background:

Deoxyribonucleic acid (DNA) is a complex chemical present in nearly all cells in living organisms. DNA is packaged in humans in discrete packages along with proteins called chromosomes. These chromosomes can be targeted for repeating information called Short Tandem Repeats (STR). Currently, forensic DNA profiling techniques uses a commercial STR kit with capillary electrophoresis detection. The current kit used in the laboratory is the PowerPlex® 21 STR kit and

the previous kit was the Profiler® Plus STR kit. These STR kits are used to compare the profile generated from crime scene samples to a reference sample to assess the likelihood that a person contributed to a DNA profile. STR kits provide an indication of gender along with the repeating information.

Y-STR testing:

Human chromosomes can be either allosomes (sex chromosomes) or autosomes (non-sex chromosomes). Approximately half of the DNA is inherited from the mother and half from the father. Y chromosomes are passed from fathers to sons only and make a useful target in DNA profiling where routine (autosomal) DNA testing has not been able to produce a useful DNA profile.

Y-STR testing is a specialised technique that would not be applied to all casework samples. There are two main uses for this technique. One would be samples that contain a high proportion of female than male and would predominantly be sexual assault cases, however it could be applied to other cases in this category. The other main use would be to establish paternal lineages, which would be useful for mass disaster victim identification.

Other jurisdictions have implemented this technique into their workflow and the QPS have taken advantage of this testing by utilising the Y-STR service of New Zealand's ESR.

Massively Parallel Sequencing testing:

MPS technology is an emerging analysis technique in the forensic DNA field, which is likely in coming years to supplement and / or supersede current capillary electrophoresis DNA analysis methods. The QPS have utilised this type of service from an overseas provider – Parabon.

Recently FSS purchased an MPS instrument and have successfully collaborated with the QPS on the research project 'Massively Parallel Sequencing as an Investigative Tool', which resulted in a publication in the Australian Journal of Forensic Science in July 2020. The research project used MPS technology to analyse samples from solved cases where the ancestry and EVC were already known from QPS photographs and case information. The MPS results of ancestry, hair and eye colour were presented to detectives, who were asked to assess its utility in a workshop environment. Although the workshop didn't accurately replicate an active criminal investigation, the results were encouraging and suggest that MPS investigative information could be operationally effective and a valuable tool. FSS are currently designing a validation plan for this service.

In the first instance, this specialised technique would not be applied to all casework samples and FSS would work with the QPS to identify relevant cases such as Cold Cases or high profile, unsolved cases to develop criteria to capitalise on this technique.

CA-136

Forensic Services Liaison Group

10:30am - 11:30am, Wednesday 27 January 2021
By Teams

Attendees:

Brian Connors, A/g Assistant Commissioner, Operational Support Command, QPS

Bruce McNab, Superintendent, Forensics Services Group, QPS

John Doherty, Executive Director, Forensic and Scientific Services, HSQ

Michel Lok, General Manager, Community and Scientific Services, HSQ

Philip McCarthy, A/Deputy Director of Public Prosecutions, DJAG

Fiona Regan, Senior Administration Manager, Secretariat, HSQ

Notes and Actions

Item	Topic	Lead
1	Welcome and Introduction • Actions from October meeting – Accepted and updated	Chair (ML)
2	Business Outlook • 2021-22 Budgets and resourcing **HSQ** Commencing budget build for FY. Various saving measures are being considered across all departments. All business units reviewing efficiencies. Nil specific budget bids across forensic portfolio. **QPS** Ongoing COVID pressures in regard to resourcing. Increase in BAU/routine and serious crime cases. Current HOLD on reviewing and renewing MOU's in place. Significant resources allocated to support The Commissioner's priority is the Service Alignment Program. Review and optimisation of business units. **JAG** Courts are returning to BAU. Likely to involve larger cases with forensic evidence, so impacts may be significant for QPS and QHFSS. Looking at options to work smarter and more efficiently. Access to Forensic Register for prosecutors could provide more timely responses and fewer requests directly to QPS. QPS to investigate this as an option. Jury Trials have returned to BAU in 3-4 courts in Brisbane and regions running jury trials. All supreme court trials relisted.	All

	ACTION: QPS to Investigate access to Forensic Register for investigator prosecutors QPS advised current format of Forensic Register does not support read-only. Read-only capability in development for next release. Current training package is delivered online (2hrs). Option to explore forensic liaison/coordinator roles to access register. • Terms of Reference ➢ It was agreed not to include the Magistrates Court as a member but to invite when discussion relevant ***Action: Draft TOR in line with audit guidelines*** • Discuss inclusion of activity data as standing item ➢ Share data volumes and case loads with a focus on priorities, backlogs and turnaround times.	
3.	Business Items	
	3.1 Service alignment program for drugs ➢ Initial engagement ➢ Process is underway ➢ Concern with lack of ongoing consultation with QHFSS ➢ Stakeholder Reference Group meeting held two weeks ago ➢ It is the Commissioner's priority ***ACTION: Invite Project lead – Service Alignment Project to next meeting.***	FSS
	3.2 Roadside drug testing invoicing ➢ For information. ➢ Potential issues with invoicing. DDG escalation if no response from AC Road Policing. ➢ FSS to share letter sent to AC Road Policing with QPS to see if they can see where it is at before escalation actioned.	FSS
	3.3 Update on Forensic Register ➢ Governance process for access to Forensic Register between QLD Health and QPS ➢ Agreement with bdna is with QPS only (QH not a signatory) ➢ Old MOU for access to current forensic Register. Currently good working relationship and understanding. ➢ Governance process needed to ensure correct terms for access to new forensic register (and benefits flow on to FSS in the contract with QPS such as pricing and access to development hours) into the future ***ACTION: Forensic Register access update MOU with addendum***	FSS
	3.4 Opportunities for strategic research collaboration ➢ Request for cross agency collaboration with Research Governance Office and QPS ethics committee. ***ACTION: FSS to send contact details for FSS Research Coordinator to BMc***	FSS

	3.5 Taking of Reference Samples from Victims of Sexual Assault (Papers attached) ➢ QH need to work through and change process ➢ Need to be clear in communicating updated process changes to all parties ➢ Training of clinical staff will take some time ➢ Decision to implement changes needs to be set. Define the new process, then determine what will it take to make it happen. ➢ Proposed change date - 01 July 2021	QPS
4	Other Business • Recommendation 5 from the Audit Report to be discussed at next meeting.	
5	Meeting closed	Chair

Action List

Meeting Date	Description	Responsible Officer	Update/Comments
26 October 2020	Discuss MOU for DNA Service	JD and BM	Ongoing discussions.
26 October 2020	Draft a letter on behalf of QPS to send to QLD Health outlining their position and seeking QH assistance in transitioning to new arrangements	Closed	BM sent letter to JD and letter was acknowledged.
27 January 2021	Investigate access to Forensic Register for prosecutors	BMc	
27 January 2021	Forensic Register ongoing access	JD/BMc	Update MOU and/or add addendum
27 January 2021	Terms of Reference	ML	Draft terms of reference to be prepared
27 January 2021	Invite Project lead – Service Alignment Project to next meeting.	FR	Confirm with QPS and send invitation
27 January 2021	FSS to send researcher contact details to BMc	JD	

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Queensland Government

Operational Command
Queensland Police Service

Forensic and Scientific Services
Queensland Health

Director of Public Prosecutions
Department of Justice and Attorney-General

Terms of Reference

Forensic Services Liaison Group (FSLG)

The Forensic Services Liaison Group (FSLG) has been established between the agencies to enhance the leadership, performance and accountability of the delivery of forensic testing services in Queensland. It builds on the extensive and ongoing operational engagement that exists between the agencies to strengthen system governance, planning, coordination and scientific collaboration.

This document establishes the purpose, functions, membership and accountabilities of the FSLG.

Authorisation

The FSLG is established through mutual interest to enhance strategic collaboration and continuous improvement in operational performance. The FSLG is an advisory forum and has no delegated decision-making authority.

Purpose and functions

The FSLG will:

- Review forensic testing demand and resourcing across agencies.
- Oversight system performance, including the establishment and monitoring of KPIs for forensic testing services and devising strategies to reduce bottlenecks and testing backlogs.
- Monitor systemic risk and develop collaborative strategies to mitigate threats.
- Foster inter-agency collaboration and scientific cooperation to enhance the effectiveness and quality of forensic evidence.
- Lead implementation of system reforms, including those arising from the findings and recommendations of the Queensland Audit Office performance audit Report No. 21 2018-19: *Delivering Forensic Services*.
- Review and make recommendations for prioritising enhancements to the Forensic Register.

Guiding Principles

Consistent with the expectations of effective public sector management set out in section 25 of the *Public Service Act 2008*, the FSLG will function with the aim of:

- providing responsive, effective and efficient services to the community and the Government;
- maintaining impartiality and integrity in informing, advising and assisting the Government;
- promoting collaboration between Government and non-government sectors in providing services to the community;
- continuously improving public service administration, performance management and service delivery; and
- managing public resources efficiently, responsibly and in a fully accountable way.

Membership

Co-Chairs:

- Assistant Commissioner, Operations Support Command, QPS
- General Manager, Community and Scientific Services, Health Support Queensland

Members:

- Superintendent, Forensic Services Group, Operations Support Command, QPS
- Executive Director, Forensic and Scientific Services, Health Support Queensland
- Deputy Director of Public Prosecutions. Office of the Director of Public Prosecutions

Meeting Arrangements

Role of the Chair

The Chair will:

- oversight the development of the meeting agenda
- ensure that all views are heard
- maintain a strategic focus
- ensure the actions recorded are agreed at the end of the meeting

The Chair's role will alternate between the co-chairs.

Quorum and Proxies

Quorum is half of the member plus one, including a member from both Queensland Health and QPS. Where a quorum is not available, the meeting will be rescheduled as soon as practicable.

Proxies are permitted and are expected to be fully briefed on the matters being considered.

Attendance

Meetings will be attended in person or via Microsoft Teams.

Guests and observers may attend with the prior approval of the meeting Chair.

Frequency of meetings

Meetings will be held every three months in January, April, July and October each year.

Additional meetings may be convened at the request of either of the co-chairs.

Secretariat

The Chair's office will alternate to arrange administrative support for planning, convening and taking the record of a meeting.

Confidentiality

Members and attendees may receive information that is commercially sensitive, private and/or confidential and which may be protected by certain doctrines.

Members and attendees will act in a proper and prudent manner in the use of information acquired in the course of their attendance at FSLG meetings. This duty to maintain confidentiality and to exercise discretion is paramount and survives the expiry of attendance and membership.

Members should endeavour to avoid or minimise the need to include commercially sensitive, private and/or confidential information in meeting papers and during discussions to the extent practicable.

Conflicts of Interest

Conflicts of interest (actual, perceived, or likely to arise) will be declared and managed in consultation with the Chair.

A conflicted Member will leave the room whilst the remaining members determine whether the conflicted Member is entitled to attend the applicable agenda item for the purpose of providing information (but excluding any consideration or decisions) or should remain absent for the duration of the item. A record of any absence is to be recorded in the meeting summary.

Record Keeping

Files must be kept securely and confidentially in accordance with the requirements of the Public Records Act 2002 and retained in accordance with Queensland Government's General Retention and Disposal Schedule for Administrative Records.

Evaluation

An annual review of the performance of the FSLG in meeting its objectives will be undertaken.

Reporting

A summary of testing submissions, completion times and outstanding items will be tabled at each meeting.

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Delivering Forensic Services Implementation Update

Current as at 10 February 2021

Legend - status		
Green	Amber	Red
Implementation is in progress	Implementation is on hold or actual timeframes are dependent on decisions/actions from other stakeholders	Implementation is stalled with key risks that need to be addressed

RECOMMENDATION	UPDATE	RESPONSIBLE AGENCIES	RISKS/ISSUES	TIMEFRAME
We recommend that the Queensland Police Service and Queensland Health: **1.** implement a governance structure to effectively coordinate and provide accountability for managing forensic services across agencies The terms of reference should include: • identifying current and future demand and the required resources for forensic services • establishing processes to capture the extent and impact of delays from forensic services, including the impact on courts • implementing a performance framework to measure and report on the effectiveness and efficiency of forensic services. This should include ensuring each agency has appropriate performance targets • ongoing consultation with the Department of Justice and Attorney-General about the delivery of forensic services and impact on the justice system. (Chapters 2 and 3)	Jun-19 Agencies acknowledge long history of collaboration and agree to develop an MOU Jul-19 Letter from QH to QPS (DC Gollshcewski) initiating MOU discussion Oct-19 Liaison meeting – MOU proposal Nov-19 Draft MOU drafted outlining: • An MOU Committee and scope of role • Cooperation and Scientific collaboration • Performance of Services and Fees • Services Schedules July-20 Liaison meeting – postponed Nov-20 Forensic Services Liaison Group meeting, MOU postponed due to PQS priorities Jan-21 Forensic Services Liaison Group meeting, MOU remains postponed due to PQS priorities Feb-21 Draft Terms of Reference – Forensic Services Liaison Group meeting.	Queensland Police Service and Queensland Health	▲ MOU drafted, though progress delayed by COVID-19 pandemic response priorities. Interim (alternate) governance approach through establishment of formal liaison group.	December 2019
We recommend that the Queensland Police Service and Queensland Health: **2.** implement a process to coordinate and manage collecting, transporting, prioritising, and destroying illicit drugs. The revised process should reduce the risks to security, occupational health and safety, and the cost of unnecessary handling (Chapter 2).	Sep-20 Service alignment program commenced. CIB is leading optimisation of internal processes. Jan-21 QH has been consulted, but request further engagement on options	Queensland Police Service and Queensland Health	▲ Progress delayed by COVID-19 pandemic response priorities.	December 2020

We recommend that the Queensland Police Service: **3.** improves its quality assurance processes and practices to ensure all police property facilities conduct an annual audit of all property and exhibits. These audits should be standardised and documented, with findings reported to senior management (Chapter 3).	Sep-20 A service-wide High Risk property Audit was finalised Dec-19, implementation date on 4 recommendations extended to Dec-20. Property dashboard redeveloped on a Power BI platform and trialled, but not yet distributed for use. Jan-21 No update	Queensland Police Service	Progress delayed by COVID-19 pandemic response priorities.	**Third Quarter 2020**
The Department of Health, in collaboration with the Queensland Police Service and all hospital and health services: **4.** continues to develop and deliver reforms to forensic medical examinations to improve services to victims, including: • implementing service agreements to deliver forensic medical examinations • developing strategies to recruit and retain appropriately trained physicians and nurses for forensic medical examinations across the state • implementing a range of reporting pathways and supporting processes for all victims requiring forensic medical examinations • improving clinician's awareness of reporting options for victims of sexual assault • improving the availability of, and access to, paediatric services for child victims of sexual assault • establishing local interagency support services which better integrate clinicians, police and non-government services (Chapter 2).	Sep-20 HHS Service Agreements 2019-22 amended to include responsibility to provide forensic medical examinations. Health Service Directive Caring for people disclosing sexual assault effective from 22 July 2019. QH Medical officer professional education sessions schedule delivered. Sexual Assault Nurse Examiner training program launched in September 2019 in collaboration with Central Queensland University. Resource material published to QH Intranet site. QPS victim centred training package developed. Pathways developed for victims of sexual assault to offer informed choice. QH launched just-in-case examination option. QPS introduced online sexual assault reporting in Aug-20 to supplement alternate reporting options, with Police Link alerting urgent reports.). Patient referral to support service is part of the pathway. Post-acute counselling support services supplemented with telephone-based service through the RBWH sexual assault response team. Information resources on sexual assault pathways included in clinician professional education and available on QH Intranet site. The Health Service Directive and pathway require each HHS to establish a pathway for child victims of sexual assault. Examinations must be conducted by a Paediatrician. Support and assistance is available through the state-wide Child Protection and Forensic Medical Service based at Queensland Childrens Hospital. HHS and police commands have been encouraged to establish local interagency groups and consult with local support agencies regarding the effectiveness of sexual assault responses. It is expected the revised interagency Guidelines on Responding to People who have Experienced Sexual Assault will further promote the establishment of local sexual assault networks.	Department of Health Queensland Police Service Hospital and Health Services	Completed	**December 2019**
We recommend that the Queensland Police Service, Queensland Health and the Department of Justice and Attorney-General: **5.** improve the prioritisation and timely sharing of case information between agencies. This should include establishing systems and processes (and where possible automation) to ensure there is real-time notification of changes in priority or status to avoid unnecessary analysis (Chapter 3).	Sep-20 Coronial service working group is exploring options to share information and data across IT platforms of the agencies. Opportunity to leverage. Oct-21 QH meet with Chief and Deputy Chief magistrate and DJAG to discuss illicit drug testing process and timelines and confirm contact arrangements for priority analysis Jan-21 DPP requested view access to FR for investigating prosecutors QH invited to participate on a Streamlining Criminal Justice working group examining forensic evidence.	Queensland Health Queensland Police Service Department of Justice and Attorney-General	Delayed by COVID-19 pandemic response priorities.	**December 2020**

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Status update 21 February 2021 – QAO Audit: Delivering Forensic Services

Recommendation 1:
Implement a governance structure to effectively coordinate and provide accountability for managing forensic services across agencies.

Status: In-progress
Queensland Health has led the establishment of a working group with members of the QPS and FSS to progress a Memorandum of Understanding (MoU) to improve the management of illicit drugs and other forensic services provided by FSS.

Recommendation 2:
Implement a process to coordinate and manage collecting, transporting, prioritising, and destroying illicit drugs. The revised process should reduce the risks to security, occupational health and safety, and the cost of unnecessary handling.

Status: In-progress
Actions agreed between QH and QPS in November 2021 include an audit of current illicit drug exhibit holdings and identification of key collaborative Forensic Register (FR) developments in the illicit drugs area.

Recommendation 3:
Improves quality assurance processes and practices to ensure all police property facilities conduct an annual audit of all property and exhibits. These audits should be standardised and documented, with findings reported to senior management.

Status: In-progress
A service-wide high-risk property Audit was finalised Dec-19. Property dashboard redeveloped on a Power BI platform and trialled.

Recommendation 4:
Continues to develop and deliver reforms to forensic medical examinations to improve services to victims, including:

- implementing service agreements to deliver forensic medical examinations
- developing strategies to recruit and retain appropriately trained physicians and nurses for forensic medical examinations across the state
- implementing a range of reporting pathways and supporting processes for all victims requiring forensic medical examinations
- improving clinician's awareness of reporting options for victims of sexual assault
- improving the availability of, and access to, paediatric services for child victims of sexual assault
- establishing local interagency support services which better integrate clinicians, police and non-government services

Status: Complete
HHS Service Agreements 2019-22 amended to include responsibility to provide forensic medical examinations. Health Service Directive Caring for people disclosing sexual assault effective from 22 July 2019.

QH Medical officer professional education sessions schedule delivered. Sexual Assault Nurse Examiner training program launched in September 2019 in collaboration with Central Queensland University. Resource material published to QH Intranet site. QPS victim centred training package developed.

Pathways developed for victims of sexual assault to offer informed choice. QH launched just-in-case examination option. QPS introduced online sexual assault reporting in Aug-20 to supplement alternate

reporting options, with Police Link alerting urgent reports.). Patient referral to support service is part of the pathway. Post-acute counselling support services supplemented with telephone-based service through the RBWH sexual assault response team. Information resources on sexual assault pathways included in clinician professional education and available on QH Intranet site.

The Health Service Directive and pathway require each HHS to establish a pathway for child victims of sexual assault. Examinations must be conducted by a Paediatrician. Support and assistance is available through the state-wide Child Protection and Forensic Medical Service based at Queensland Children's Hospital.

HHS and police commands have been encouraged to establish local interagency groups and consult with local support agencies regarding the effectiveness of sexual assault responses. It is expected the revised interagency Guidelines on Responding to People who have Experienced Sexual Assault will further promote the establishment of local sexual assault networks.

Recommendation 5:
Improve the prioritisation and timely sharing of case information between agencies. This should include establishing systems and processes (and where possible automation) to ensure there is real-time notification of changes in priority or status to avoid unnecessary analysis.

Status: In-progress
Queensland Health is actively working with relevant agencies to develop an automated case-sharing portal with QPS and DPP through the established Streamlining Criminal Justice working group.

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Forensic Services Liaison Group

QAO 2018-19 DELIVERING FORENSIC SERVICES: RECOMMENDATION 5

AGENDA ITEM	TBC
MEETING DATE	13 May 2021
SPONSOR	Michel Lok, General Manager, Community and Scientific Services

RECOMMENDATION

It is recommended that the Forensic Services Liaison Group:

1. **AGREE** what actions are required to implement Recommendation 5 of the Auditor-General's report to Parliament No.21:2018-19 – *Delivering forensic services*.

CONTEXT

- The QAO performance audit report *Delivering forensic services* (Report 21: 2018–19) was tabled in Parliament in June 2019.
- The objective of this audit was to assess whether agencies deliver forensic services efficiently and effectively in order to investigate crime and prosecute offenders.
- The report identified that strategic management and planning was limited and ad hoc as there was no formal structure to promote or facilitate strategic management and improve efficiency and outcomes.
- It was noted that each agency delivers individual forensic services largely without considering the collective needs across the entirety of the process. Therefore, the process is constrained by individual agency priorities and limitations.
- Better interface of systems, supported by notifications that alert agencies to the status of a criminal investigation, could improve timeliness and information flow for supporting forensic services.
- The QAO recommended that the Queensland Police Service (QPS), Queensland Health (QH) and the Department of Justice and Attorney-General (DJAG) improve the prioritisation and timely sharing of case information between agencies (Recommendation 5). This should include establishing systems and processes (and where possible automation) to **ensure there is real-time notification of changes in priority or status to avoid unnecessary analysis**.
- In response, agencies stated:
    - QH will work collaboratively with the QPS and DJAG to identify options to improve information sharing of case information (by Dec 2020)
    - Meetings with QH and DJAG have already occurred to address this recommendation and a review will occur to identify solutions. The focus of this review will be upon the management and sharing of information in respect to DNA and illicit drugs (by Dec 2020)
    - DJAG is committed to working in partnership with QPS and QH to undertake a review of current processes and explore opportunities for system enhancement.

ISSUES

- Action to implement recommendations arising from the QAO performance audit were delayed due to COVID pandemic response commitments by affected agencies.
- Agencies operate custom IT systems that manage sensitive data with varied security policies for access control.
- Early thinking assumed there would be translatable benefits from work underway through the Coronial Services Governance Board (CSGB) that was exploring integration products to share data and forms between PRIME, CMS and AUSLAB.
    - This work has stalled due to limited investment and time available to test and deliver the pilot project.
    - An unfunded, partially complete, workplan has been developed by the CSGB IT Working Group.
- New investment in IT systems has been severely limited due to adherence with the government's Savings and Debt plan. Accordingly, proposals must have strong public good value and deliver significant benefits to be prioritised. These controls are ongoing.
- A number of initiatives have been underway that may contribute to ensuring the timely delivery of forensic results for court cases. These include:
    - Provisioning DPP with access to the forensic register
    - Developing triage processes for illicit drug testing (see also Recommendation 2)
    - Magistrates working group examining the value of forensic evidence submitted to courts.
- FSLG members are asked to consider what current and further actions are needed to ensure the objective of the QAO recommendation can be met, and in what timeframe.

ATTACHMENTS

- Nil

Details	Author	Cleared by
Name	Noreen Walton	Michel Lok
Position	Manager	General Manager
Work Area	Office of the General Manager	Community and Scientific Services
Telephone	[redacted]	[redacted]
Date	**28 April 2021**	**7 May 2021**

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Financial Year	QAO Audit Type	Audit Reference	Audit/Report Title	Division	Issue No.	Issue Title	QAO Risk Rating	Recommendation No.	Recommendation	Management Agreed Actions	Management Update	Management Proposed Status	Original Recom Due Date	Extended Due Date	Current Status agreed with QAO/SSU	Overall QAO Recom Status
2018/19	Performance Audit	2018-19 Report 6	Delivering coronial services	CHOPD - Chief Health Officer & Prevention Division	N/A	N/A	No Risk Rating	4	It is recommended that the Department of Justice and Attorney-General, Department of Health, and the Queensland Policy Service, in collaboration with coroners improve processes and practices across the coronial system by • ensuring there is a coordinated, state-wide approach to triaging all deaths reported to the coroners to help advise the coroner of the need for autopsy • ensuring sufficient counselling services are available and coordinated across agencies to support families and inquest victims.	In line with recommendations 1 and 3, the Department of Health will work with agencies to design and implement improvements to triage processes and practices. The Department of Health will work with agencies to develop and implement a protocol regarding the role and responsibilities of the Coronial Counsellors employed by Forensic and Scientific Services and their role relative to other agencies. Agency resourcing is a matter for the government.	8/09/2021: Recs 4(a), (b) and (d) all remain open and are largely held up by Department of Justice and Attorney-General resourcing constraints. 4(c) was closed in October 2020. The new Coronial System Board (formerly Coronial Services Governance Board) has governance responsibility for remaining QAO recommendations. Board Secretariat provides regular reports to QAO and A-G on progress. • The Coronial Services Governance Board closed recommendation 4(c), and noted recommendation 4(a) would be closed in December. • An enhanced triage model for apparent natural cause deaths was developed and is being piloted. The 2019 state budget allocated additional funding to pilot the model (Strengthening Coronial Services) which involved the establishment of a second Coronial unit, supported by Queensland Health medical staff. A recent CBRC submission requesting 2.0FTE Department of Health staff be made permanent to support this work was approved, however the funding and MOHRI for the positions is required to come from within the existing Department of Health budget and MOHRI. A brief for approval of funds and MOHRI is	In Progress	31/12/2019		In progress	Overdue
2018/19	Performance Audit	2018-19 Report 21	Delivering forensic services	CHOPD - Chief Health Officer & Prevention Division	N/A	N/A	No Risk Rating	1	(Queensland Health and Queensland Police Service) implement governance structure to effectively coordinate and provide accountability for managing forensic services across agencies. The terms of reference should include: • identifying current and future demand and the required resources for forensic services • establishing processes to capture the extent and impact of delays from forensic services, including the impact on courts. • implementing a performance framework to measure and report on the effectiveness and efficiency of forensic services. This should include ensuring each agency has appropriate performance targets • ongoing consultation with the Department of Justice and Attorney-General about the delivery of forensic services and impact on the justice system.	13.1 A Memorandum of Understanding between the Department of Health and the Queensland Police Service is under development to establish a governance structure to oversight the effective and efficient delivery of analytical services and promote collaboration and cooperation between agencies.	8/09/2021: Remains open. • Queensland Police Service is not pursuing an MOU due to other Queensland Police Service priorities and COVID-19 response, so in lieu, an alternate governance model (Forensic Services Liaison Group) has been established. • The Forensic Services Liaison Group met quarterly with senior officers from Queensland Police Service, a Director from the Office of the DPP, GM Community and Scientific Support and the ED Forensic and Scientific Services, however a complete change-over in all senior officers involved in this group (Queensland Health and Queensland Police Service) has hampered continuity of discussions. 19/08/2021: Further progress on these items has effectively ceased	In Progress	31/12/2019		In progress	Overdue
2018/19	Performance Audit	2018-19 Report 21	Delivering forensic services	CHOPD - Chief Health Officer & Prevention Division	N/A	N/A	No Risk Rating	2	Implement a process to coordinate and manage collecting, transporting, prioritising, and destroying illicit drugs. The revised process should reduce the risks to security, occupational health and safety and the cost of unnecessary handling.	14.1 Queensland Health will work with Queensland Police Service to review processes for the collection, transport, prioritising and destruction of illicit drugs and implement improvements identified.	8/09/2021: CIB (Queensland Police Service) is leading optimisation of internal processes, however progress has been delayed by COVID-19 pandemic response priorities. Queensland Police Service is seeking funding to establish a drug triaging pilot – with the outcome to be advised. 19/08/2021: Further progress on these items has effectively ceased due to limited QPS capacity and significant recent staffing changes at QPS. Of note, due to QPS officer unavailability (and other reasons), the Forensic Services Liaison Group (FSLG) has only met on a handful of occasions, with the last informal meeting in June seeing a 100% change in QPS membership. This was a fairly informal meeting held as a meet and greet for the new members and for broader discussion of issues (no minutes).	In Progress	31/12/2020		In progress	Overdue
2018/19	Performance Audit	2018-19 Report 21	Delivering forensic services	CHOPD - Chief Health Officer & Prevention Division	N/A	N/A	No Risk Rating	5	Improve the prioritisation and timely sharing of case information between agencies. This should include establishing systems and processes (and where possible automation) to ensure there is real-time notification of changes in priority or status to avoid unnecessary analysis.	16.1 Queensland Health will work collaboratively with the Queensland Police Service and the Department of Justice and Attorney-General to identify options to improve information sharing of case information.	8/09/2021: The legacy systems involved are not readily capable of integration, so the focus is on prioritising and communication. Forensic and Scientific Services have communicated processes and contact for urgent requests, which was appreciated by the Chief Magistrate. The Courts, DPP and Queensland Police Service are responsible for managing evidence briefs and coordinating these. Queensland Police Service should be prioritising samples, but does not have a process in place, leaving it up to Forensic and Scientific Services to try and follow court dates and react to emergent demands. Both Forensic and Scientific Services and Queensland Police Service are working with Magistrates Working Group to review the nature and need for forensic evidence in court cases. 19/08/2021: Further progress on these items has effectively ceased due to limited QPS capacity and significant recent staffing changes at QPS. Of note, due to QPS officer unavailability (and other reasons), the Forensic Services Liaison Group (FSLG) has only met	In Progress	31/12/2020		In progress	Overdue

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Queensland Government

Enquiries to: Ms Cathie Allen
Managing Scientist
Police Services Stream,
Forensic and Scientific
Services

Telephone: [redacted]
File Ref:

Queensland Health

Katarina Carroll APM
Commissioner
Queensland Police Service
GPO Box 1440
BRISBANE QLD 4012

Email: [redacted]

Dear Commissioner Carroll

Management of illicit drug testing

I am writing to you in relation to our mutual interest in improving the timeliness and efficiency of illicit drug testing and to seek assistance from the Queensland Police Service (QPS) on tackling this important matter.

In the past 12 months, Forensic and Scientific Services (FSS) has received around 12,000 illicit drug items which are submitted from QPS stations across Queensland, usually without any designated priority or related court date. Despite our best efforts through numerous internal strategies, untested drug exhibits are continuing to rise, and thus new additional solutions need to be explored. By August 2021, FSS held in excess of 5,000 illicit drug exhibits in backlog, relating to 2,948 cases, an increase of 7% on the same time last year. The ongoing increases in submissions year on year are causing significant delays in turnaround times. This was highlighted through the Australian and New Zealand Policing Advisory Agency (ANZPAA) National Institute for Forensic Science (NIFS) workflow mapping project for illicit drugs conducted in mid-2020, which showed an average submission time for the QPS to be 46 days, with an average turnaround time for laboratory processes of 97 days. This brings the total combined turnaround time for both organisations to 143 days, and the Courts have advised that this is becoming unacceptable. Urgent testing is conducted on a small number of appropriately identified items, with an average turnaround time of 5 days for laboratory processing in these instances.

Recently, Queensland Health had the opportunity to participate in the QPS Service Alignment Program where options were explored for improving the prioritisation of illicit drug exhibit tests, aiming to meet the needs of police investigators, prosecutors and the Courts alike. The 2018-2019 Queensland Auditor-General's report *Delivering Forensic Services* suggested ways to mitigate such delays, avoid unnecessary forensic testing, and implement a governance structure to more effectively, coordinate and manage forensic services. We recommend that a high-level Memorandum of Understanding (MoU) between QPS and FSS (as part of Queensland Health) is the best way to manage forensic services and would go a long way to addressing the current issues being faced in forensic testing.

[redacted]

With your assistance, developing a MoU with the QPS will assist in defining a prioritisation schedule for illicit drug submissions to our FSS laboratories. In turn, it would contribute significantly to meeting our joint obligations regarding the outstanding Queensland Audit Office (QAO) recommendations.

Until such time as an MoU is agreed and developed, FSS respectfully propose the following solutions to address the backlog of illicit drugs exhibits requiring testing:

1. FSS will return to the QPS any unprocessed illicit drug exhibits that were submitted more than 12 months ago (prior to 31 August 2020), unless there is a current court date assigned to the case. In this case, these exhibits will be prioritised for testing prior to the court case; and
2. QPS are requested to review all outstanding illicit drug cases and eliminate items or cases for which testing is either no longer required or is of low priority. Any returned items may of course be re-submitted to FSS should a matter progress to court and testing/analysis is required.

Combined, these actions will go a long way to ensuring minimal delays in court processes, reducing the public cost of items for which investigations have been discontinued or where court cases have already concluded.

Taken together, we estimate these actions will reduce the outstanding caseload by 30 to 40 per cent and assist scientific staff at FSS in focussing on active cases and emergent priorities as identified by police or the courts, until such time as a sustainable prioritisation process via an MoU can be developed between our agencies.

Finally, we are seeking your assistance in enabling FSS (guaranteed) development hours in the Forensic Register (FR) software. The FR is used by both forensic officers and teams at FSS, and your approval for the QPS Forensic Services Group to collaborate with FSS on the allocation of development hours would assist us greatly in reducing the turnaround time for testing, which in turn benefits both organisations.

Thank you in advance for your assistance and consideration of the above. I look forward to continuing to work in partnership with the QPS to support an efficient Queensland coronial and judicial system.

To progress these initiatives and/or discuss the above matters further, please contact Ms Cathie Allen, Managing Scientist – Police Services Stream, Forensic and Scientific Services, on telephone [redacted] or by email [redacted]

Yours sincerely

[redacted]

Dr John Wakefield PSM
Director-General
18/10/2021

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QUEENSLAND POLICE SERVICE

COMMISSIONER'S OFFICE
200 ROMA STREET BRISBANE QLD 4000 AUSTRALIA
GPO BOX 1440 BRISBANE QLD 4001 AUSTRALIA

Email: [redacted]

Our Ref:

Your Ref:

8 November 2021

Dr. John Wakefield PSM
Director-General
Queensland Health
GPO Box 48
Brisbane Qld 4000

Dear ~~Doctor Wakefield~~ John,

I refer to your letter of 18 October 2021, seeking assistance from the Queensland Police Service (QPS) to improve the timeliness and efficiency of illicit drug testing conducted by Queensland Health (QH), Forensic and Scientific Services (FSS).

I share your interest in improving the management of illicit drug testing and propose progressing development of a Memorandum of Understanding (MoU) through a working group consisting of members from Queensland Health (QH), QPS Forensic Services Group, Operational Support Command and QPS State Property Unit, Road Policing and Regional Support Command.

With reference to your proposed interim solutions prior to the development of the MoU, I agree to have officers conduct an audit of current exhibit holdings to assist with reducing the current backlog of illicit drugs submitted for testing. Additionally, I support the collaboration between FSG and FSS for development hours in the Forensic Register software. However, I respectfully request that QH maintains the status quo in relation to FSS returning any unprocessed illicit drug exhibits, until the QPS State Property Unit has had time to consider whole of service implications should large amounts of exhibits be returned to the QPS.

I look forward to continuing our partnership with Queensland Health to more effectively manage illicit drug testing.

To progress the MoU and agreed interim solutions, please contact Inspector Jim McKay, Manager, State Property Unit, Road Policing and Regional Support Command on [redacted] or via email [redacted]

Yours sincerely

[redacted]

KATARINA CARROLL APM
COMMISSIONER

CA-144

Queensland Government

Enquiries to: Lara Keller
A/Executive Director
Forensic & Scientific Services

Telephone: [redacted]
File Ref:

Queensland Health

Katarina Carroll APM
Commissioner
Queensland Police Service
GPO Box 1440
BRISBANE QLD 4012

Email: [redacted]

Dear Commissioner Carroll

Management of illicit drug testing

Thank you for your letter dated 8 November 2021, regarding your mutual agreement to progress with initiatives to improve the timeliness and efficiency of illicit drug testing.

To assist in progressing these actions, Queensland Health Forensic and Scientific Services (FSS):

- will lead the establishment of a working group with members of the QPS and FSS to progress a Memorandum of Understanding (MoU) to improve the management of illicit drugs and other forensic services provided by FSS;
- will provide the current illicit drug exhibit holdings to be audited by QPS to assist in reducing the current backlog of illicit drugs submitted for testing;
- has identified key areas for collaborative Forensic Register (FR) development in the illicit drugs area which include, but are not limited to, development of batch processing to enable a paper-lite environment, development of an FR-based Standards database, and data search functionality. FSS will liaise with QPS to have the necessary FR development hours allocated before 30 June 2022;
- will arrange monthly progress meetings between QPS and FSS to maintain inter-agency focus; and
- accepts the QPS request for FSS to retain unprocessed illicit drug items, until the QPS State Property Unit has had time to consider whole of service implications.

Thank you again for your support of these initiatives and I look forward to continuing to work in partnership with the QPS to support an efficient Queensland coronial and judicial system.

[redacted]

Forensic and Scientific Services A/Executive Director, Lara Keller, will be in contact with the relevant senior officers in QPS to commence progress on these actions. Ms Keller can be contacted on telephone [redacted] or via email at [redacted] should your officers wish to contact her directly.

Yours sincerely

[redacted]

Professor Keith McNeil
Acting Deputy Director-General and
Chief Medical Officer, Prevention Division and
Chief Clinical Information Officer
Queensland Health
30 / 11 / 2021

CA-145

Nicole Watt

From: Alison Slade
Sent: Tuesday, 3 May 2022 3:14 PM
To: Cameron Lane
Subject: RE: QAO audit updates

Hi Cameron,

Please see below additional detail re current status of actions for "Delivering Forensic Services" recommendations (noting that the recommendations for the "Delivering Coronial Services" QAO report are governed by the Coronial Services Governance Board – QH rep is Keith McNeil).

Delivering Forensic Services:

- **Recommendation 1:** implement a governance structure to effectively coordinate and provide accountability for managing forensic services across agencies
  - The Queensland Health Director General and QPS Commissioner exchanged letters in November 2021 agreeing to progress the development of an MOU, which had been delayed due to COVID priorities throughout 2020-21. Queensland Health has since led the establishment of a working group with members of the Queensland Police Service (QPS) and Forensic and Scientific Services (FSS) to progress a Memorandum of Understanding (MoU) to improve the management of illicit drugs and other forensic services provided by FSS. A draft MOU header agreement has been developed and provided to the QPS for review and consultation.
- **Recommendation 2:** implement a process to coordinate and manage collecting, transporting, prioritising, and destroying illicit drugs.
  - Actions agreed between Queensland Health and QPS in November 2021 include an audit of current illicit drug exhibit holdings and identification of key collaborative Forensic Register (FR) developments in the illicit drugs area. Increased communication sharing regarding illicit drugs samples requiring testing is now occurring. A new Client Portal in the FR is now allowing QPS officers to advise if testing is required and set a priority rating for the test.
- **Recommendation 5:** improve the prioritisation and timely sharing of case information between agencies.
  - Queensland Health is actively working with relevant agencies to develop an automated case-sharing portal with QPS and the Department of Public Prosecutions through the established Streamlining Criminal Justice working group.

Kind regards,
Alison

From: Cameron Lane [redacted]
Sent: Friday, 29 April 2022 11:55 AM
To: Alison Slade [redacted]
Cc: Cameron Lane <[redacted] Yvonne Li [redacted]
Subject: QAO audit Delivering Coronial Services

Dear Alison

Yvonne has her monthly catch up with Internal Audit Unit scheduled for 4 May 2022. She asked me to check to see if the team had an update on the QAO audit – Delivering coronial services.

The following recommendations are marked as in progress and partially implemented:

Area	Financial Year	QAO Audit Type	Audit/Report Title	QAO Risk Rating	Recommendation no.	Recommendation
PQ/FSS	2018/19	Performance Audit	Delivering coronial services	No Risk Rating	4	It is recommended that the Department of Justice and Att General, Department of Healt the Queensland Policy Servic collaboration with coroners im processes and practices acro coronial system by • ensuring is a coordinated, state-wide approach to triaging all death reported to the coroners to he advise the coroner of the nee autopsy • ensuring sufficient counselling services are avail and coordinated across agen support families and inquest v
PQ/FSS	2018/19	Performance Audit	Delivering forensic services	No Risk Rating	1	(Queensland Health and Queensland Police Service) Implement governance struct effectively coordinate and pro accountability for managing fo services across agencies. Th of reference should include • identifying current and future demand and the required res for forensic services • establis processes to capture the exte impact of delays from forensi services, including the impact courts. • implementing a performance framework to me and report on the effectivenes efficiency of forensic services should include ensuring each agency has appropriate perfo targets • ongoing consultation the Department of Justice and Attorney-General about the d of forensic services and impa the justice system.
PQ/FSS	2018/19	Performance Audit	Delivering forensic services	No Risk Rating	2	Implement a process to coord and manage collecting, transp prioritising, and destroying illi drugs. The revised process sl reduce the risks to security, occupational health and safet the cost of unnecessary hand

PQ/FSS	2018/19	Performance Audit	Delivering forensic services	No Risk Rating	5	Improve the prioritisation and sharing of case information be agencies. This should include establishing systems and pro (and where possible automati ensure there is real-time notif of changes in priority or statu avoid unnecessary analysis.

Let me know if there is any way I can support you with this?

Thank you so much.

Kind regards
Cameron

Chat with me on Teams!

Queensland Government

Cameron Lane
Team Leader
Office of the Deputy Director-General Prevention Division | Queensland Health
Working hours Monday to Friday

P [redacted]
E [redacted]
W health.qld.gov.au
A [redacted]



Queensland Health acknowledges the Traditional Custodians of the land across Queensland, and pays respect to First Nations Elders past, present and future.

CA-146

Nicole Watt

From: Lara Keller
Sent: Friday, 27 May 2022 10:17 AM
To: [redacted]
Subject: Today's meeting

Hello Bruce

I waited for a while on Teams, but then figured your day was too hectic to meet 😉

I understand that a meeting regarding the SAIK document was convened yesterday, and that there was QPS representation there.
According to Cathie, A/Supt Stephen Blanchfield and Debbie Jones (not sure of her rank but she was from a QPS Children's portfolio) attended.

I would like to talk with you (?next week), about SAIKs and the TOR for the QAO Forensics report, and MOU.

I'll ask my Executive Assistant to make the arrangements.

Wishing you a great weekend ahead.

Thanks and Kind Regards
Lara

Lara Keller B App Sc (MLS), Grad Cert Health Mgt, MAIMS, CMgr FIML
A/Executive Director

Forensic and Scientific Services
Prevention Division, Queensland Health
[redacted]

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CA-147

Financial Year	QAO Audit Type	Audit Reference	Audit/Report Title	Division	Recommendation No.	Recommendation	Management Agreed Actions	Management Proposed Status	Original Recom Due Date	Extended Due Date	Current Status agreed with QAO/IAU	Overall QAO Recom Status	Recommendation Close Date	Description of action taken	Evidence received and reviewed	Outcome of action taken?	Planned future action required for recommendations not yet completed	Are additional actions required?	Is more evidence required?	From who?	Current Status	HHS involvement?
2018/19	Performance Audit	2018-19 Report 21	Delivering forensic services	Prevention Division	1	(Queensland Health and Queensland Police Service) Implement governance structure to effectively coordinate and provide accountability for managing forensic services across agencies. The **terms of reference** should include: • identifying current and future demand and the required resources for forensic services • establishing processes to capture the extent and impact of delays from forensic services, including the impact on courts • implementing a performance framework to measure and report on the effectiveness and efficiency of forensic services. This should include ensuring each agency has appropriate performance targets • ongoing consultation with the Department of Justice and Attorney-General about the delivery of forensic services and impact on the justice	13.1 A Memorandum of Understanding between the Department of Health and the Queensland Police Service is under development to establish a governance structure to oversight the effective and efficient delivery of analytical services and promote collaboration and cooperation between agencies.	In Progress	31/12/2019		In progress	Overdue		The former Director-General, Queensland Health and the Queensland Police Service (QPS) Commissioner exchanged letters in November 2021 with an agreement to progress with the development of an MoU. This had been delayed due to COVID-19 priorities through 2020-21. Queensland Health has since led the establishment of a working group with members of the Queensland Police Service (QPS) and Forensic Scientific Service (FSS) to progress a MoU to improve the management of illicit drugs and other forensic services provided by FSS. A draft MoU header agreement has been developed and provided to the QPS of review and consultation.	[redacted]	[illegible] meetings are held between FSS and QPS, to discuss [illegible] across [illegible]. There are no terms of reference for these meetings at this time. The [illegible] meeting was held on [illegible]	Finalise the MoU between QPS and QH. Meeting is scheduled on 27/05/2022 to begin formalisation of revised MoU		No ToR exists at this time	PD	Partially Implemented	Possibly
2018/19	Performance Audit	2018-19 Report 21	Delivering forensic services	Prevention Division	2	(Queensland Health and Queensland Police Service) Implement a process to coordinate and manage collecting, transporting, prioritising, and destroying illicit drugs. The revised process should reduce the risks to security, occupational health and safety and the cost of unnecessary handling.	14.1 Queensland Health will work with Queensland Police Service to review processes for the collection, transport, prioritising and destruction of illicit drugs and implement improvements identified.	In Progress	31/12/2020		In progress	Overdue		Actions agreed between QH and QPS in November 2021 include: 1) conduct an audit of current illicit drug exhibit holdings to assist with reducing the current backlog of illicit drugs submitted for testing - [illegible] 2) identification of key collaborative Forensic Register (FR) software developments in the illicit drugs area - [illegible] 3) Increased communication sharing regarding illicit drugs samples requiring testing is now occuring - [illegible] 4) A new Client Portal delivers information into the FR and is now allowing QPS officers to advise if testing is required and set a priority rating for the test. [illegible]	[redacted] The QPS and QH are working together and liaising through regular [illegible] scheduled for [illegible] June 2022	The audit has identified that approx. 12% of cases are no longer required for testing. The cases required for testing have been prioritised and testing will begin based on [illegible]. QH and the QPS will work together on an efficient process for destruction of illicit drugs [illegible] identified through the audit	The QPS and QH will work together on improvements to [illegible] regarding occupational health and safety		The QPS approved the use of a Client Portal and documentation [illegible] with the QPS	PD	Partially Implemented	Possibly
2018/19	Performance Audit	2018-19 Report 21	Delivering forensic services	Prevention Division	4	(Department of Health, in collaboration with the Queensland Police Service and all HHSs) Continue to develop and deliver **reforms to forensic medical examinations** to improve services to victims, including: • implementing service agreements to deliver forensic medical examinations • developing strategies to recruit and retain appropriately trained physicians and nurses for forensic medical examinations across the state • implementing a range of reporting pathways and supporting processes for all victims requiring forensic medical examinations • improving clinician's awareness of reporting options for victims of sexual assault • improving the availability of, and access to, paediatric services for child victims of sexual assault • establishing local inter-agency support services that better integrate clinicians, police and non-government services.	15.1 Queensland Health will continue to contribute to the finalisation of the **Response to sexual assault - Queensland Government Interagency Guidelines for Responding to People who Experienced Sexual Assault** and will develop a **communication strategy** to support Hospital and Health Services (HHSs) implement the guidelines at a local level. Queensland Health has commenced consultation with HHSs on a **Health Service Directive** to establish mandatory sexual assault service standards. **Funding and service accountabilities to support implementation of the reforms have been included in HHS Service Agreements for 2019-20.** A nursing education program is in development to expand the number of clinicians able to conduct assault examinations. Queensland Health is working in collaboration with Queensland Police and HHSs to ensure patients disclosing sexual assault are supported in deciding to have a forensic examination or whether to defer police investigations if they	Completed	31/12/2019		Resolved	Completed	31/01/2020	Health Service Directive (HSD) *Caring for People Disclosing Sexual Assault* (QH-HSD-051:2019) has been developed published on the QH website. Resources supporting the delivery of the requirements set out in the above HSD are available on the QH intranet site, including information about the Sexual assault nurse examiner course. HHS responsibilities relating to adult sexual health clinical forensic examinations have ben included in the HHS Service Agreement 2019/20 - 2021/22	HSD - Caring-for-people-disclosing-sexual-assault Supporting doc - Response-to-sexual-assault QHEPS - Sexual-assault-nurse-examiner-course	The Health Service Directive (HSD) *Caring for People Disclosing Sexual Assault* (QH-HSD-051:2019) requires HHSs to take a consistent approach to managing clinical and psychosocial needs of people who have experienced sexual assault. This includes the person-centred provision of forensic examinations. One of the mandatory requirements included in the HSD is for HHS to ensure everyone who discloses that they are a victim of sexual assault informed of their choices about forensic examinations and reporting the assault to the police, including the benefits of early reporting. Extra support materials were made available on the QH intranet site and QH website to help staff better understand and provide greater care in forensic medical examinations to improve services to victims. These include: 1) *Guideline for the management of care for people 14 years and over disclosing sexual assault* - provides recommendations regarding best practice to support the management	N/A	N/A	N/A	N/A	Completed	Yes
2018/19	Performance Audit	2018-19 Report 21	Delivering forensic services	Prevention Division	5	(Qld Police Service, Queensland Health and the Dept. of Justice and Attorney-General) Improve the prioritisation and timely sharing of case information between agencies. This should include establishing systems and processes (and where possible automation) to ensure there is real-time notification of changes in priority or status to avoid unnecessary analysis.	16.1 Queensland Health will work collaboratively with the Queensland Police Service and the Department of Justice and Attorney-General to identify options to improve information sharing of case information.	In Progress	31/12/2020		In progress	Overdue		Queensland Health is actively working with relevant agencies to develop an automated case-sharing portal with QPS and the Department of Public Prosecutions (DPP) through the established Streamlining Criminal Justice working group. [illegible]	[redacted]	A secure [illegible] containing details of [illegible] QPS [illegible] information, and ODPP court information has been published and is in use	Regular review of effectiveness will be [illegible] between organisations	No	No		[illegible]	Possibly

CA-148

QUEENSLAND POLICE SERVICE

QPS & FSS Meeting

MINUTES

Meeting Date: Thursday 19 May 2022
Location: Microsoft Teams
Time: 12:00pm – 1:00pm
Chair: Superintendent Bruce McNab
Secretary: AO3 Jenna De Marco
Attendees:

Superintendent Bruce McNab, QPS (BM)
Inspector David Neville, QPS (DN)
Ms Lara Keller, FSS (LK)
Ms Cathie Allen, FSS (CA)
Ms Paula Brisotto, FSS (PB)

	Item	Responsible
1.0	**Welcome and Apologies**	
1.1	Opening and Welcome	BM
1.2	Apologies	BM
2.0	**Review Previous Minutes/Action Items**	
2.1	• **ACTION ITEM:** Both agencies to assess potential for using FR as primary search engine and only uploading unknown crime scene profiles and new person profiles to NCIDD. To be reviewed at next meeting – risks/impacts from QHSS regarding FR as main search database. **CARRY OVER NEXT MEETING** ○ DN questioned if FSS see any obstacles with changing process of uploading data to QPS Database and only uploaded to NCIDD if there are not hits on QLD Database. • **ACTION ITEM**: QHFSS to provide a report to the QPS regarding the testing thresholds used to triage continuation of DNA testing. The report is anticipated to be provided by 25/03/2022 **CARRY OVER NEXT MEETING**	All
3.0	**Review – Summary of FSS Systems and Processes**	
3.1	• Hon Yvette D'Ath MP tabled a paper in parliament – Terms of Reference titled 'Summary of FSS Systems and Processes Review'. • LK advised a Reviewer has not been finalised. Once this has been confirmed, the review will commence. • BM noted that he was unaware of any consultation taking place with QPS in the development of the TOR and that it does not include consideration of any customer feedback. LK indicated that the TOR may increase in scope and this should be considered.	LK
4.0	**General Business**	
4.1	• Strategic/Research Projects ○ CA asked if QPS have any Strategic or Research Projects in progress, in particular DNA or Drug related. CA advised QH is happy to offer their assistance.	All



QUEENSLAND POLICE SERVICE

QPS & FSS Meeting



	○ BM/DN advised they don't believe there is any but will make some enquires and advise FSS. • Frequency of FSG/FSS meetings ○ Discussed the frequency of these meetings. ○ Previously they were held bi-monthly when Supt Frieberg was in the chair. ○ Currently they are scheduled monthly. ○ Will review and make changes as required. • Forensic Register ○ General discussion regarding the new FR system and feedback. ○ FSS advised they had some minor issues which they have raised with Bdna. ○ FSG raised similar issues. • Success Rate/Thresholds Levels ○ As per the above action item 2, FSS are waiting on legal advice on the release of this information.	
5.0	**Meeting Finalisation**	
5.1	Next Meeting – 16/06/2022	BM
5.2	Close	

CA-149

Nicole Watt

From: Lara Keller
Sent: Tuesday, 21 June 2022 7:05 AM
To: McNab.BruceJ[OSC]; Neville.DavidH[OSC]
Cc: Cathie Allen; Peter Culshaw
Subject: FSS agenda items for today's meeting

Good morning All

Here are our agenda items for this afternoon's QPS-FSS meeting, noting that some already appear on the previous minutes:

1. Commission of Inquiry
   https://statements.qld.gov.au/statements/95380
2. Follow up report regarding thresholds
3. Research collaboration
4. FR development hours
5. Turnaround times
6. DNA reference samples for SAIKs
7. Terms of reference for this group
8. MOU

As Cathie is taking leave soon, Peter Culshaw will also attend from FSS.
We look forward to seeing you then.

Thanks and Kind Regards
Lara

Lara Keller B App Sc (MLS), Grad Cert Health Mgt, MAIMS, CMgr FIML
A/Executive Director

Forensic and Scientific Services
Preventive Division, Queensland Health
[redacted]

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CA-150

QUEENSLAND POLICE SERVICE
QPS & FSS Meeting
AGENDA/MINUTES

Meeting Date: Thursday 23 June 2022
Location: Microsoft Teams
Time: 11:38am – 12:06pm
Chair: Superintendent Bruce McNab
Secretary: AO3 Jenna De Marco (JDM)
Attendees:

Superintendent Bruce McNab, QPS (BM)
Inspector David Neville, QPS (DN)
A/Executive Director Lara Keller, FSS (LK)
Cathie Allen, FSS (CA)
Mr Peter Culshaw FSS (PC)

	Item	Responsible
1.0	**Welcome and Apologies**	
1.1	Opening and Welcome Meeting opened – 11:38am	Chair
1.2	Apologies	Chair
2.0	**Review Previous Minutes/Action Items**	
2.1	• Both agencies to assess potential for using FR as primary search engine and only uploading unknown crime scene profiles and new person profiles to NCIDD. To be reviewed at next meeting – risks/impacts from QHSS regarding FR as main search database. **SEE AGENDA ITEM 3.1 *GENERAL DISUCSSION*** • QHFSS to provide a report to the QPS regarding the testing thresholds used to triage continuation of DNA testing. The report is anticipated to be provided by 25/03/2022. **SEE AENDA ITEM 5.0 *FOLLOW UP REPORT REGARDING THRESHOLDS***	All
3.0	**General**	
3.1	**RECORDING OF FUTURE MEETINGS** • Superintendent Bruce McNab (BM) proposed all future meetings between FSG and QHFSS should be recorded. A copy of the transcript can also be provided. All attendees were in favour. **MANAGING SCIENTIST – ABSENCE OF LEAVE** • A/Executive Director Lara Keller (LK) advised Ms Cathie Allen (CA) would be commencing recreation leave shortly and will be backfilled by Mr Peter Culshaw (PC). **ACTION: Secretary AO3 Jenna De Marco (JDM) to include PC in the next meeting QPS/FSS meeting.** • LK also advised she would be taking 6 weeks leave in July. Reliever will be advised in due course. **LOCAL DATABASE FOR DNA SEARCHING** • DN asked with DNA searching is only going to NCIDD when it's a new profile that's not on there or when there's no hit against on the local database and the benefits that we see is that.	





QUEENSLAND POLICE SERVICE
QPS & FSS Meeting
AGENDA/MINUTES

	We're not clogging inside with duplicate or triplicates or whatever or replicates of profiles, and there's less lines of reporting coming back. So rather than getting the match reported twice, it's just once, as indication that might be a change management issue out there, I just wondered how that looked, what obstacles, what risks you might have identified? • CA advised due to other commitments and current events, FSS have not been able to progress this request. • BM asked what time frame this would be completed by. CA indicated potentially by the end of the year but this could not be firm on this date due to the Commission of Inquiry and other commitments. • LK advised FSS would have a conversation in house and provide a response back to FSG by the next meeting with what they will need to complete this request. • BM acknowledge that FSS may have some resources being diverted off, and we'd be really interested to further discussion around some of the time frames and and hurdles and anything we can do to assist in that space. **ACTION: LK to advise by next meeting the expected timeframe to respond to risks/impacts from QHSS regarding FR as main search database.** • CA asked DN if any progress in regards to the removal of duplicates or has there been an update on that process? DN indicated they are trying to stop the replicates being added in the first place. • BM added he has requested DN not to progress that because we're removing stuff that constantly gets added back in	
4.0	**Commission of Inquiry**	
4.1	• LK Table within group – Terms of Reference (TOR) have been announced. • LK confirmed internal review has been placed on hold.	
5.0	**Follow up report regarding thresholds**	
5.1	• CA advised FSS have been able to obtain data from the Forensic Register (FR) for a specific period. • FSS have reviewed the data and drafted a report indicated suitable/not suitable percentages. • This report has been reviewed and peer reviewed and is approved for release. LK advised she would forward a copy to BM to review.	
6.0	**Research collaboration**	
	• FSS advised there were very interested in being involved in any collaborative research projects. • DN indicate that QPS are working on a project around Phenotyping. This project is being managed by Senior Sergeant Ewen Taylor.	





QUEENSLAND POLICE SERVICE
QPS & FSS Meeting
AGENDA/MINUTES

	• DN advised there are no other projects. • BM asked if there was an opportunity for the respective research or project officers to meeting regularly for a collaborative session. CA indicated their research officer has meet the QPS research officer Dr Matt Krosch. • Proposed by BM that research officers attend these meetings every 2nd month to provide an update on current projects. **ACTION: FSG & FSS to speak with their research officers to commence meeting regularly and to provide an update at every 2nd meeting.**	
7.0	**FR development hours**	
	• LK seeking clarification through the illicit drug space about the FR development hours. • BM explained in the original commercialisation negations, Bdna offered a series of royalty payment over a fixed number of years. • In previous discussions with the previous ED John Doherty, BM and Bdna, structure of development hours was suggested. 80% of development would sit with QPS and 20% to FFS (would need to review and confirm these stats) Both agencies would have an opportunity to discuss what needs were required and the potential to share each other's development hours. • If FSS were to enter into a further relationship with Bdna to obtain services in addition to the original agreement, then those development hours wouldn't relate to that. • LK indicated she has been in discussions with Bdna to explore the coronial space with the FR but this would be a separate body of work.	
8.0	**Turnaround times**	
	• LK had requested if herself and CA could be given access to the Turn Around Time (TAT) figures. LK indicated that they would like to review these stats themselves as it would give them an opportunity to look at process improvements and opportunities. • DN indicated he will send an email to Bdna to allow access to FSS. The TAT will appear on their stats function. **ACTION: DN will send an email to Bdna to grant access to FSS to the TAT data.**	
9.0	**DNA reference samples for SAIKs**	
	• LK made enquires when the next meeting will be scheduled as she would like to finalise the multi-jurisdictional document. • BM has not had an opportunity to speak with the Deputy Director, DPP. • There was a proposed amendment to the document in terms of wording around when the reference sample should be taken and by whom.	





QUEENSLAND POLICE SERVICE
QPS & FSS Meeting
AGENDA/MINUTES

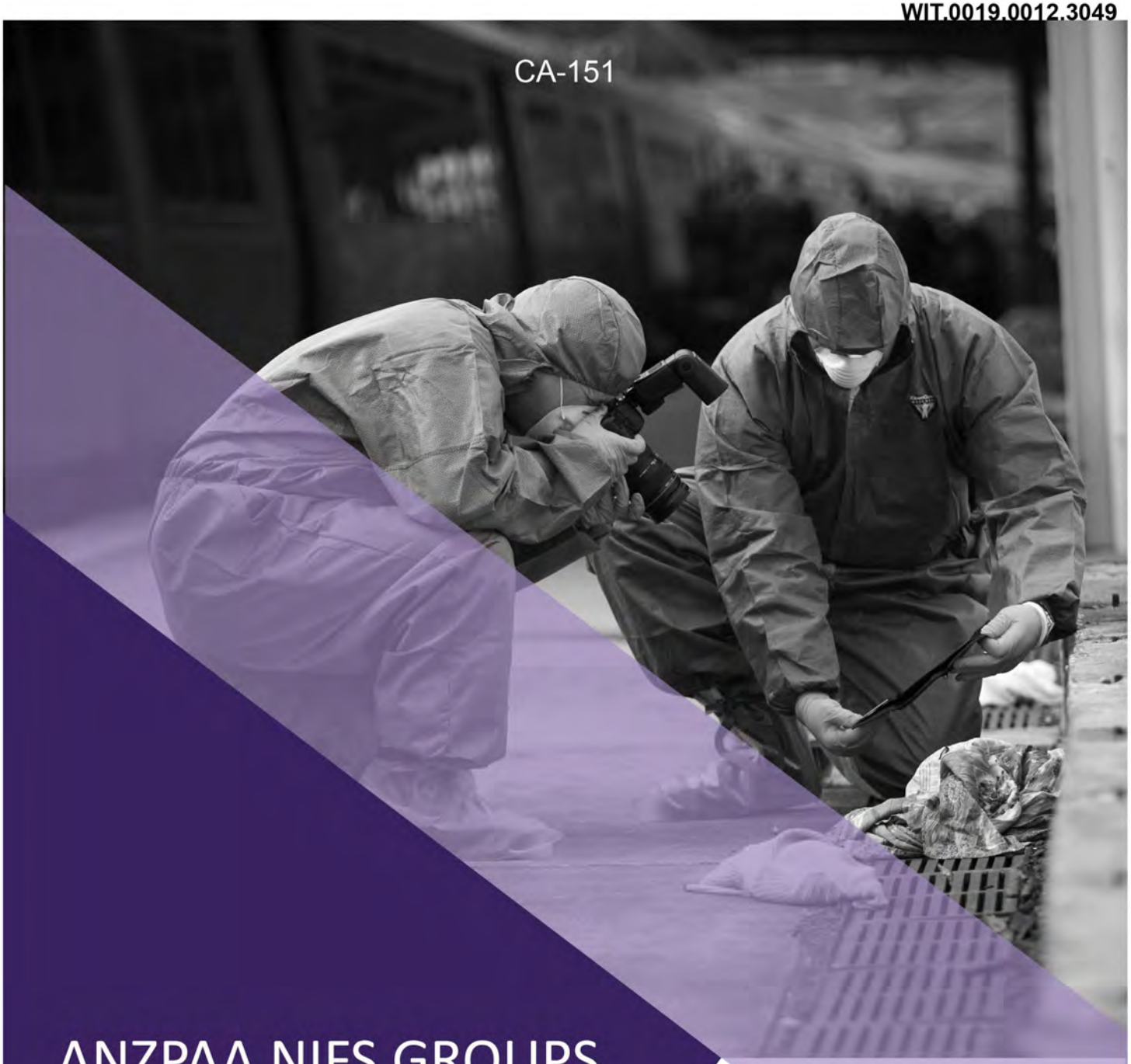
	• BM advised this document would go back to the next meeting and has requested the DPP to be involved in future meetings. • **ACTION: BM to include LK in his response email to DPP re: amendment to document, reference samples** • LK also mentioned there has been a lot of activity happening in the training space. Jackie Thompson, who is managing the same program, is starting to work out the training needs, collection of DNA samples etc. • Need to also clarify the kits – what will they contain and how to keep reference DNA samples separate. • LK indicated she has a health collector for DNA reference samples.	
10.0	**Terms of reference for this group**	
	• FSS are regularly requested to provide updates to the board regarding the QAO report, in particular the TOR. • Also have been requested to provide an update on the MOU and recommencing those discussions. • BM indicated FSG have not had to provide regular updates on the QAO report. • BM understood that one of the TOR was around the communication between agencies. • BM is supportive of a TOR being drafted if FSS wish to do so. BM requested a copy be sent him for his review.	
11.0	**MOU**	
	• Previous discussions between BM and former ED John Doherty to formalise the MOU. • QPS had no issues with the MOU, but the schedule of fees was incomplete. • It was requested FSS submit a schedule of fee for consideration with the MOU. • Delays impacted the progression of the MOU – previous Director Michael Lok departed FSS and COVID. • BM expressed to Michael Lok that the QPS needed little bit of space to deal with a global pandemic and then the next part of the conversation was, Clause 8 outlines the financial responsibilities and payment terms contained within scheduled to the service schedule, but it's incomplete with respect to cost for service. • This portion of the MOU will need to be finalised prior to the MOU being executed. • LK asked if QPS were happy to recommence MOU conversations. BM agreed to recommence MOU discussions.	
12.0	**Meeting Finalisation**	
12.1	Next Meeting –	Chair
12.2	Close Meeting closed – 12:06pm	Chair

QUEENSLAND POLICE SERVICE
QPS & FSS Meeting
AGENDA/MINUTES

ACTION ITEMS

Meeting Date	Item	Actioner
17/03/2022	Both agencies to assess potential for using FR as primary search engine and only uploading unknown crime scene profiles and new person profiles to NCIDD. To be reviewed at next meeting – risks/impacts from QHSS regarding FR as main search database. **CARRY OVER - LK to advise by next meeting the expected timeframe to respond to risks/impacts from QHSS regarding FR as main search database**	FSG & FSS
17/03/2022	QHFSS to provide a report to the QPS regarding the testing thresholds used to triage continuation of DNA testing. The report is anticipated to be provided by 25/03/2022 **CARRY OVER**	FSS
23/06/2022	PC in the next meeting QPS/FSS meeting.	FSG
23/06/2022	Speak with their research officers to commence meeting regularly and to provide an update at every 2nd meeting.	FSG & FSS
23/06/2022	Send an email to Bdna to grant access to FSS to the TAT data.	FSG
23/06/2022	Include LK in his response email to DPP re: amendment to document, reference samples	FSG

CA-151



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References in this notice to ANZPAA are references to the Members of ANZPAA and the Members of ANZFEC.

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INTRODUCTION

The National Institute of Forensic Science (NIFS) is a directorate within the Australia New Zealand Policing Advisory Agency (ANZPAA). The strategic intent of ANZPAA NIFS is to promote and facilitate excellence in forensic science through a number of defined programs of work that are approved by the ANZPAA Board, which comprises the Police Commissioners of Australia and New Zealand and the Chief Police Officer of the Australian Capital Territory. Within these programs of work, there are a number of ongoing and project activities that are approved by the Australia New Zealand Forensic Executive Committee (ANZFEC), which comprises the Director or Head of Department from each recognised government forensic science service provider that are signatories to the ANZPAA NIFS Service Level Agreement.

The ANZPAA NIFS Groups provide an important mechanism for ANZFEC and ANZPAA NIFS to support and promote the continuous improvement of forensic disciplines, encouraging collaboration and innovative thinking. They also provide a mechanism for ANZFEC and ANZPAA NIFS to seek discipline specific technical advice and guidance in relation to contemporary issues affecting science service provision in Australia and New Zealand.

This document provides information on the Terms of Reference (TOR) for the ANZPAA NIFS Groups and covers key elements including:

- purpose
- roles
- governance and accountability
- membership and responsibilities
- protocols and procedures.

This TOR is applicable to all ANZPAA NIFS Groups and any additional information or deviations are detailed in the relevant Group's Annexe.

PURPOSE

The purpose of the ANZPAA NIFS Groups is to provide discipline specific technical advice and opportunities for capability development to inform strategic policy and decision makers through:

- identifying and addressing critical issues
- forecasting emerging challenges
- informing best practice
- identifying opportunities to collaborate and leverage resources, between agencies and disciplines.

Additional information in relation to purposes for specific Groups are detailed in the relevant Group's Annexe.

ROLES

The roles of the ANZPAA NIFS Groups are detailed in *Table 1*. Any variation to these roles are detailed in the relevant Group's Annexe.

Table 1: ANZPAA NIFS Groups Roles

ANZPAA NIFS Groups Roles
Co-ordination ▸ Provide specialist advice regarding technical issues, emerging challenges and capability development. ▸ Identify agreed best practice and promote cross-jurisdictional standardisation. ▸ Collaborate in initiatives to improve forensic science capabilities.
Research and Innovation ▸ Identify and prioritise trends, research and innovation needs and new technology to inform projects and initiatives. ▸ Participate in research projects and initiatives.
Information Exchange ▸ Share and exchange information to reduce duplication and leverage resources across jurisdictions. ▸ Communicate the activities of the Group to ANZPAA NIFS and ANZFEC through quarterly reporting. ▸ Represent the Australia New Zealand forensic science community at national and international meetings and groups and liaise and communicate between the groups. ▸ Liaise with equivalent international groups.
Education and Training ▸ Identify and prioritise opportunities for cross agency and cross discipline training workshops and co-ordinate applications to ANZPAA NIFS. ▸ Co-ordinate and run cross agency workshops.
Quality ▸ Identify cross agency discipline specific or general quality issues and initiatives to promote continuous improvement and recommend actions to address the issues. ▸ Action approved recommendations that address quality assurance issues.

GOVERNANCE AND ACCOUNTABILITY

The ANZPAA NIFS Groups are advisory groups managed by ANZPAA NIFS, with reporting lines to ANZFEC. The ANZPAA NIFS Groups governance model is provided in *Figure 1*. Ultimate responsibility of the ANZPAA NIFS Groups is to the Police Commissioners of Australia and New Zealand and, where reporting to the ANZPAA Board is required, this will be facilitated through the Chief Executive Officer (CEO) of ANZPAA.

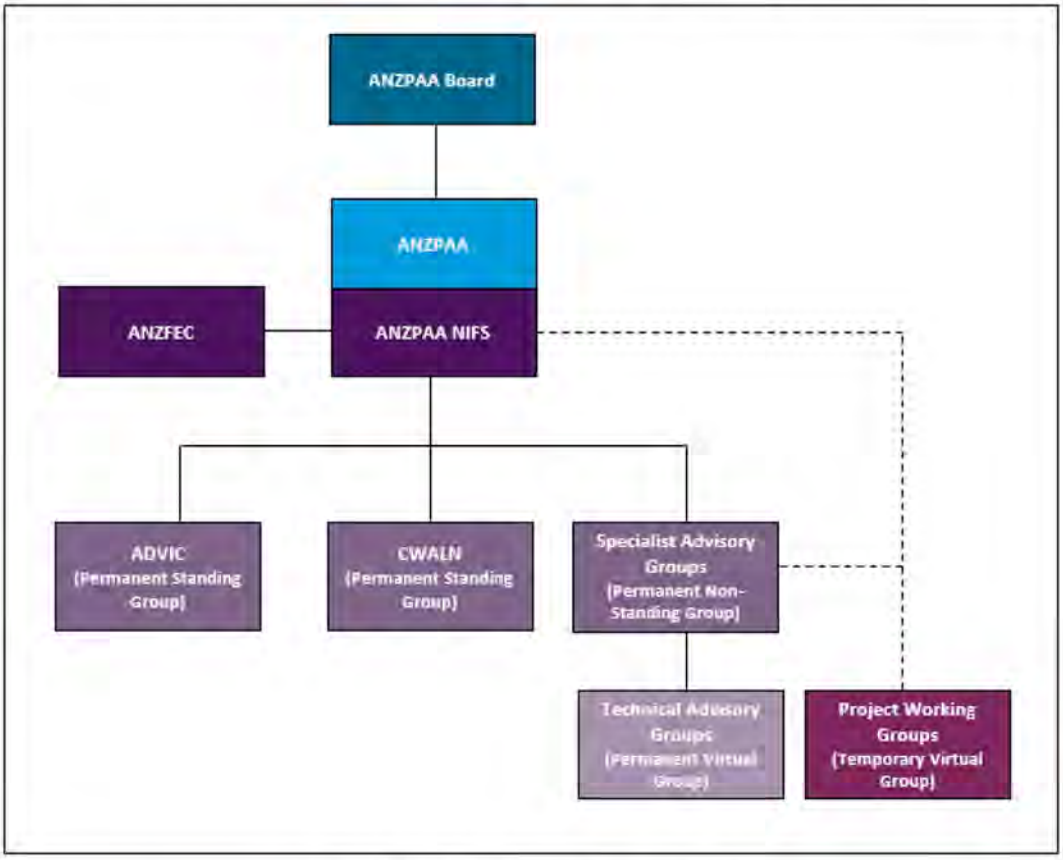


Figure 1: ANZPAA NIFS Groups Governance Model

ANZPAA NIFS GROUPS

The ANZPAA NIFS Groups are detailed in *Table 2*.

Table 2: ANZPAA NIFS Groups and Descriptions

Name	Descriptions
ANZPAA Disaster Victim Identification Committee (ADVIC)	Permanent Standing Group
Chemical Warfare Agent Laboratory Network (CWALN)	Permanent Standing Group
Specialist Advisory Group (SAG)*	Permanent Non-Standing Group
Technical Advisory Group (TAG)*	Permanent Virtual Group
Project Working Group (PWG)*	Temporary Virtual Group

*See *Appendix A* for a diagram of the current ANZPAA NIFS Groups Structure.

A **Permanent Standing Group** is an ongoing Group that engages and participates in discussions through technology-supported means and in person at an annual meeting. These Groups report to ANZFEC through ANZPAA NIFS.

A **Permanent Non-Standing Group** is an ongoing Group that engages and participates in discussions through technology-supported means and/or in person at meetings, based on need. These Groups report to ANZFEC through ANZPAA NIFS.

A **Permanent Virtual Group** is an ongoing Group that engages and participates in discussions generally through technology-supported means. The activities of these Groups are reported to ANZFEC through ANZPAA NIFS via the relevant SAG.

A **Temporary Virtual Group** is a non-ongoing Group that engages and participates in discussions through technology-supported means and/or in person at meetings, based on need. These groups have a finite life span and defined outcomes. Temporary Virtual Groups may be cross-discipline, with reporting lines to ANZFEC through multiple SAGs, or directly to ANZPAA NIFS.

CREATION, DISBANDMENT AND ELEVATION OF GROUPS

The creation, disbandment and elevation of Groups is the remit of ANZFEC.

ANZPAA NIFS Groups may request the creation or disbandment of SAGs, TAGs or PWGs for ANZFEC consideration. A business case, developed in consultation with ANZPAA NIFS and the relevant ANZFEC Mentor, shall be submitted to ANZPAA NIFS by the Group's Chair for ANZFEC approval. Support from the ANZFEC Mentor should be received before submission. ANZPAA NIFS Groups may also request the elevation of a PWG to a TAG or TAG to a SAG through this mechanism.

The business case should address, but is not limited to, the following considerations:

- forensic environment as it relates to the Group
- proposed outcomes that would be delivered
- benefits and risks
- resource implications
- proposed membership.

MEMBERSHIP AND RESPONSIBILITIES

MEMBERSHIP

Members should ideally have demonstrated appropriate credentials as specified below, and be part of an agency or institution with a recognised forensic science capability. Membership is comprised of predominately representatives from recognised government forensic science service providers; however, the broader science community such as representatives from academic institutions may be engaged as appropriate. ANZFEC agencies may nominate a representative for any Group related to a forensic science service they provide. All decisions in relation to membership will be at the discretion of ANZFEC.

The membership structure is depicted in *Figure 2*.

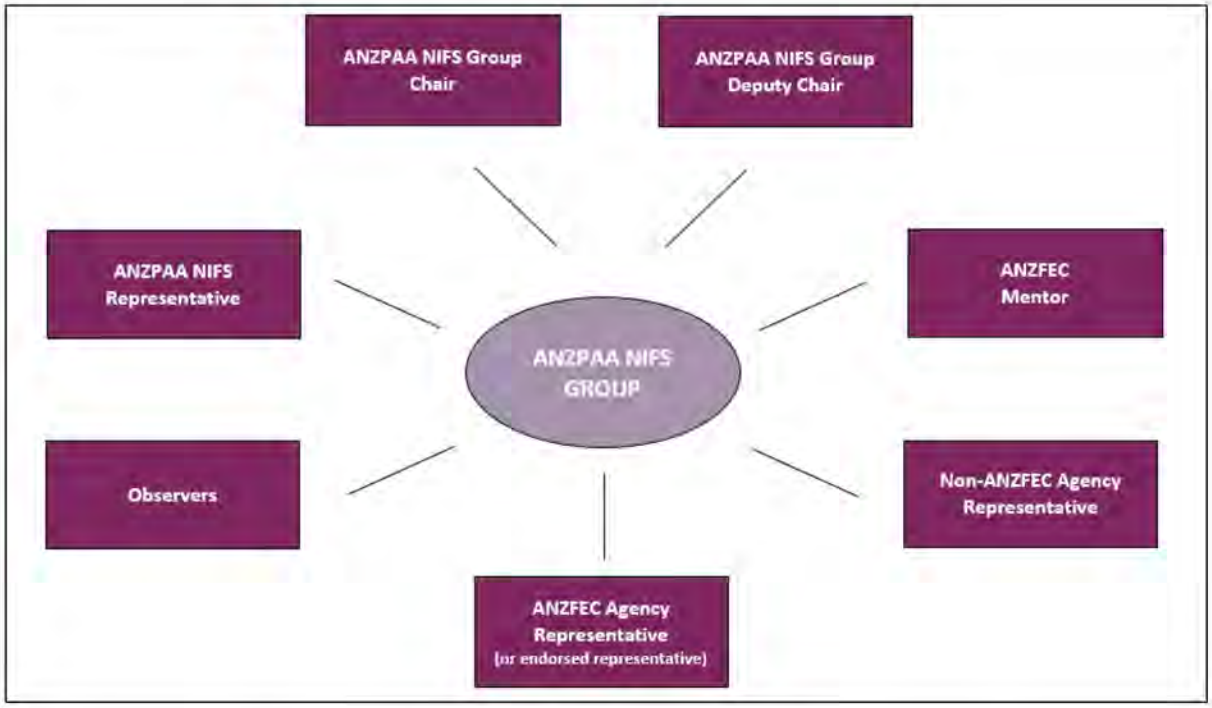


Figure 2: ANZPAA NIFS Groups Membership

There are three operating models for SAG membership. The variation in these models is due to the different structure and functionality of the Groups. The models are as follows:

1. Discipline Specific SAG

   This model is applicable to standalone SAGs that do not have any reporting TAGs (e.g. Toxicology). SAG membership is as depicted in *Figure 2*.

2. SAG with one or more sub-discipline TAGs

   This model is applicable to SAGs that have reporting TAGs which are a sub-discipline of their field (e.g. Crime Scene). In addition to the membership structure presented in *Figure 2*, the TAG Chairs sit on the SAG as observers to facilitate reporting and continuity.

3. SAG consisting of one or more distinct discipline TAGs

   This model is applicable to SAGs that have reporting TAGs which are recognised as being distinct disciplines (e.g. Electronic Evidence). The SAG does not have its own individual members, but rather is comprised of the TAG's members. An ANZPAA NIFS Representative and ANZFEC Mentor also sit on the SAG.

As per *Figure 1*, the activities of TAGs and PWGs are reported to ANZFEC through a SAG or ANZPAA NIFS. Similarly, these Groups may be tasked with actions from ANZPAA NIFS, ANZFEC through the SAG or directly from the SAG. To aid in the timely completion of action items and increase communication flow, where a representative of the relevant SAG is not a TAG or PWG member, the SAG may nominate a liaison person to provide advice and assistance as required.

MEMBER DUTIES AND REQUIREMENTS

The specific duties and requirements of members are detailed in *Table 3*. All members are also required to:

- participate in discussions at meetings in person or through technology-supported means
- contribute to the annual review and update of the Roadmap Questions document in consultation with ANZPAA NIFS, ANZFEC and the Research and Innovation Advisory Committee (RIAC)
- report on the status of the Group's activities to ANZPAA NIFS, ANZFEC and the agency they represent.

Table 3: Duties and Requirements of ANZPAA NIFS Groups Members

ANZFEC Mentor	
Criteria for Membership	▸ Recognised voting member of ANZFEC.
Nominations and Appointment	▸ Non-voting member of the ANZPAA NIFS Group. ▸ ANZPAA NIFS will notify the Group Chair of changes to the Mentor, as required.
Term of Appointment	▸ Reviewed every two years.
Duties	▸ Represent ANZFEC. ▸ Provide guidance, advice and strategic direction to inform action plans, research initiatives and capability development. ▸ Attend face-to-face meetings and provide an ANZFEC update. ▸ Be a conduit of information between the ANZPAA NIFS Group and ANZFEC. ▸ Review requests and agendas for face-to-face meetings. ▸ Review and prioritise workshop proposals. ▸ Review and endorse submissions for the creation of a new Group. ▸ Seek an ANZFEC member to attend Group meetings, as a proxy, if they are unavailable.

Chair/Deputy Chair	
Criteria for Membership	▸ An ANZFEC agency representative who is an existing Group member.
Nominations and Appointment	▸ Recognised ordinary voting member of the ANZPAA NIFS Group. ▸ Also sits as their ANZFEC agency representative on the Group. ▸ Nominations are accepted at the end of each term with an election, if required (in or out-of-session). ▸ The Chair's nomination must be endorsed by the nominee's ANZFEC member before commencement. ▸ The ANZPAA NIFS Group Chair handover occurs on 1 January in the year following the election of the new Chair. The outgoing Chair shall actively involve the incoming Chair, with respect to the activities of the Group between the election and handover.

Chair/Deputy Chair	
Term of Appointment	▸ Two years, with the eligibility of re-appointment for a second two-year term if supported by the Group.
Duties	▸ Co-ordinate the development and submission of meeting agendas, strategic discussion papers and workshop proposals in consultation with the ANZFEC Mentor. ▸ Mediate and manage discussions between Group members. ▸ Be a conduit between the Group and ANZPAA NIFS. ▸ Record and distribute, or delegate the recording and distribution, of minutes from meetings in a timely manner. ▸ Oversee and manage the completion of action items and action plans in a timely manner. ▸ Appoints a Webmaster to co-ordinate the NIFS Secure Server folder structure and user access.

ANZFEC Agency or ANZFEC Agency Endorsed Representative	
Criteria for Membership	▸ An ANZFEC agency representative. OR ▸ A forensic service provider endorsed by an ANZFEC agency to represent the interests of the relevant jurisdiction.
Nominations and Appointment	▸ Recognised ordinary voting member of the ANZPAA NIFS Group. ▸ The relevant ANZFEC member, or a delegate, is responsible for approving their agency representative. ▸ Membership is limited to one voting member per ANZFEC agency, however an agency may send additional representatives as observers (see Non-ANZFEC Agency Representative/Observer for further information).
Term of Appointment	▸ Ongoing role, subject to review by relevant ANZFEC member.
Duties	▸ Represent the best interests of their agency. ▸ Be a conduit of information between the Group and their agency. ▸ Assume responsibility to complete action plan items in a timely manner.

Non-ANZFEC Agency Representative/Observer	
Criteria for Membership	▸ A non-ANZFEC agency that provides a service relevant to a Group. OR ▸ An additional ANZFEC agency representative.
Nominations and Appointment	▸ Non-voting member of the ANZPAA NIFS Group. ▸ Non-ANZFEC agency representatives shall be endorsed by the Group and the ANZFEC Mentor. ANZFEC is responsible for final approval. ▸ ANZPAA NIFS Groups may nominate non-ANZFEC agencies for representation on the groups for ANZFEC consideration and approval. Requests received by ANZPAA NIFS directly shall be forwarded to ANZFEC for approval. ▸ Observers may hold a standing invitation or be invited on an ad hoc basis in consultation with the Group's Chair.
Duties	▸ Represent the best interests of their agency. ▸ Be a conduit of information between the Group and their agency. ▸ Assume responsibility to complete action plan items in a timely manner.

ANZPAA NIFS Representative	
Criteria for Membership	▸ ANZPAA NIFS team member.
Nominations and Appointment	▸ Ex officio member of the Group and does not hold voting rights.
Duties	▸ Co-ordinate the ongoing support of the ANZPAA NIFS Group, facilitates reporting to ANZFEC and provides advice on matters with national implications, as required. ▸ Ensure the ANZPAA NIFS Group undertakes their roles and responsibilities in accordance with the ANZPAA NIFS Groups Terms of Reference. ▸ Attend face-to-face to meetings and provides an ANZPAA NIFS update. ▸ Liaise with Chair and Mentor in relation to matters that require ANZFEC approval.

INVITED GUESTS

A guest may be invited by the Group to present, facilitate or engage in discussions in relation to a topic of interest. Invitations shall be endorsed by the Group's Chair and ANZFEC Mentor.

CODE OF ETHICS AND DECLARATION OF INTERESTS

ANZPAA NIFS Groups members and attendees acknowledge that they will:

- work collaboratively to achieve outcomes
- disclose any actual or perceived conflicts of interest
- be responsive and engaged and exercise honesty, care and diligence in the discharge of their duties on the Group.

PROTOCOLS AND PROCEDURES

The protocols and procedures for the ANZPAA NIFS Groups are detailed below. Any variation to these protocols and procedures are detailed in the relevant Group's Annexe.

MEETINGS

Meetings of the ANZPAA NIFS Groups may be face-to-face (ADVIC, CWALN and SAGs) or through technology supported means. All meetings of the Groups shall be agenda-led and the agenda should be provided to participants upon finalisation of the meeting details. The approval process for face-to-face meetings of the SAGs is detailed in *Figure 3*.

Meeting minutes shall be taken by a delegate and provided to all participants in a timely manner after completion of the meeting. The minutes shall reflect the discussions held and record decisions, recommendations and actions.

Agendas and minutes should be stored on the NIFS Secure Server.

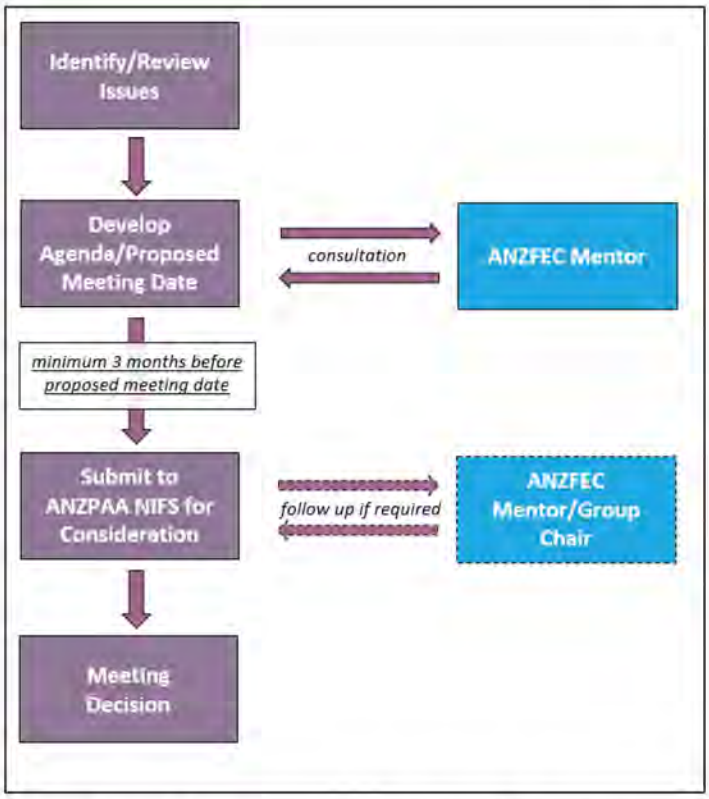


Figure 3: Approval process for face-to-face SAG meetings

AGENDA

The agenda is set by the ANZPAA NIFS Group Chair in consultation with the Group's ANZFEC Mentor and consideration is given to:

- review of the Roadmap annual questions document
- any taskings and referrals from ANZFEC
- current and emerging issues warranting the attention of the Group
- workshop proposals for submission to ANZPAA NIFS
- any matters raised by Group members, ANZPAA NIFS or ANZFEC.

The agenda should indicate the preferred location, including relevance or reason for selection. If the location is not crucial to the outcomes of the meeting, ANZPAA NIFS may change the location of the meeting based on previous meeting locations, funding provisions and alignment to other meetings.

The agenda shall be submitted to ANZPAA NIFS for consideration no less than 3 months before the intended meeting date.

The agenda should include the following standing agenda items:

- review of action items and action plan
- ANZPAA NIFS update
- Australasian Forensic Science Assessment Body (AFSAB) update (for relevant disciplines)
- emerging/critical issues and trends
- research, innovation and development opportunities or requirements
- workshop proposals
- training, quality and accreditation
- review of the ANZFEC capability matrix
- TAG and/or PWG reports (for relevant disciplines).

DECISIONS

Although the primary role of the ANZPAA NIFS Groups is to provide advice to ANZPAA NIFS and ANZFEC, where a decision is required resolutions will be based on a majority vote. Only one vote is permitted per voting member.

ATTENDANCE AND ENGAGEMENT

ANZPAA NIFS Groups members will make every effort to prepare for and attend all meetings, whether virtual or in person. Where a member of an ANZPAA NIFS Group is not able to attend a meeting in person, a proxy may be nominated by the relevant agency. A member of an ANZPAA NIFS Group may attend the meeting by way of telephone or other technology-supported means and the meeting agenda may be adjusted to provide for the maximum participation of that member.

FINANCIAL SUPPORT

ANZPAA NIFS will provide the following financial support to facilitate Groups discussions:

1. Flights to attend face-to-face meetings

For discipline specific SAGs, ANZPAA NIFS will fund and book one return flight per ANZFEC agency representative and for the ANZFEC Mentor. Where a SAG has one or more reporting sub-discipline TAGs, a flight will also be provided for each TAG Chair.

For each SAG consisting of one or more distinct discipline TAGs, ANZPAA NIFS will fund and book up to 12 return flights across the TAGs and a flight for the ANZFEC Mentor. This will include flights for the SAG and TAG Chairs. Preference for TAG member flights will be given to ANZFEC agency representatives. The distribution of flights will be determined in consultation with the Group Chair and ANZPAA NIFS representative.

ANZPAA NIFS is bound by Victorian government policy to book the cheapest reasonable flight option. As such, requests for specific airlines or flexible flights are unlikely to be accommodated.

Any charges incurred by ANZPAA NIFS for flight changes as a result of unforeseen personal or agency requirements shall be the responsibility of the relevant agency.

Financial support may not be reallocated from SAG to TAG members or between jurisdictions without approval from the relevant ANZFEC member(s).

2. Venue Hire

Where possible, a face-to-face meeting of the ANZPAA NIFS Groups should be hosted by an ANZFEC agency with appropriate facilities to accommodate the meeting, however, consideration will be given to a meeting being held at an external venue to facilitate information exchange and encourage maximum attendance.

ANZPAA NIFS will contribute up to $500 for the hiring of an appropriate meeting venue. Any remaining fees associated with the venue hire will be the responsibility of the hosting agency.

3. Teleconference facilities

Teleconference meetings may be organised in consultation with the relevant ANZPAA NIFS representative to progress action items, provide jurisdictional updates, develop workshop proposals or discuss critical issues. Sufficient notice and an agenda should be provided to all teleconference participants.

4. Catering

ANZPAA NIFS will provide funding for catering at ANZPAA NIFS Group meetings up to the value of $30 per person/per day. This funding is applicable to all registered attendees.

5. Funding for Permanent Standing Groups

In addition to the above funding, some specific funding arrangements exist for ADVIC and CWALN. These arrangements are described in the relevant Annexes.

OTHER SUPPORT

ANZPAA NIFS maintains the infrastructure for ANZPAA NIFS Groups email distribution lists. Distribution list membership is the responsibility of the Group's members. ANZPAA NIFS will facilitate the addition of email addresses to the distribution lists as soon as practicable after receipt and authorisation of the addition(s).

ANZPAA NIFS engage an external IT provider to maintain the infrastructure of the NIFS Secure Server. The content of any information on the server is the responsibility of the relevant Group. The Group Chair or Webmaster are responsible for approving access to the server.

REGISTRATION FEE

A registration fee will be charged for the attendance of non-ANZFEC agency representatives at ANZPAA NIFS Group meetings. The fee is subject to annual review.

WORKSHOPS

Workshop proposal shall be submitted to ANZPAA NIFS in September each year for consideration by the ANZPAA NIFS Groups ANZFEC Mentors.

Proposals may be submitted by Permanent Standing Groups, SAGs, TAGs and PWGs to assist in fulfilling their role and purpose. TAG and PWG workshop proposals shall be submitted to the relevant SAG for discussion and prioritisation. All workshop proposals shall be developed in consultation with the ANZFEC Mentor.

The financial support received for workshops will be determined as part of the workshop approval process.

REPORTING AND COMMUNICATION RESPONSIBILITIES

Each quarter, the ANZPAA NIFS Groups shall update their action plans and report their progress and activities to ANZPAA NIFS via the 'Action Plan and Quarterly Reporting' template (see ANZPAA NIFS Groups Documents). A SAGs report should also include the activities of any relevant TAGs and PWGs.

ANZPAA NIFS will disseminate a summarised quarterly report of all of the ANZPAA NIFS Groups to the Group's Chairs after each ANZFEC meeting.

RAISING ITEMS TO ANZFEC

ANZPAA NIFS Groups may raise items to ANZPAA NIFS or ANZFEC through the 'Raising Issues to ANZFEC Template' for the following reasons:

- strategic discussion
- approval
- noting.

The item should be raised in consultation with the Groups Chair, ANZPAA NIFS representative and ANZFEC Mentor. Formal endorsement by the ANZFEC Mentor of the item shall be sought by the Groups Chair prior to submission to ANZPAA NIFS.

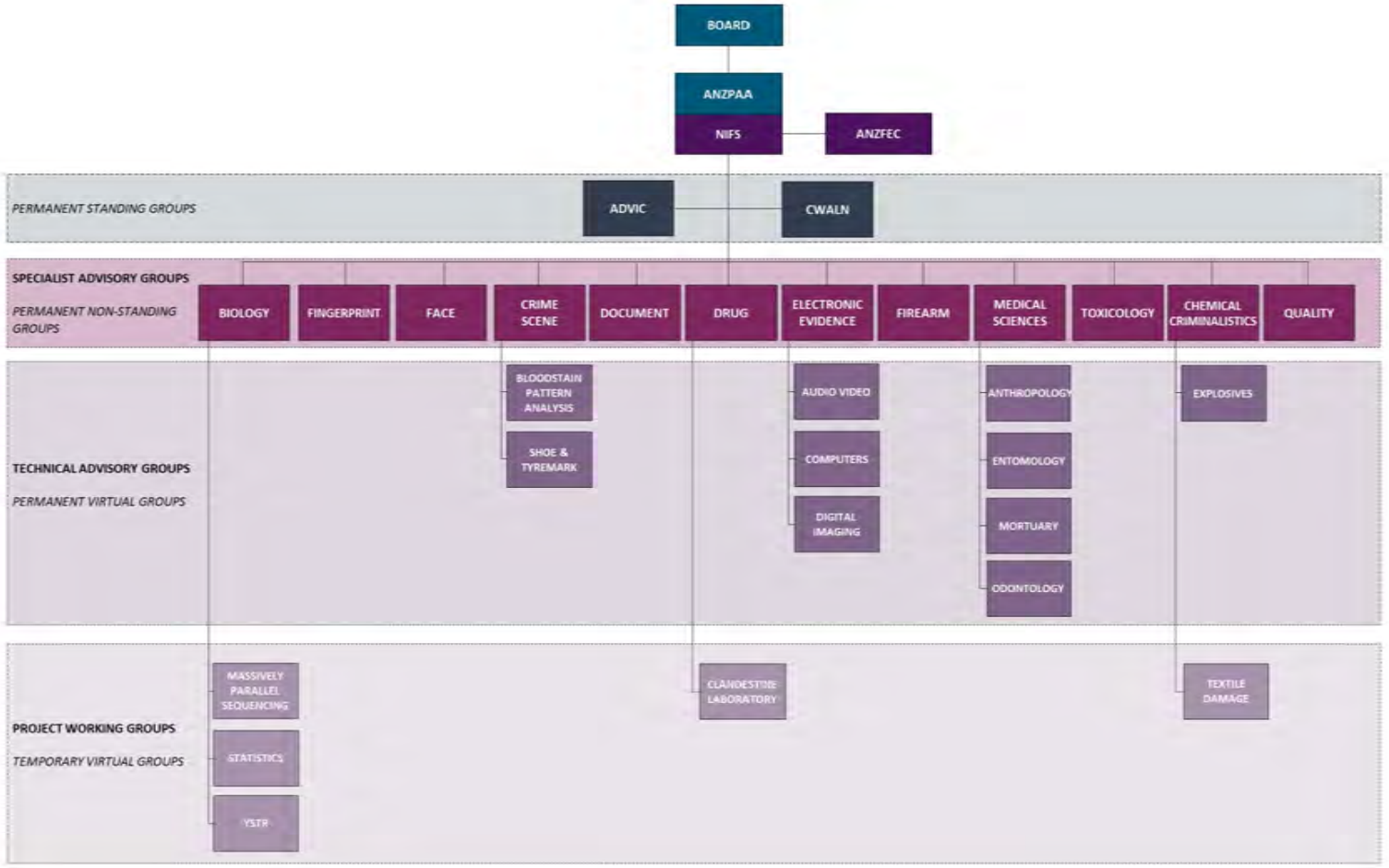
ANZPAA NIFS GROUPS DOCUMENTS

The following are a list of documents for use by the ANZPAA NIFS Groups and are available on the ANZPAA NIFS website at http://www.anzpaa.org.au/forensic-science/resources/sags.

- Registration and Flight Booking Form
- Agenda Template
- Action Plan and Quarterly Reporting
- Annual Presentation Template
- Raising Issues to ANZFEC Template
- Guidelines Template
- Australia New Zealand Representation Framework
- Workshop Proposal Form
- Workshop Attendee List.

All requests from external agencies for documents created by ANZPAA NIFS Groups should be directed to ANZPAA NIFS. The provision of documents to external agencies will be made on a case by case basis.

APPENDIX A – ANZPAA NIFS GROUPS STRUCTURE



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CA-152

Lab	Robotic platform	Extraction casework	Differential method	Quant method casework	Amp volume casework	Amp amt casework	Instrument casework	Extraction reference	Quant method reference	Amp volume reference	Amp amt reference	Instrument reference	Thermal cyclers	Confirmatory/ presumptive testing eg Semen, Saliva, Blood	Typing software (version)	Available kits	Interpretation software (version)	Currently validating/verifying	MPS status Equipment/kits	STATS 1/07/2020 - 30/06/2021				Sampling devices used
																				# EXHIBITS	# REFERENCE SAMPLES	# REPORTS	# FTE	
WA	Extraction: TECAN Fluent 1080 (x2) Automate Express (x4) Quiagen QIAcube HT Qiasymphony SP Qiagen EZ1 Advanced XL Biomerieux VidiTo 90 (x1, minimise use) **FTA Punch:** EDC Quin (x2), EDC 600 Biomek (x1)	PrepFiler (Forensic) PrepFiler (Biomolecular)	Swab: Chelex extraction, PrepFiler extraction	Quant Trio	PP21: 25ul YFlex Plus, 25ul	0.4ng PP21, 0.4ng YFlexPlus	1000W, x 1	Chelex (blood card, swab, FTA excision), PrepFiler (Plain, Trace) Direct amp on FTA	Quant Trio	Direct Amp FTA: 12.5 µl PP21 & YFlexPlus Extracted samples: 25ul	Extracted samples: 0.2ng PP21, 0.5ng YFlexPlus, NA (Direct Amp	6800W x 2	9700 (x2), ProFlex (x4)	CM: Hemastrow (Blood), RSID (Saliva), AP, RSIDCreamy, Microscopy - Clearmax, tree scan (semen), Lone (saliva reactions), Fences (microbiome) -	GMID-X v1.1	PP21 & YFlex Plus	GTFlex v2.7	Verifier Plus, Self vacuum YFlex Plus -	NA	37,940	23,100	727 Trial Reports	105.7 FTE (Includes Admin, IT, Drivers)	Trace DNA – SD BIO™ CollumSwab™ (2 Sterile + MRQ Water - Biological Fluid – Copan Rayon Swab, Sterile + MRQ Water - Small Insects – Copan aluminium shaft (sterile) + MilliQ water - Toothbrush – 4MRL-IQ Lysis/DNA Prep + MRQ Water - Tape/lift – Scotch Transparent Tape 3M-
SA	Extraction: 24 Applied Biosystems (ABI) Automate Express (x1) for challenging samples; Qiagen EZ1 Advanced XL (x2) for Forensic Swabs & Low Concentration Kit.	DNA IQ Sec Analysis & Manual methods. Use for challenging samples; Qiagen EZ1 Advanced XL DNA IQ Forensic Tissue & Low Concentration Kit.	DNA IQ Manual	Quant Trio	GlobalPlex, YFlex Plus & Argus X-12: 25uL	0.4ng GF, 0.5ng YFlex Plus	1500 x1	Direct amp on FTA with ESO Ascent v1, DNA IQ manual for liquid extracts	Quant Trio for liquid samples	GlobalPlex, YFlex Plus & Argus X-12: 12.5uL for FTA & liquid extracts	Extracted samples: 0.4ng GF, 0.5ng YF Plus	9600 x1	ProFlex x1	Amylase, Alkaline Phos & Luminol (Blood); Sentiti paper & RSID (Saliva); Acid Phosphatase, RNA card x30 & microscopy (Semen)	GMID-X v1.1	GF & YFlex Plus, Finishing Qiagen & ETF Argus 12	GTFlex v2.2	ExpertRT ID with STRmix (demo until) PLATE, RSID Feeder Memo until, Qiagen EZ1 for extraction (demo) Until, Quant Studio 5 (new purchase)	NA	10,527	7,599	Not measured	32	Trace DNA - Isohelix Handy + Nonsupported Biological fluids - Sarstedt 80.634 + water- Tape/lift - Lasec surgical supplies.
NSW	Tecan: Freedom Minicell, Automation, ITAR Extraction: Tecan Freedom EVO 150 & Automate Express Quant & PCR Set Up: Tecan Freedom EVO 100. QI Set up: Tecan Freedom EVO 150	PrepFiler Demonstration method & Qiagen's (manual) for compromised Swab Samples, PrepFiler ITA (Automate Express) for Fresh Areas	7 - Gill Differential Extraction method manual to assist, then PrepFiler automated extraction	Quant Trio (QuantStudio 5)	PP21, 25 uL YFlex Plus: 12.5ul	0.7ng PP21 (29 cycles) 0.7ng YFlex Plus (30 cycles)	ISOBAL v 2	Direct amp on FTA with ESO Ascent v2; Prep Flex extraction from Hairs, usiFTA card samples and Mini rati.	Quant Trio (ProFlex extracts only); Real-time (post PCR quant for Mini)	Direct Amp FTA PP21 (25 cycles) & YFlex Plus (27 cycles): 12.5ul	Extracted samples: 0.7ng PP21; 0.7ng YFlex Plus; NA Direct Amp	2800 x 2, 9700 x 1 (Mini)	ProFlex x3 7- Mini; 9700 (x1) ProFlex (3 heat x2)	Gold & Identifiler (Blood); RSID (Saliva); Acid Phosphatase & RNA card x30 (semen); Microscopy & SpermFinder (Sperm); Urine (Semen); - Faeces - - Trichomonas)	GMID-X V1.1	PP22, YFlex Plus,	GTFlex v2.4	Validating MPS for full mtDNA genome. Using nuclear for replacement of nuclear, Sanger sequencing approx. Oct 2021, will be evaluating NextGen and automated differential lysis/ extraction soon.	Ion Chef and GS Amateur on Converge software); Interpretation performed externally (S Precision ID kit; for NGM/SNC on ion s530 chip, ion AmpliSeq DNA Phumanology panel) Validation: Identity-seq - Precision ID - mtDNA whole genome sequencing run on 530 chip.	Approx. 7,000 (Prisca Lab samples - approx 67,000; Whole exhibits - approx. 8,000)	Approx. 10000	Approx. 2400 (more statements and approx. 85,000 from lead reports)	Approx. 30 (inc/ specimen receipt x 9 staff)	Biological Fluids and Trace: Rayon Swabs + water (Qinwada, Medical Work Equipment, SCI Heated Locosteff), Fingernail clippings: 4MI-IQ (Sarstedt, Germany) + water/ if Cotton, subungual/vulgar - 4MI-IQ, Tape/lift: 3M 9425 Tape (Cowell surgical supplies, ED treated)
VIC	Hamilton Auntra (x2) Biomek i7 Series (x2) Biomek i5 Series (x2) Hamilton EasyFetch (x2)	DNA-IQ (Hamilton Auntra & Biomek i7 series) Organic/Chelex/ QIAGEN (manual)	DNA-IQ - Organic	Quant Trio (To 7500)	PP21 - 25 ul YFP- 15ul	0.5ng PP21 0.5ng YFP	ISOBAL V 1	Automated DNA IQ (Hamilton Auntaya + Beckman Coulter i7) Direct amp (Promega GeneMarkQ on EasyCollect Plus cards	- Quant Trio (Non-Direct PCR)	PP21 - 12.5ul YFP - 25ul (Non and Direct PCR)	0.25ng PP21 0.5ng YFP 6x30 Direct PCR	9800W X 1	Veriti 96-well cole Veriti 60-well/x96	Hemastrow (Blood) Hemastrow (Blood), Luminol (Blood) MM camera (Blood) AP (Semen) - FSO (Semen) - M & T (sperm) RSID (saliva) ProBlow (Blood/semen/saliva) 6dfh reactions control) Evolve test (urine) - Histokompan (Blood) mmo actinary (vomit)	GMID-X V1.1	PP21 Y Flex Plus -	GTFlex v2.6	New PCR Kit: Verifier Plus / Veriti Flex 27 / Investigator 24plex GTFlex v2.4	NA	7,500	17,000	Total Statements (for cases): 4MI Total Case Result Summaries (CSR): 6607 ISO reviewer - 7GH ISO trainer - 1,650	Total ESC FTE (inc/ admin) - 97.80 FTE inc casework - 41.2 FTE for database - 1.5	Cotton cotton swabs (sterile 15ml) + water- Sarstedt DNA free soft driving rayon swab + water- Sarstedt DNA free cotton swab + water- swabCollect+ (References)...
APP																								
TAS	Quant, PCR and CE Setup: Gregory	organic	manual organic	Power Mf	PP21, 12ul YFlex, 12ul	0.5ng PP21 0.5ng YFlex	15 (ECC but very exactly will be moving to 2 x 3500	Quant Amp -	none	PP21, 12ul YFlex, 12.5ul	NA	ex-ten Cetamerx	Veriti 12	Blood - Hemastrix, Luminol, consequent Semen - AP, Hemt, Haemoglobin Saliva - Phadebas tube and paper	GMDX v1.5 will move to v1.6 with move to 3500; PP21, YFlex (soon to move to YFlexPlus)	GTFlex 2.4.35 (v2.6 will move to v2.7 with move to 3500)	NA	NA	8307	5601	no count available	17.4	In lab - Lysmodo synthetic swabbin sizes, DNA-free; Copan cotton microswab; No scarves, and SWAT - Sarstedt Forensic 4(DNA - free
WT	Quant and amp setup: Hamilton Microlab.	DNA(I) Maxwell	Chelex with microcon	Quant Trio on 7500	40 - 15ul	GF 1ng	3500 (x1) with QCA	Direct amp on FTA, Chelex for exceptions	Quant Trio on 7500 - extracted samples only	FTA (GF5): 15ul, extracted samples (GF): 25ul, YFP: 30ul,	GF, YFP 1ng	3500 (x1) with QCA	NTB x2, Proflex x1	Semen/sperm: AP, FSO, rsidni (Blood: O-tol, Amastrow; Saliva: Phadebas, SSID saliva	GMDx v1.1	GF, GFE (GF Express), YFlexPlus	GTBriti v2.6.1	GTBriti v2.6: YFP on casework	Nil	~2,200	1,463	166	17	Sarstedt self drying forensic visual, Lysed Storage/Lysed DNA from HFL,
QLD	Extraction: Qiahamathrity (x2) Maxwell 16 (x2) Maxwell FSC (x2) Quant, PCR and CE Setup: Hamilton Starlet (x2)	QIAamp Investigator (DNA) DNAIQ (Maxwell).	DNAIQ	Quant Trio - QuantStudio 12 Setup also on QIAamphora integrated runs	PP21: 25uL	0.5ng PP21	3500xL x2 (2 = verification)	Direct amp on FTA, DNA Investigator (QIAamphora) and DNAIQ for Extracted samples	Quant Trio only extracted samples)	Direct amp FTA and Extracted Samples: 12.5uL	Extracted samples: 0.5ng	Ion Casework	9700 (1)	All (x3) Amylase (Semen), TMB (Blood), Phadebas (Saliva)	GMDx v1.6	PP21	GTBriti v2.6	Ellen Plus, Verifier Plus, Proflex, MPS	Ion Chef and Genetyper GS Plus (DNA and EVC) -	17,042	14,027	722	69	Copan Flock Dry (wet lysate) + or tap, and - Copan Flock Dry Swab (plastic) for SAMO - Majority of sampling materials at crit /DP)

Lab	Robotic platform	Extraction casework	Differential method	Quant method casework	Amp volume casework	Amp amt casework	Instrument casework	Extraction reference	Quant method reference	Amp volume reference	Amp amt reference	Instrument reference	Thermal cyclers	Confirmatory/ presumptive testing eg semen, saliva, blood	Typing software (version)	Available kits	Interpretation software (version)	Currently validating/verifying	MPS status Equipment/kits	STATS 1/07/2020 - 30/06/2021				Sampling devices used
																				# EXHIBITS	# REFERENCE SAMPLES	# REPORTS	# ITO	
VIC / VFM																								
NZ	Casework extraction and quant set up: HamiltonStarlet; Database&Reference extraction: Hamilton AGS; Plate set up: HamiltonMicroLab	DNA IQ	Differex/DNA IQ	Quant Trio	HamiltonMicroLab: 12.5ul; GlobalFiler: 12.5uL MicroAmp: 25ul Y Filer Plus: 12.5ul iDe - ICM: 12.5ul	HamiltonMicroLab: 1ng; GlobalFiler: 0.5ng; MicroAmp: 0.2ng; Y Filer Plus: 0.25ng; iDe - ICM: 50pg	9700 x2	Direct PCR and Chelex	Quant trio if needed	GlobalFiler: 12uL; Y Filer plus: 12.5uL	GlobalFiler: 0.5ng; Y Filer plus: 0.4ng	9700	2700, Veriti, ProFlex	mRNA AP/PSM/ HACE+ TMB/AHB/semen/ Anastase (rapid) amylase paper and tube test	GM iDe v1.4	MicroPlex™ Rediscover Plus™ Kit, mRNA/DNA/Panel 2™ Identifiler Plus	Effirm v1.7	Qiaseuner nano for SARS-CoV-2 work	MiSeq FGx (Forensic Panel, Hereigen genealogy kit); GeneMiSeq for Seldo Core 1 work.	3,210 cases with approx. 9,000 exhibits	approx 750 case specific references and 8,000 reference samples for the DNA Database	1,570	66	MiniTapes: Standard twist; Scotch Speed-DNA tamper-proof genetic tape; Swabs for LCN: Double swabs - wood, CTT created; DNA free ventilated swab; Zymosafe, Catalogue number R4660-100ETO - Swabs for standard work (Super Cotton tipped wooden stems) in an index genetic shaft (Ex:1000pcs/Box); Protected Samples: Thermo Fisher Scientific AE Ltd, CP1122590