Paula Brisotto

From: Cathie Allen
Sent: Friday, 2 February 2018 4:00 PM
To: Justin Howes; Paula Brisotto
Subject: FW: Options Paper for consideration

Sensitivity: Confidential

Hi Paula and Justin

The QPS have agreed with Option 2, so we can proceed with that option. I will send out further information to management team but I will not be sending the below email. This is just for your information only at this stage.

Cheers
Cathie

Cathie Allen
Managing Scientist – Police Services Stream

Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

p | [redacted] m | [redacted]
a | 39 Kessels Road, Coopers Plains, QLD 4108
w | www.health.qld.gov.au e | [redacted]

HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

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.

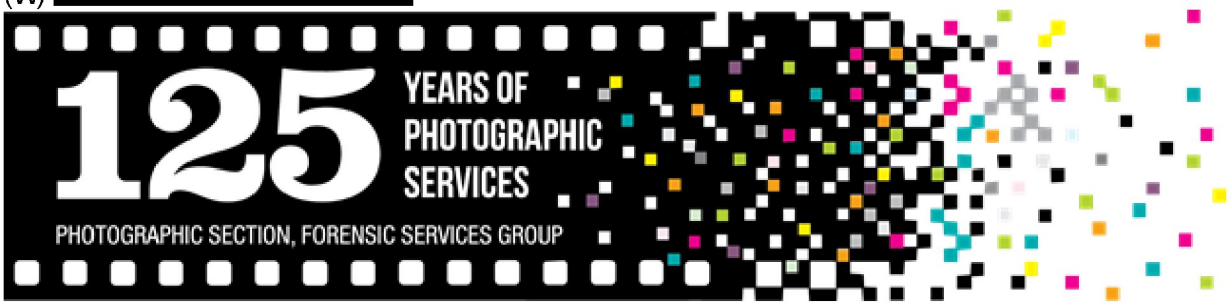
- It would be beneficial to amend the Forensic Register to provide an automated Q-Prime update advising the Investigators of the option to request further 'Auto-microcon' processing for those samples for unsolved crime, which may prove worthwhile.
- DNA staff can request this additional processing if/when 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]



From: Cathie Allen [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**

p | [redacted] m | [redacted]
a | 39 Kessels Road, Coopers Plains, QLD 4108
w | www.health.qld.gov.au e | [redacted]

HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

****

This email, including any attachments sent with it, is confidential and for the sole use of the intended recipient(s). This confidentiality is not waived or lost, if you receive it and you are not the intended recipient(s), or if it is transmitted/received in error.

Any unauthorised use, alteration, disclosure, distribution or review of this email is strictly prohibited. The information contained in this email, including any attachment sent with it, may be subject to a statutory duty of confidentiality if it relates to health service matters.

If you are not the intended recipient(s), or if you have received this email in error, you are asked to immediately notify the sender by telephone collect on Australia +61 1800 198 175 or by return email. You should also delete this email, and any copies, from your computer system network and destroy any hard copies produced.

If not an intended recipient of this email, you must not copy, distribute or take any action(s) that relies on it; any form of disclosure, modification, distribution and/or publication of this email is also prohibited.

Although Queensland Health takes all reasonable steps to ensure this email does not contain malicious software, Queensland Health does not accept responsibility for the consequences if any person's computer inadvertently suffers any disruption to services, loss of information, harm or is infected with a virus, other malicious computer programme or code that may occur as a consequence of receiving this email.

Unless stated otherwise, this email represents only the views of the sender and not the views of the Queensland Government.

****

****
CONFIDENTIALITY: The information contained in this electronic mail message and any electronic files attached to it may be confidential information, and may also be the subject of legal professional privilege and/or public interest immunity. If you are not the intended recipient you are required to delete it. Any use, disclosure or copying of this message and any attachments is unauthorised. If you have received this electronic message in error, please inform the sender or contact [redacted]
This footnote also confirms that this email message has been checked for the presence of computer viruses.
****

HealthSupport Queensland

Forensic and Scientific Services

Procedure for Case Management

Not Current

Not Current

1 Purpose

The purpose of this procedure is to describe the components of a case record, processes involved in compiling and completing a case record and tracking of case records.

2 Scope

This procedure shall apply to all Forensic DNA Analysis staff that case manage any component of a case record.

3 Definitions

AmpF*l*STR® Profiler Plus®	The amplification kit made by Life Technologies – This is used for low priority cases (Volume crime cases).
AmpF*l*STR® COfiler®	The amplification kit made by Life Technologies – this was used for additional loci in paternity cases. This is no longer used.
Case managing scientist	The scientist(s) that has (or have) been involved in the assessment of results and compilation of the case file in preparation for statement writing or peer review.
Case record	All information relating to a particular case. This can include all case histories, receipts, communication with clients, examination notes, Analytical data, internal communications, results and reports.
DNA Mgt	DNA Management Unit – A QPS Unit that transfers the exhibit results and link results from the Forensic Register to QPRIME. They also perform quality checks on the validity of the information/results received.
EPG	Electropherogram
Examining scientist	The scientist/s who has/have examined exhibits for a case.
FR	Forensic Register – Laboratory Information Management System since July 2017.
GMIDX	GeneMapper ID-X, software used for allele designation after capillary electrophoresis
In tube	An item that has been sub-sampled by the QPS and submitted to the laboratory in a tube ready for analysis.
NCIDD	National Criminal Investigation DNA Database
OLA	Off ladder allele
PDA	Profile Data Analysis – page in the FR to record the DNA profile interpretation and actions
P+	AmpF*l*STR® Profiler Plus®
PP21	PowerPlex® 21 system kit
Paperless	A type of case that does not involve a traditional paper case file. Work is performed almost entirely in AUSLAB
PowerPlex® 21 system kit	The amplification kit made by Promega that is currently used for all reference samples and high priority case work samples.
QFLAG	Quality checking procedure to investigate potential staff and elimination database matches
QPRIME	Queensland Police Records and Information Management Exchange (Post 2008)

Not current

Reporting Scientist	The scientist who is responsible for writing a Statement of Witness outlining the results of a case and for presenting evidence in a court of law.
SCI	QPS Scientific Officer
SOCO	QPS Scenes of Crimes Officer
SSLU	Scientific Services Liaison Unit
STATSWG	Statistics Working Group
STRmix™	A statistical program used during case management to interpret certain types of DNA profiles.
ULP	Unlabelled allele
VAR	Variant allele
XOVER	Cross over allele, allele migrates into an adjacent marker bin.

4 Case file overview

Since the 1st of September 2009, low priority Volume Crime cases have been treated as 'paperless' and therefore do not have case files. In April 2010, paperless case management and review was expanded to also include all cases of both high and low priority (Volume and Major Crime) and some Sexual Assault cases (Yellow Team cases) except for cases involving excessive numbers of crime scene/reference samples or complex profiles. In April 2015 all cases are initially managed as paperless cases.

Case files are generally created

- At the time of case management (for complex cases) or
- When a statement is requested or
- When a case manager/reporter deems it necessary for efficient case management.

A case that has been initially managed paperlessly may be converted to a paper file if further exhibits are received at a later date. Case and examination notes are stored in 'Paperless' folders stored in Evidence Recovery, Reporting and Admin areas.

If a case has been converted from paperless to paper, it is not necessary to annotate all of the epgs with the item description or interpretations unless a statement has been requested. The reporter of the statement will update the epgs with interpretations.

4.1 How to create a case file

To request a casefile to be created, email FSS.FDNA[redacted] with instructions. Admin edit the Statement Request/Task that a casefile is being created, assign a barcode for the casefile and create a storage location (see QIS 33773 and 34248).

4.2 Additional Elements of a case file

Upon completion, a case file may also contain:

1. Examination notes
2. Diagrams, photographs and/or photocopies
3. Statistical calculations.
4. Copies of results (GeneMapper ID-X printouts).
    a. As a minimum, reference samples require the final/reported profile. Casework samples should have all EPGs printed.
5. Interpretations of results
6. Copy of statement or intelligence report

Not Current

7. Records of any internal or external communication relating to the case, e.g. Casefile Notations, Requests/Tasks or emails.
8. STRmix™ output files/report. STRmix v2.6 it is not recommended to include the STRmix report, rather a printout of the PDA page with the EPG is sufficient.

4.3 Handwritten results and corrections within a case file

As is required by NATA ISO 17025 - as case notes etc. are subject to subpoenas; no pencil is to be used in the case file (unless used in diagrams or pictorial representations).

Any calculations, interpretations or changes to notes or results must be initialled and dated by the person performing the action.

4.4 Case file storage and movement

Case files are required to be kept indefinitely as per accreditation requirements.

1. No exhibits are to be stored in the case file. This includes external proficiency samples. Original QPS property tags or reference sample envelopes are also NOT to be stored in the case file.
2. Case file movement is to be recorded in the FR.
3. Active case files are stored with the case analyst or in a designated storage location for the work area.
4. Upon completion, scientists should transfer cases to Admin via the FR. Administration assistance slips are available to attach to the front of the case file to direct the storage of the file or to outline any further administrative tasks that need to be performed prior to storage.
5. Admin In-Tray – Casefile Finish is the location from which administrative staff will track case files (sequentially) into the compactus or another designated storage location. No further administrative tasks will be carried out on these cases.

5 Workflows

5.1 Priorities

Table 2 details the DNA priorities that are used in Forensic DNA Analysis. These are not to be confused with case priorities eg. one sample may be processed as Priority 1, but the case as a whole is Priority 2 (Major Crime).

Table 1 - DNA Priorities in Forensic DNA Analysis

Priority	Description	CW Use	Ref Use
1~SS	Urgent	Urgent	Priority/investigation
2~SS	High Pri	Major crime	High priority
3~SS	Med Pri	Volume	Normal

Urgent (5 day TAT) cases are specifically allocated to a case scientist and/or reporting scientist as they arrive into the department. The Managing Scientist and Team Leaders will be notified of the arrival of an urgent case by email and appropriate notes will be entered. A supervising scientist will allocate to an appropriate case manager. This does not mean that the case managing scientist will necessarily become the reporting scientist should a statement be required, however this is preferred to maintain consistency in reporting.

P1 samples must be managed as soon as results become available and reviewed as soon as results are interpreted. To ensure there is no delay in QPS being informed of 5 day TAT

Not Current

results as soon as they are available, a workflow has been created for samples that are expected to be completed on a Friday (see QIS 23968, 33773 and 34006).

5.2 PowerPlex®21 system kit vs AmpFℓSTR® Profiler Plus® case management

Since the end of testing with AmpFℓSTR® Profiler Plus® (P+) in January 2018, all samples are received and processed with PowerPlex®21 system kit (PP21). This does not mean the reporting method for P+ samples is invalid; therefore, in consultation with a senior scientist, samples may be re-processed with PP21 for case consistency or only newly received items will be processed and reported with PP21 and STRmix™.

5.3 STRmix versions

Any cases with a priority 1 or 2 received from 01 Jan 2015 are processed with STRmix™ version 2.0.6 Refer to QIS 31523. All likelihood ratios (LRs) are generated using STRmix™ v2.0.6 regardless of the version of the deconvolution. See Table 3 below.

Table 2 – STRmix version use

Date case received	Decon	LR (at time of receival)	LR (New comparison)
19 Dec 2012 – 30 June 2014	v1.05	v1.05	v2.0.6
1 July 2014 – Jan 2015	v2.0.1	v2.0.1	v2.0.6
30 Jan 2015 – present	v2.0.6	v2.0.6	v2.0.6

5.4 Case management workflows

For the process to allocate samples and/or cases, see QIS 33773.

For worklists and information on how these are populated, refer to QIS 33773.

Allocation of cases to a particular scientist usually only happens if a statement is required, the case is large or has been assigned an Operation by QPS. These cases will otherwise be routinely case managed by the competent case managers. However, to reduce the amount of double handling by case managers, individual samples initially case managed by a particular person will be completed by the same person. This includes reworking and STRmix™ deconvolutions.

Unallocated paper case file may be stored in the filing cabinets stored in the far end of the reporting area in Block 3.

Internal controls, external and internal proficiency, internal and external environmental monitoring samples case managed by the Analytical, Evidence recovery and Quality teams.

Various tools may be employed to assist in meeting timeframes and to cover absence such as scheduling Outlook appointments or tasks.

6 Case management

The purpose of case management is to collate and report any DNA results that have been obtained and to prepare the case file for a statement (if required) or for peer review. To achieve this, the case managing scientist may be required to:

Not Current

1. Assess DNA results to determine whether reworking is required to improve or confirm results.
2. Enter final Exhibit reports via the Profile Data Analysis (PDA) page in the FR.
3. Compile case file.

The steps for case management are listed below and a checklist provided in Appendix 2.

6.1 Check quality

Samples should not be progressed or reported until the various quality checks that are in place have been completed. These checks are designed to identify potential issues with samples before they are reported to the QPS.

6.1.1 Batch statuses

Check that the statuses of the processing batches are fully completed (see QIS 33773).

If there has been an issue noted during processing of a sample, the Analytical staff member/delegate will enter a status of 'See batch'. The case manager **MUST** check the batch audit and add a Sample Note to indicate what the issue is and that it has been assessed and they have deemed the sample OK to report.

6.1.2 Casefile Notations

Check Case Management tab in the FR for Casefile Notations and Request/Tasks (and UR notes for cases processed with AUSLAB) for relevant information related to the case. This may include information such as allocation to an individual case manager/reporter, court timeframes, communication with DNA Management etc.

6.1.3 Notations

Check for relevant information in the Exhibit Testing tables for notations and Analytical Notes (see QIS 33773), and Specimen Notes for cases processed with AUSLAB.

6.2 Check case information

Case information may be relevant to only particular samples or the whole case. This information may be used to guide the case manager's choice of processing and reporting.

6.2.1 Check for reference samples associated to the case

The presence or absence of reference samples may affect the workflow path a sample takes. If reference samples have been received for a case, these will be compared against representative single source DNA profiles, and all interpretable mixed DNA profiles to generate a LR.

See QIS 33773 and 34006.

Not Current

6.2.2 Check for case allocation

It is necessary to check if a case has been allocated to a particular case manager or reporter before case managing a sample.
Check the Case Management tab in the FR for details or on the PDA page, it can be viewed in the 'Case Scientist' field. See QIS 33773.
In AUSLAB (if some of all of the case was processed with AUSLAB (pre July 2017), it may be recorded in the UR notes and/or the CS page.

6.2.3 Check for paper file/case notes.

Check the Exhibit Register for a barcode created for a casefile to enable storage and tracking (see QIS 33773).

6.2.4 Check ownership of item

Ownership of an item may be required before interpretation of a DNA profile or an exhibit is sampled. If unknown, send a Request/Task to the SOCO or SCI to obtain this information.

6.2.5 Finalising samples no longer required

See QIS 34006.

6.3 Assess results

All samples have alleles designated as per QIS 34112.

When results become available for a sample, an assessment needs to be made as to whether reworks are required or whether sufficient information has already been obtained. This can be performed as each result becomes available. Not all results need to be available at the same time for these assessments to take place.

Samples that have been processed in Profiler Plus may have their epgs saved to AUSLAB via digital imaging. Otherwise, samples prior to the use of FR that were major crime, had their epgs saved to the P drive.

To aid in the assessment of results, several macros have been created. The PDF finder macro locates the epgs (both zooms and standard) for a particular laboratory number or a whole case.

1. Open the macro (I:\Macros\PDF Finder.xls)
2. Click the Find all .pdf files button
3. Enter the required laboratory number or case number
4. Select the years to search by ticking the year required
5. Press the Search button or 'Enter' key
6. A list of .pdf files will be displayed
7. Select the .pdf required and double click or press the open .pdf button.

The Stutter check macro is a tool used to check the stutter and potential pull up for a whole plate or a single sample. The macro uses the allele sizes, allele peak heights, and validated stutter thresholds. This macro is only used for the assessment of PowerPlex®21 samples as stutter is left on and modelled by STRmix™.

Not Current

1. Open the macro (I:\Macros\Macros to update\Stutter Check.xls)
2. Click the Check for Stutters (1 sample) button
3. Enter the laboratory number in the Sample ID field
4. Enter the GeneMapper plate ID in the Plate field
5. Press Ok button.

6.3.1 Assess the number of contributors to the DNA profile

The number of contributors to a DNA profile is required to perform interpretation. Counting the number of alleles at each locus (above and below threshold) is the first step in assessing the number of contributors.

However, counting called peaks (above and below Limit of Reporting threshold) alone may not be suitable in determining the number of contributors due to the presence of PCR artefacts such as stutter. Allelic imbalance (AI) also known as heterozygote balance (Hb) can also be used as an indication of the number of contributors. Forensic DNA Analysis does not have a threshold for AI for casework DNA profiles because STRmix is designed to model the heterozygote balance as a continuous system. Although internal validation studies indicate that the calculated AI threshold varies depending on the DNA input, the values detailed in the study can be used as a guide.

The document '*Assessment of the Number of Contributors for Mixed PowerPlex® 21 DNA Profiles within Forensic DNA Analysis_version 2*' is used as a guideline for determining the number contributors within a PowerPlex 21 sample.

The validated stutter thresholds (as published in QIS 34112) are used as a guide to aid in the determination of contributors to a DNA profile.

Additional information (for Profiler Plus samples only) is detailed in the document '*A guideline for the assessment of complex DNA profiles*'.

6.3.2 Assess the overall quality of the DNA profile

The quality of the DNA profile in conjunction with the number of contributors will determine if a DNA profile is suitable for interpretation.
The following factors should be considered

1. Whether a reasonable assumption of the number of contributors can be made.
2. The degradation slope (the tendency for higher molecular weight loci to have lower peak heights compared with smaller molecular weight loci).
3. The total amount of DNA input used in the amplification.
4. Adverse events affecting the sample.

6.3.3 Check VAR/OLA/ULP/XOVER calculations

If a variant and/or off ladder allele or stutter has been observed on a GeneMapper ID-X (GMIDX) profile it is not necessary to re-amplify to confirm its presence.

For mixed DNA profiles with variant and/or off ladder alleles, the repeat of these samples is at the case manager/reporter's discretion. Things to consider include whether the profile with variant and/or off ladder alleles has already had this questioned allele confirmed, matches a deconvoluted contribution, or if the sample description suggests the mixed DNA profile could be conditioned on the reference DNA profile (with variant and/or off ladder alleles).

Not Current

The case manager must independently perform the calculation for allele designation including if the calculated allele falls in the stutter position. Refer to QIS 33773.

Variant/OLA/ULP/crossover calculations do not require checking if the DNA profile has been assessed as unsuitable for interpretation.

6.3.4 NAD samples

If a sample is flagged as No Analysed Data (NAD) at CE quality checking stage, the sample will be re-prepared by Analytical staff. To confirm the DNA profile is correct and has not been taken from a different well the sample needs to be re-amplified to confirm.

6.3.5 Edit DNA profiles

See QIS 33773 and 34006.

6.3.6 Rework DNA extract if necessary.

For processes relating to ordering reworks, see 33773. If a sample has been completed in DNAMaster/DAD and AUSLAB, any subsequent reworks that are required are requested in the FR.

QPS in conjunction with Forensic DNA Analysis have decided that if reworking is required, that additional testing will only be conducted on Major Crime samples and selected Volume Crime samples (high priority cases - DNA priorities 1 & 2) via any means available.

Internal validation studies have shown that samples with low template DNA (~132 pg) that are amplified with PP21 may exhibit significant stochastic effects such as large allelic imbalance and allele drop-out. These effects can complicate the interpretation of both single source and mixed DNA profiles. Reworking may improve the quality of the DNA profile.

Low priority Volume Crime (DNA priority 3) cases are only to be reworked via re-amplification, re-running (previously known as re-Genescanning) or re-reading in GMIDX until 12 alleles are obtained (National Criminal Investigation DNA Database-NCIDD uploading threshold). No NucleoSpin cleanups or Microcon concentrations are to be ordered on low priority samples, unless in exceptional circumstances. Other valid reasons for reworking these samples include investigations of adverse events or other quality issues are suspected.

If a partial profile or NSD profile is obtained for a sample, an assessment should be made as to whether reworking that sample will be beneficial or if there are other profiles within the case that satisfy reporting requirements.

Amplification products are not kept indefinitely. The availability of a PCR product should be checked prior to ordering a re-run. For more recent batches, the Analytical Section enters audit notes against the amplification batch when the PCR product has been discarded.

Rework strategies:
If it is determined that a better profile is required, the following should be considered when determining the best rework strategy:

Not Current

1. **The type of sample**
   e.g. blood versus cells. Due to the generally high number of nucleated white cells in whole blood, a DNA profile is usually obtained from such samples. On the other hand, shed skin cells contain few or no nuclei and therefore it is more difficult to obtain a profile of DNA that has been deposited on an item through casual contact.

2. **The quantitation value**
   The quantitation value is displayed in the FR. The quantitation value is an estimate and should be assessed in conjunction with other factors. Sample workflows based on the quantitation value are listed below:

   1. PP21 samples with a quantitation value <0.001 ng/µL will not be further processed and will be reported post-quant with the result line 'No DNA detected', regardless of priority.
   2. PP21 samples with an initial quantitation value between 0.001 ng/µL and 0.0088 ng/µL will be reported post-quant with the result line of 'DNA insufficient for further processing'. Priority 1 samples will proceed to a microcon concentration step prior to re-quant and amplification as per QPS –Forensic DNA Analysis agreement.
   3. Samples reported as 'No DNA detected' or 'DNA insufficient for further processing' can be requested by QPS for further processing via the Request/Task system to the senior scientist of the Analytical section.
   4. PP21 samples with an initial quantitation value of > 0.0088 ng/µL are amplified.

   A partial or NSD profile from a sample with a high quantitation value may indicate inhibition. It should be noted that while quantitation values can be used as an indicator for the presence of inhibitory compounds in an extracted sample, lack of inhibition in a quantitation amplification (as indicated by the IPCCT and possibly the CT as well) does not necessarily mean there will be no inhibition in an STR amplification. This is because 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, 2 µL of extracted sample is added to a quantitation 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). Up to 15 µL of DNA extract can be used for a PP21 full volume amplification (which would change the relative concentration of inhibitory substances in the amplification reaction). Further information on DNA quantification is found in QIS 34045.

3. **The number of alleles obtained**
   A full DNA profile is the aim of any DNA amplification but a partial DNA profile does not necessarily need to be reworked.

   The minimum number of alleles required to upload to NCIDD is 12 alleles. Samples below this stringency, but above 6 alleles, may be loaded to NCIDD under special circumstances and searched against the database (refer to QIS 34246 and 33773).

   If an assumption of a single contributor has been determined, Partial DNA profiles do not have to be reworked to obtain a full DNA profile.

Not Current

4. **Examination notes**
   Certain substances are known to be inhibitory to the PCR process. This includes a variety of commonly encountered substances, such as dyes used in clothing (particularly denim dyes) and some biological material (in particular, the haem in blood). Semen samples have also been observed to return an NSD profile after initial extraction with no indication of inhibition. Performing a NucleoSpin clean up may result in improved or full profiles for these samples.

5. **Offence Details (if available)**
   Information from the QPS entered into the FR, present on item packaging, or from case conferences may assist in determining the evidential value of a particular item.

6. **Results already obtained**
   If multiple samples have been submitted for an item and one or more full profiles or mixtures 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 must be considered carefully and in the context of the case. If it is a possibility that there may be a different profile present, such as in the case of multiple offenders, then reworks should be considered.

6.4 Manage samples

The sample management tab in the FR contains the worklists relevant to PDA entry and review (see 33773 and 33744).

Cases are not usually allocated to an individual case manager/reporter. The exception to this rule may be some urgent cases, QPS operations, linked cases or sensitive matters. Samples are case managed by staff from the worklists in the FR.

Cases with paper files may have epgs annotated with the results and interpretations, although if the PDA page is also printed, this may be not required (see 33773). If annotated, as a minimum, the type of DNA profile. e.g. single source matching UKM1 is required. These annotations need to be signed and dated by the case manager.

6.4.1 Interpret

6.4.1.1 Paired Kinship/Paternity Trios

Any samples for Paternity trios etc. are interpreted as detailed in QIS 25303 *Statistical Analysis for Paired Kinship and Paternity Trio / Missing Child Scenarios*.

Reporting of the analysis outcomes is detailed in QIS 34006 and QIS 34308.

6.4.1.2 PP21 interpretation

Statistics for PP21 results are generated by the STRmix™ program as outlined in QIS 31523.

If a sample has replicate amplifications they must all be included in the STRmix™ deconvolution unless they have a particular processing issue such as different amplification volumes (half volume vs full volume PCR amplifications), excess peak heights and pull up, a Re-run has been performed or the runs are not consistent with each other (at the discretion of the case manager). A Re-run and the source amplification results cannot be included in the same deconvolution as they come from the same amplification, a choice as

Not Current

to the best or most appropriate run must be made by the case manager, and replaces the less informative result. At minimum, a Sample Note may be added to explain why particular amplifications were not included.

All reference samples received for a particular case are to be compared against all interpretable mixtures (to generate a Likelihood Ratio - LR) and single source samples within a case.

The number of contributors will have been determined as per section 6.3.1 above.

Samples processed with STRmix™ V2.0.6 use three populations (Australian Caucasian, Aboriginal and Asian) for the calculation of LRs, the figure that is quoted is the most conservative of the three with a factor of N and 99% one tailed HPD. The case manager is to ensure that this is the figure that is used to determine which EXH line will be used.

Table 3 – Quick reference when to use STRmix™

Scenario	Decon	LR
SS <32 & matches assumed known contributor	No	No
SS <32 & matches a reference sample	Yes	Yes
SS <32 & new Unk & NCIDD	Yes	N/A
SS <32 & matches an Unk	No	N/A
First SS >32 DNA profile & matches a reference sample & NCIDD	Yes	No
First SS >32 DNA profile & matches a reference sample no NCIDD	No	No
SS >32 DNA profile & new Unk & NCIDD	Yes	No
Subsequent SS >32 DNA profile and matches a reference sample/Unk	No	No
2P or 3P & no reference samples & not likely to resolve for NCIDD	No	N/A
2P or 3P cond & no other reference samples & not likely to resolve for NCIDD	No	N/A
2P or 3P & reference samples	Yes	Yes

Single source DNA profiles

Deconvolution with STRmix™ is required:

1. If the sample is the first single source DNA profile that matches a reference sample and needs to be loaded to NCIDD or
2. The sample requires loading to NCIDD (e.g. UNK). And/or
3. This DNA profile has a less than 32 alleles.

LR generation with STRmix™ is not required for single source DNA profiles:

1. If a reference sample does not match the single source sample.
2. If a matching reference sample has previously had an LR generated (and the new interpretation would not be more probative).
3. If the single source DNA profile has 32 or more alleles, the sample can be reported with the appropriate EXH line (as per QIS 34229) and doesn't require deconvolution and an LR generated as per the recommendations in the document 'The determination of the threshold number of alleles, above which single source DNA profiles can confidently be ascribed a likelihood ratio in excess of 100 billion.' [Parry et al 2014].

If a single source DNA profile has one peak at a locus and another peak is visible sub threshold, STRmix™ may designate the locus as a homozygote (with a ≥99 % weighting), the case manager should consider ordering a rework in an attempt to amplify the second peak.

Not Current

Homozygote alleles for single source samples that will not be loaded to NCIDD do not require editing in the FR.

A mixed DNA profile would be reported as a single source profile with sub-threshold peaks using the appropriate exhibit result line in the following circumstances:

1. If the only indication of a mixture is a labelled Y peak at Amelogenin or
2. If the only indication of a mixture is a labelled Y peak at Amelogenin and sub-thresholdpeaks that do not affect the called alleles.

This is done because STRmix™ cannot 'see' Amelogenin or sub-threshold peaks and the low level contribution does not affect the interpretation of the 'single source' profile.

Two and three person mixtures

Deconvolution with STRmix™ is not required:

1. If the case does not have any reference samples and the profile is not likely to be deconvoluted by STRmix™ into contributions for NCIDD or
2. If the case does not have any reference samples and if the DNA profile is likely to be deconvoluted into a contribution that matches an already reported unknown in the case.

If reference samples are later received they will be compared against the mixture and the LRs reported back via exhibit result lines.

Deconvolution with STRmix™ is required for all other two and three person mixtures. All three person mixtures have the number of iterations increased to 100 000 burn in and 500 000 accepts.

Two and three person mixtures may run for extended periods of time, additional support is provided by other staff in Forensic DNA Analysis (mostly Forensic Technicians) to run deconvolutions on dedicated STRmix™ computers. This releases Reporting Scientists' computers for other tasks.

To have another staff member run a deconvolution, see QIS 33773.

Conditioning mixtures

It may be possible to condition mixtures from intimate swabs and items (said to have come from a person). The decision to condition is at the discretion of the case manager (and reviewer). Additional information regarding ownership may be required.

Four-person mixtures

As per *Interpretation of four person mixtures using STRmix™ v2.0.6,* there is limited scope for the interpretation of four-person mixtures with STRmix™ v2.0.6.

Mixtures that have been assessed as having more than four contributors, or not within the scope of the four-person validation with STRmix™ v2.0.6 are considered unsuitable and are not interpreted.

STRmix™ results output

After the STRmix™ deconvolution and/or reference comparison has been completed and processed with the QIS 32139, the following quality checks must be performed on each result produced by STRmix™.

Not Current

1. STRmix™ version
2. Casework sample number is correct
3. Reference sample number (if any) is correct
4. Number of contributors assumed to be present is correct
5. Casework DNA profile (correct allelic designations entered and correct run(s) have been included)
6. Individual locus LRs appear have an intuitive fit
7. Check all loci had successfully deconvoluted (component interpretation complete)
8. Settings values (especially check full vs. half variances)
9. Reference DNA profile (correct allelic designations entered)
10. The overall LR is reasonable given the reference and casework DNA profiles

It is important when a STRmix™ analysis is carried out, that the results are interpreted by examining the weightings of various genotypes and the DNA profile(s) observed. There are instances when the results obtained do not intuitively seem correct. Sometimes (particularly if the model must account for drop-in) the failure of the Markov chain to properly converge means that some parameters will not have optimised properly. Examples of this are:

1. Large LRs are obtained for each locus, except one where the LR is low or 0
2. The mixture proportions do not reflect what is observed
3. The degradation does not reflect what is observed
4. Genotype combinations do not reflect all likely allele sets (especially likely if sub-threshold peaks are present at a locus)
5. The probability of dropout at a particular locus has been given a low value but sub-threshold peaks are clearly visible in the DNA profile.

Effectively, a zero LR means that the genotype of the POI has not been accepted by the MCMC at any time through the course of the analysis. Common causes for making a genotype an unlikely contributor are large required dropouts, drop-ins or imbalances, or when the peak heights at a locus exceed the general degradation slope (and are therefore penalised). The standard values for an increased iteration analysis is 100K/500K for burn-in and MCMC respectively. If further iterations are chosen, then the MCMC will have more opportunity to accept the less supported genotypes, however a reference sample with a poor fit to the DNA profile will still have a low LR for a particular locus or loci. It is best practice to attempt to resolve the mixture biologically first, that is through rework, prior to resorting to increased iterations.

If it is noted that the epg has a plate reading error, such as a stutter peak that has been inappropriately removed or an artefact that has been left in, then the sample must be reread and the corrected GMIDX file exported.

Paper cases have the STRmix™ report printed and added to the case file. This is not necessary for STRmix™ v2.6 as the report contains a large number of pages; a printout of the PDA page and EPG is sufficient. All cases have the pdfs imported and retained in the FR (see QIS 33773).

Repeated Analysis

Each time a DNA profile is analysed using STRmix™ the results will vary slightly. This is a natural consequence of the random nature of the Monte Carlo property. To be as unbiased as possible, each analysis should only ever be run once and the result reported. If a STRmix™ result has been generated for a DNA profile at case management stage, then that same result should be the one used for statement writing. If additional reference

Not Current

samples are received in the case, the reference sample(s) should be run against all original deconvolutions for all samples in the case where mixtures are present. The exception to this is when an analysis has produced a result that requires further investigation and hence further analysis or if the underlying assumptions made about the profile have changed (eg. a two-person mix is reassessed as being a three-person mix).

Consequently, if at review or at a subsequent stage in reporting it is decided that a different number of contributors better fits the DNA profile, the deconvolution for that sample can be rerun using the new assumption. Case-managers/Reporters should discuss any decision to change a reviewed result with the original reviewer.

If multiple analyses have been conducted, then only the STRmix™ results from the most appropriate analysis should be included in the casefile (e.g. the higher number of acceptances or the more appropriate number of contributors). All relevant STRmix™ results will need to be included in the casefile and previous results removed from the casefile. NB. this is not necessary for STRmix™ v2.6 as the report contains a large number of pages; a printout of the PDA page and EPG is sufficient.

The electronic STRmix™ results from the multiple analyses that are not used must be moved into a sub-folder labelled “Do not use” in the case folder in the STRmix results folder.

Use of Ignore Loci function

In certain circumstances a particular locus or loci may be dropped from the interpretation. These include where a Tri-allele pattern has been observed in a reference profile and inconsistent sizing of an allele is observed. There is an option in STRmix™ version 2.0.6 to exclude these loci from the calculations. The Ignore Loci option in the STRmix™ options menu is used. See QIS 31523 Section 8.

If a case has a reference sample with a mutation, all scene profiles within the case (except single-source profiles that do not match the reference sample in question) should have the loci removed from the interpretation. If the reference sample is received after the initial deconvolution was performed, the deconvolutions should be repeated in with the relevant locus/loci ignored.

Use of the database Search

If there is a large number of reference samples associated to a case, the database (DB) search function in STRmix™ is used. This is the preferred method in this scenario as the number of LR results to be checked and reviewed will be kept at a minimum. The database search function will generate a LR for each reference sample in the file.

Reference DNA profiles that contain partial loci information (e.g. 15, NR) cannot be used in STRmix™ v1.05 or 2.0.6 Database searches. Reference DNA profiles that are partial (whole locus/loci missing) can only be used in STRmix™ v2.0.6 database searches.

A database of reference samples for a particular case is created as per Database search section in QIS 31523.

The created database must be checked by a second case manager/reporter before the database is used in STRmix™. After checking the alleles and sample IDs are correct the checker must replace the case ID on each line with their AUSLAB login mnemonic.

Not Current

The STRmix DataBase macros incorporates the Factor of N. When the macro is run on STRmix™ V2.0.6 database results, it will ask whether the mixture is 2 or 3 people so that the correct factor can be applied. The reviewer must check that the correct Factor of N has been applied on the printout. It should be 2 for two person mixtures and 6 for three person mixtures.

The results of the DB search are reported back via an exhibit result line. Reference DNA profiles that generate LRs supporting low or non-contributions can be excluded if there are sub-threshold peaks that support the exclusion.

As the DB search does not incorporate the HPD (Highest Posterior Density) or θ (Theta/FST) correction, when a statement is requested, reference samples that give an LR > 0 (except if an exclusion can be made on sub-threshold peaks) need to be compared directly against the original deconvolution to generate an LR incorporating HPD & θ. This ensures that the most appropriate LR is reported in the statement.

Donors of reference samples may be intuitively excluded, in which case the DB search output can be overridden by case managers making this decision (see Appendix 2 – Intuitive Exclusion Guide).

6.4.1.3 P+ interpretation

Since January 2018, P+ DNA profiles were no longer produced by Forensic DNA Analysis. Samples may still be added to statements (if requested) and reported in a binary fashion.

Samples that are processed with P+ are not interpreted using STRmix™ as this system has not been validated for use with P+ data. Interpretation of P+ samples is outlined in QIS 17168 and 25302.

See QIS 33773 for the use of the FR in reporting P+ DNA profile interpretation results.

6.5 Report Results

All results are to be communicated as outlined in QIS 23968 and 34308.

Statements and intelligence reports are to be prepared according to QIS 34006 and 34308.

For cases processed and reported via AUSLAB, all new items received and/or updated interpretations should be reported via the FR.

If a sample cannot be explained by one of the EXH results available, an intelligence letter should be sent to QPS to outline the interpretation. See QIS 34308.

6.5.1 Exhibit Result lines

See QIS 33773 and 34006 for details on how to report result lines in the FR.

For urgent/Priority 1 samples only, an interim exhibit report may be entered.

Not Current

6.5.2 Exhibit Result line updates

Exhibit result lines may require updating after additional information is available or additional testing has been completed. Commonly, these lines are updated after a reference sample for case has been received and new information needs to be sent back to QPS.

If a result has been reported incorrectly (or further information such as ownership becomes available) the line(s) must be incorrected by FRIT Senior Scientists or Team Leader. See QIS 33773 and 34006.

If a sample is reported as 'incorrect', the result should be added when requesting the Profile Review process in the FR (see QIS 34006).

6.5.3 Suspect checks

If a suspect check has been requested by QPS for a reference sample profiled in P+ and the sample is not intuitively excluded from the mixture, the reference sample needs to be reworked in PP21 to increase the amount of data available to NCIDD.

Instructions for reworking reference samples are documented in QIS 34245.

Suspect checks have reserved Exhibit result lines for reporting; refer to QIS 34229.

6.5.4 STRmix™ Database searches

If after the LR for the reference samples changes then:

- Add 'This sample has undergone further processing' result line
- Add all relevant lines to the interpretation just like it is being done for the first time. This means, the slate was wiped clean with the further processing notification, so re-add '3MX' etc. etc..
- Do not incorrect any lines
- Do not send an email (DNA Management understand the situation may occur)

6.5.5 Samples with undetermined quantitation values or insufficient DNA

It is understood by QPS that samples reported post-quant as 'No DNA Detected' or 'DNA Insufficient for further processing' can be requested for processing at any time.

This request for further processing is made by sending a Request/Task to the Senior Scientist of the Analytical section to reactivate the sample for processing.

Similarly, case managers may at their discretion order a rework in cases where the only results are low quant samples.

6.5.6 Paternity Samples

For paternity cases, results are reported via the barcode for the child (see QIS 33773).

Not Current

If the putative father sample is an intelligence sample, the relevant result line would be 'Intel report required for further Interpretation'. The Intel Report is issued as per QIS 34308.

.

6.5.7 Using Coronial samples as Reference Samples in Exhibit results.

- If a sample has been processed with casework conditions is to be used as a reference sample, it needs to be deconvoluted in STRmix because there is no homozygote threshold. This deconvoluted DNA profile is used as the reference in all comparisons.

7 NCIDD

Case managers are responsible for choosing a representative profile for each unique profile seen within a case for upload to NCIDD. These profiles must have at least 12 alleles for NCIDD matching.

To upload an allele to NCIDD for PP21 samples, a 99% deconvolution is required at a locus as per the Statistics Working Group (STATSWG) recommendations.
e.g.

- [9,11] 99% = 9,11 uploaded
- [9,11] 98% [9,9] 2% = 9,NR uploaded
- [9,11] 98.8% [9,9] 0.6% [11,11] 0.6% = 9,11 uploaded
- [9,11] 98.8% [9,10] 0.6% [10,11] 0.6% = NR,NR uploaded
- If four alleles exist in a deconvolution [9,11] 98.1%[9,10] 0.4% [9,12] 0.5% = 9,NR uploaded
- If in doubt as to the combination to load e.g. [9,10] 98.5% [9,NR] 0.5% [10,NR] 0.5% = NR,NR uploaded
- If in doubt as to the combination to load and the allele count is borderline for NCIDD load (11 alleles) refer to a senior for direction.

≥99% deconvolution at all PP21 loci is known as a 'full' NCIDD load
≥99% deconvolution at ≥ 12 PP21 loci is known as an 'Intel' NCIDD load.

Profiles of less than 12 alleles may be loaded to NCIDD in special circumstances. Please consult with Senior Scientist in the Intelligence Team prior to uploading. All matches generated will be reported through an Exhibit result line in the FR.

In certain circumstances, a profile with less than 12 alleles (including sub-threshold information) can be loaded to NCIDD, and any matches will be reported back to QPS via an Intelligence report written by the case scientist or Intelligence Team member. This is an intel/upload process and is not for court purposes. Intel/NCIDD work does not get heard in court unless special authorisation is given by the Judge/Justice due to potential to prejudice court.

Only one representative DNA profile is loaded to NCIDD for a person in a case. Profiles that match known deceased persons or complainants in sexual assault cases are not to be uploaded to NCIDD. By the same rationale, unknown DNA profiles previously loaded to NCIDD that match known deceased and sexual assault victims are also removed from NCIDD. Refer to QIS 34246 and 33773.

Not Current

7.1 Conditioned DNA profiles loading to NCIDD

After a mixed DNA profile has been conditioned in STRmix™, the deconvolution will list that each conditioned allele has been deconvoluted to 100%, a conditioned component of a mixed DNA profile can be loaded to NCIDD provided that :

- The upload alleles are able to be visually separated (i.e. major or minor)
- Upload matching alleles in an even mixture where there is a strong representation

Do not upload contributions from low level mixed minors where we may be confident enough to condition but not load to NCIDD.

8 Peer review

All results must be peer reviewed prior to release to the QPS. Peer review can be at a sample level or case level, Technical or Administrative (see QIS 34322 and 34006).

Peer review of 'No DNA detected' and 'DNA insufficient for further processing' is performed by a competent Analytical Section staff member.

9 Reference sample management

Refer to QIS 34245.

10 File compilation

10.1 Suggested order of pages (from top to bottom)

1. Case file particulars page (QIS 17038)
2. Copy of final statement (if written)
3. Most recent printout of UR notes, emails and other communications*
4. DNA results table (if deemed necessary)
5. Reference samples – receipt page then profile
6. QP127 (if available) and receipt page
7. Examination notes:
    i. Description of item
    ii. Diagrams
8. Photos/photocopies/AUSLAB images*
9. Profiles
10. Mixture interpretation sheets (if applicable)
11. Statistical calculations (if applicable)#
12. Subsequent QP127 (if available), receipt page and examination notes etc…

* these items are not required to be printed if the case is not going to court
# STRmix v2.6 deconvolution and likelihood Ratio reports are not necessary for casefiles. The PDA page may be substituted as it displays the LRs.

Not Current

10.2 Page numbering

Only cases that are going to court (Statements of Witness or Evidentiary Certificates) need to be page numbered. Assistance is available from the Administrative Team for page numbering.

1. The Case File Particulars page is always Page 1 (except upon reactivation when the additional Case File Particulars page will be numbered page 1 and the original Case File Particulars page will be renumbered as the next consecutive number in the case file).
2. Case Files are numbered from the back of the case file to the front.
3. Number and initial each page, including the reverse of the page if both sides have been used.
4. Ensure the Case number is recorded on each page.
5. Write the total number of pages on the front of the case file and initial and date as indicated.

For those cases that aren't going to court, the total number of pages simply needs to be counted and noted on the front of the case file, that is, each individual page does not need to be numbered.

10.3 Statement compilation

Refer to QIS 34006 for the correct format for statements or reports issued by Forensic DNA Analysis.

FBCALC – order an FBCALC (for 9PLEX samples only) from the registration page if Kinship has been used. Complete and validate

10.4 Preparing a case file for peer review

Prior to submitting a case file for final review or prior to a statement being issued, the following is required:

- Ensure that all items/exhibits have been examined or prioritised appropriately.
- Ensure that appropriate reworks have been performed.
- Establish whether further testing needs to be performed
- Ensure that all samples are finalised
- Samples that have been reported as 'No DNA detected' or 'DNA insufficient for further processing' need to be documented in the case file. This can be done by either printing the PDA page, annotation of the receipt or annotation of the packaging image.
- All profiles have been printed and included in the case file. It is not necessary for epgs within a casefile to be labelled, instead a copy of the PDA page can be printed to accompany the epg(s). The PDA page contains all of the sample and interpretation information and can be associated with the epg via its barcode.
- Ensure that appropriate profiles have been selected for upload to NCIDD. Only one example of each profile is to be loaded to the database.
- Ensure that the reference sample receipt is printed for each evidence sample (AUSLAB only).
- If there are multiple epgs for a particular reference sample, only the reported profile need be printed and annotated as the final profile.
- Ensure that all evidence samples associated with the case are present in the final table.

Not Current

- STRmix™ printouts for all cases that used this program for statistical calculations. It is not necessary to print the report for STRmix™ v2.6 as it contains a large number of pages; a printout of the PDA page and EPG is sufficient.
- For P+ cases: if a statement has been requested, ensure that profiles requiring a genotype frequency have had the statistical calculation performed through the Kinship program (see QIS 25368) and that the results are printed and included in the file. Any mixture interpretation pages, including Popstats where appropriate, must be included in the casefile.

11 Reactivated cases and case requiring updated interpretations

11.1 Reactivated cases

On occasion, some cases require further work after they have been finalised and reviewed.

An assessment of previously reported and uploaded profiles should be undertaken. In July 2007, it was decided (in conjunction with QPS) that all crime scene profiles (except Known Deceased and complainants in sexual assault cases) would be uploaded. Prior to this any crime scene sample that matched a complainant profile for any case type was uploaded to NCIDD. Since the introduction of GMIDX software and lower thresholds, it may also be advantageous to rework samples in an attempt to obtain more information from a profile than may have previously been reported as insufficient for interpretation (if time restrictions permit).

New evidence samples received for a case which has been profiled using P+ will be profiled using PP21. Only the 9 common loci between kits will be used for comparison purposes. It should be discussed with a Senior Scientist or Team Leader and in consultation with DNA Management as to whether the case is transitioned to PP21 profiling.

Any interstate person samples submitted for analysis by the DNA Management Section (QPS) that have been obtained from people located interstate are to be treated as Evidence samples (as per advice from the QPS).

12 Case file management off site

When case files are required for court appearances they should be tracked to the Reporting Scientist in the FR.

13 Records

1. Case file records – the location of paper case files is recorded in the FR.
2. Paperless case examination notes (FBP1 – FBPX) – all but the current folder is stored in Block 3 Reporting.
3. Batch paper records - Filing Storage area (room 6112) or the Exhibit Room (room 6106)
4. DAD-Prior to AUSLAB Batch Functionality, all results obtained were loaded into an Excel spreadsheet known as DNAmaster. In 2008 these results were transferred to the DNA Analysis Database (DAD).
5. AUSLAB
6. Electropherogram pdf/jpeg files for samples:
   - Genotyper profiles are located in J:\User3100\Results Finalised\PRE-LIMS and I:\User3100\AAARESULTS FINALISED\POST-LIMS

Not Current

- As of the 16th February 2009, results have been analysed using GeneMapper ID-X. GeneMapper ID-X profiles are located in P:\Profile PDFs and only accessible from computers with GeneMapper ID-X installed (contains all DNA profile results from 16th February 2009 until June 2012).
- As of July 2012, all DNA profile results are located in O:\Profile PDFs (accessible from all network PCs).

7. STRmix™ result files are stored on a network drive - I:\STRmix Results\

14 Associated Documentation

QIS: 17038 – Case File Particulars

QIS: 17168 – Procedure for Single Source DNA Profile Statistics

QIS: 23968 – Forensic DNA Analysis Communications Procedure

QIS: 25302 – Interpretation of Mixed DNA (STR) Profiles using Profiler Plus

QIS: 25368 – Kinship Software – Genotype Frequency Module

QIS: 25581 – Kinship Software - Paired Kinship and Paternity Trio/Missing Child Modules

QIS: 31523 – Use of STRmix™ Software.

QIS: 32139 - STRmix™ Report macro

QIS: 33744 – Forensic Register Training Manual

QIS: 33773 – Procedure for Profile Data Analysis using the Forensic Register

QIS: 34006 – Procedure for Release of Results using the Forensic Register

QIS: 34045 - Quantification of Extracted DNA using the Quantifiler® Trio DNA Quantification Kit.

QIS: 34112 – STR Fragment Analysis of PowerPlex 21 profiles using GeneMapper ID-X software – FR

QIS: 34229 - Explanations of Exhibit Results for FR

QIS: 34245 – Reference Sample Result Management

QIS: 34246 – Uploading and Actioning on NCIDD - FR

QIS: 34248 - Administrative Team - Case File related duties using the 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

Not Current

15 References

National Association of Testing Authorities (NATA). Refer to NATA website: http://www.nata.com.au

Nurthen T., Mathieson M. & Allen C., (2013) Amplification of Extracted DNA validation v2.0
Nurthen T., Mathieson M., Scott K. & Allen C., (2012) PowerPlex® 21-Direct Amplification of Reference FTA® samples validation.

Parry, R., Caunt., E & Allen C., (2012) Verification of the DNA profile module of STRmix™ using the Promega PowerPlex® 21 system.

Parry, R., Caunt., E & Allen C., (2013) Verification of the DNA profile module of STRmix™ for Full Volume Amplifications using the Promega PowerPlex® 21 system.

Parry,R., Howes, J., & Allen, C. (2014) The determination of the threshold number of alleles, above which single source DNA profiles can confidently be ascribed a likelihood ratio in excess of 100 billion.

Police Powers and Responsibilities Act 2000, Current as of 22 September 2014

Police Powers and Responsibilities Regulation 2012, Current as of 22 September 2014

Howes, J., (2010) A guideline for the assessment of complex DNA profiles.
Caunt, E., Morgan, R., Gardam, T.,Howes, J. & Allen, C. (2014) Verification and implementation of STRmix™ V2.0.1.

Morgan, R., & Caunt E. (2015) Assessment of the Number of Contributors for Mixed PowerPlex® 21 DNA Profiles within Forensic DNA Analysis.

Caunt E., Morgan, R., Howes, J & Allen, C. (2015) Assessment of the Number of Contributors for Mixed PowerPlex® 21 DNA Profiles within Forensic DNA Analysis_version 2

Caunt E, McNevin A, Howes J & Allen, C (2018) Interpretation of four person mixtures using STRmix v2.0.6

16 Amendment History

Revision	Date	Updated By	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	V Ientile	Refer to AUSLAB. Remove FACTS

Not Current

	2003	L Freney	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
12	Apr 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
Version	**Date**	**Updated by**	**Amendments**
12	10 Apr 2008	J Connell	Transferred section on preparing case file for presumptive EXR/EXH validation to Examination of Items SOP
13	12 Feb 2009	K Lee	Major rewrite; 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.
14	28 Oct 2009	K Lee	Updated with reference to GeneMapper *ID-X* software; changed “Pre/Post LIMS” references to “Pre/Post AUSLAB Batch Functionality”; removed unnecessary flow charts; updated hyperlinks and associated documents; introduced paperless case management; re-arranged for better flow and grammatical correctness; Introduced more definitions; included instruction on locating profiles for printing.
15	27 Jan 2012	K Pippia	Introduced new worklists; added section on reworking evidence samples; added VOLUND process; addressed changes in processes since last update; removed references to re-Genescanning and

Not Current

			introduced references to re-reads; updated hyperlinks; addressed comments raised against last revision; updated FBNLR process
16	12 Nov 2012	Alicia Quartermain, Emma Caunt, Justin Howes	Updated all processes to include implementation of PowerPlex®21 and STRmix™
17	Jan 2015	Thomas Nurthen	Incorporation of updated workflows, major rewrite , New template
18	August 2015	Thomas Nurthen	Fixed typos, referenced new document for number of contributors, additional steps for FBNLR process, added NCIDD removal process, updated STRmix versions, NCIDD load requirements
19	07 April 2017	Justin Howes	Changed example on p41 to [9, NR]; added information to 5.4 regarding strmix instructions; added eg P+ to PP21 to 9.3; section 6.3.6 – added info on P+ and microcon instructions; changed LOD Quant from 0.00214ng/uL to 0.001ng/uL; added information to 6.5.3 re incorrects; added first line to Table 6;added information to 6.2.5 on no further work process; added Appendix 3 – Intuitive Exclusion Guide and details to 6.4.1.2; changed 19977 to 33407; fixed title of 24126 and hyperlinking throughout; edited amendment history versions/revisions to align with QIS.
20	24 December 2018	Justin Howes	Major revision due to implementation of FR and other new SOPs (for the FR).

Not Current

17 Appendices

1 Appendix 1 Case management checklist
2 Appendix 2 Intuitive Exclusion Guide

17.1 Case Management Check list

Check Quality

- ☐ Batch statuses are fully completed
- ☐ Check Samples and PDA notes
- ☐ Check Casefile notations and Requests/Tasks
- ☐ Check the photo of the crime scene envelope.

Check case

- ☐ Check for Reference samples.
- ☐ Check for Allocation
- ☐ Check for paper file.
- ☐ Ownership of item

Assess results

- ☐ View results already reported
- ☐ Assess the number of contributors to the DNA profile.
- ☐ Assess the quality of the DNA profile
- ☐ Rework DNA extract if necessary/possible
- ☐ Variant/OLA /ULP calculations
- ☐ DNA profile edits

Manage Samples

- ☐ Interpret - STRmix™, POPSTATS etc
- ☐ Reference comparison
- ☐ LIMS completion
- ☐ Paper case files

Report results

- ☐ DNA profile type line
- ☐ Conditioning information line if necessary
- ☐ NCIDD load lines if necessary

Not Current

17.2 Intuitive Exclusion Guide

Guide for performing intuitive exclusions

Once the scientist has made an assessment of the number of contributors to a DNA profile, the next stage is to compare DNA profiles obtained from reference samples associated to the case to determine whether these people could be potential contributors. For a single source DNA profile, this is a simple process since the reference sample must match all alleles present within the crime scene profile in order for it to be considered a potential contributor. This process is more complex for mixed DNA profiles as there are more allelic peaks, and combinations of these peaks, to be considered.

As an example, for a two person mixture where there are four alleles at a locus, the reference sample must match two of those alleles to be considered as a potential contributor. If this condition is not met then, under the assumption of two contributors, the reference profile is excluded.

As the number of contributors increase and/or the contributor proportions change, the decision process for excluding a reference profile also changes.

The table below provides a guide for when a reference sample can be excluded as a potential contributor to a DNA profile when comparing the reference sample to an individual locus. It describes the following:

- the mixture type that may be encountered;
- the component of the mixture to which the reference sample is being compared (for an even mixture this would be the entire mixture, for the minor component of a major/minor mixture this would be only the minor alleles);
- the type of match to the reference sample (one or two alleles matching and whether the reference sample is homozygous or heterozygous at that locus).

Where there is an 'S', this means that the reference sample may not be able to be excluded intuitively and that a LR should be calculated using STRmix™. Where there is an 'x', this means that the reference sample can be excluded without the need to calculate a LR in STRmix™.

The number of alleles being compared does not include peaks that could be -2, -1 or +1 repeat stutter. These alleles can be either above or below the LOR but must be above the LOD.

The 'component' of the mixture being compared refers to whether the scientist is comparing to the whole mixture as in an even mixture, or to part of the mixture e.g. major, minor, remaining.

Mixture Type	Number of alleles at locus being examined in component of mixture being compared	**Reference sample**			
		Doesn't match any alleles	Homozygous matching 1 allele	Heterozygous matches 1 allele	Matches 2 alleles
2 person even mixture - drop-out is unlikely to have occurred	1	x	S	x	n/a
	2	x	S	x	S
	3	x	S	x	S
	4	x	x	x	S
2 person even mixture - drop-out is likely to have occurred	1	S	S	S	n/a
	2	S	S	S	S

Not Current

	3	x	S	S	S
	4	x	x	x	S
2 person major/minor mixture **- comparison to minor** (major is considered single source)	1	x	S	S	n/a
	2	x	x	x	S
2 person conditioned mixture **- comparison to remaining**	1	x	S	S	n/a
	2	x	x	x	S
3 person even mixture - drop-out is <u>unlikely</u> to have occurred	1	x	S	x	n/a
	2	x	S	x	S
	3	x	S	x	S
	4	x	x	x	S
	5	x	x	x	S
	6	x	x	x	S
3 person even mixture - drop-out is <u>likely</u> to have occurred	1	S	S	S	n/a
	2	S	S	S	S
	3	S	S	S	S
	4	S	S	S	S
	5	x	S	S	S
	6	x	x	x	S
3 person major/minor mixture - 2 people in major - drop-out of major is unlikely to have occurred **- comparison to major**	1	x	S	x	n/a
	2	x	S	x	S
	3	x	S	x	S
	4	x	x	x	S
3 person major/minor mixture - 2 people in major **- comparison to minor** (minor single source)	1	x	S	S	n/a
	2	x	x	x	S
3 person major/minor mixture - 2 people in minor **- comparison to minor** (major is considered single source)	1	S	S	S	n/a
	2	S	S	S	S
	3	x	S	S	S
	4	x	x	x	S
3 person conditioned mixture - 2 people in remaining **- comparison to remaining**	1	S	S	S	n/a
	2	S	S	S	S
	3	x	S	S	S
	4	x	x	x	S
3 person conditioned mixture - remaining is 2 person major/minor **- comparison to remaining minor** (single source) (major is considered single source)	1	x	S	S	n/a
	2	x	x	x	S

Not Current

Justin Howes

From: Justin Howes
Sent: Wednesday, 7 February 2018 3:18 PM
To: Adrian Pippia; Alicia Quartermain; Allison Lloyd; Amanda Reeves; Angela Adamson; Angelina Keller; Anne Finch; Cassandra James; Claire Gallagher; Deborah Nicoletti; Emma Caunt; Hannah Pattison; Helen Williams; Ingrid Moeller; Jacqui Wilson; Josie Entwistle; Justin Howes; Kylie Rika; Lisa Benstead; Matthew Hunt; Penelope Taylor; Rhys Parry; Sharon Johnstone; Susan Brady; Thomas Nurthen; Timothy Gardam
Subject: Auto-microcons

Hi all
On the back of case manager's anecdotal feedback and our lab's second round of datamining of samples that underwent the auto-microcon process, an Options Paper was presented to QPS Superintendent of Forensic Services Dale Frieberg on ways forward for QPS to consider – continue with auto-microcon process, or cease auto-microcons.

QPS have advised the laboratory that they do not wish for our efforts to be put to the auto-microcon process (including the efforts in interpretation) for Priority 1 or 2 samples.

This means samples in the range 0.001ng/uL (LOD) - 0.0088ng/uL will be reported at Quant stage as 'DNA Insufficient for Further Processing'. This is consistent with the process in place for P3 samples. The manual Microcon process may be performed upon QPS request.

To report in a statement, the following wording could be used:

Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling.

This is slightly different to the wording written in 2012/13 for these samples (P3) but after some consultation, appears a good starting point.

An enhancement has been requested to enable this to occur from 12 February. Reactivating samples for further post-extraction processing, if requested from QPS, will be directed to Luke via an FR Request. If there are changes to the 12 February date, I will let you know. As usual, appropriate comments to SOPs will follow.

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 | 39 Kessels Road, Coopers Plains, QLD 4108
w | Queensland Health e | [redacted]

HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

Justin Howes

From: Kylie Rika
Sent: Wednesday, 7 February 2018 11:35 AM
To: Justin Howes; Thomas Nurthen; Sharon Johnstone
Cc: Amanda Reeves
Subject: RE: wording for DNA insuff

I like the 2nd one better.

Kylie Rika Dip Mgt BSc PGrad Dip (Forensic)
Senior Reporting Scientist – Forensic Reporting and Intelligence Team

Forensic DNA Analysis | Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

p | [redacted]
a | 39 Kessels Road, Coopers Plains, QLD 4108
w | www.health.qld.gov.au e | [redacted]

HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

From: Justin Howes
Sent: Wednesday, 7 February 2018 11:31 AM
To: Thomas Nurthen; Kylie Rika; Sharon Johnstone
Cc: Amanda Reeves
Subject: wording for DNA insuff

Hi
The wording that we have had for 'DNA Insufficient', going back to when we used it years ago is:

DNA insufficient

This sample contained insufficient DNA to be suitable for analysis and therefore was not submitted for DNA profiling.

An alternative that we could use is:

Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling.

Please reply which one, or further variation you would prefer.

Thanks
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 | 39 Kessels Road, Coopers Plains, QLD 4108
w | Queensland Health **e** | [redacted]

HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

Justin Howes

From: Sharon Johnstone
Sent: Wednesday, 7 February 2018 11:35 AM
To: Justin Howes; Thomas Nurthen; Kylie Rika
Cc: Amanda Reeves
Subject: RE: wording for DNA insuff

I prefer the original

Sharon Johnstone
Senior Scientist – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

p | [redacted]
a | 39 Kessels Road, Coopers Plains, QLD 4108
w | Queensland Health e | [redacted]

HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

From: Justin Howes
Sent: Wednesday, 7 February 2018 11:31 AM
To: Thomas Nurthen; Kylie Rika; Sharon Johnstone
Cc: Amanda Reeves
Subject: wording for DNA insuff

Hi
The wording that we have had for 'DNA Insufficient', going back to when we used it years ago is:

DNA insufficient

This sample contained insufficient DNA to be suitable for analysis and therefore was not submitted for DNA profiling.

An alternative that we could use is:

Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling.

Please reply which one, or further variation you would prefer.

Thanks
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 | 39 Kessels Road, Coopers Plains, QLD 4108
w | Queensland Health **e** | [redacted]

HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

Justin Howes

From: Thomas Nurthen
Sent: Wednesday, 7 February 2018 11:37 AM
To: Justin Howes; Kylie Rika; Sharon Johnstone
Cc: Amanda Reeves
Subject: RE: wording for DNA insuff

The second I think is better given that the sample might be suitable for other analysis.

Cheers

Thomas Nurthen
Reporting Scientist – Forensic DNA Analysis, Police Services Stream

Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

p | [redacted]
a | 39 Kessels Road, Coopers Plains, QLD 4108
w | www.health.qld.gov.au e | [redacted]

HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

From: Justin Howes
Sent: Wednesday, 7 February 2018 11:31 AM
To: Thomas Nurthen; Kylie Rika; Sharon Johnstone
Cc: Amanda Reeves
Subject: wording for DNA insuff

Hi
The wording that we have had for 'DNA Insufficient', going back to when we used it years ago is:

DNA insufficient

This sample contained insufficient DNA to be suitable for analysis and therefore was not submitted for DNA profiling.

An alternative that we could use is:

Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling.

Please reply which one, or further variation you would prefer.

Thanks
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 | 39 Kessels Road, Coopers Plains, QLD 4108
w | Queensland Health **e** | [redacted]

HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

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)

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

Not Current

(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)

Not Current

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

Not Current

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).

Not Current

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+)

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.

Not Current

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

Not Current

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+)

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

Not Current

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+)

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:

Not Current

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

HealthSupport
Queensland
Forensic and Scientific Services

Procedure for the Release of Results

Not Current

1 Purpose

To describe the correct format for statements or reports issued from Forensic DNA Analysis.

To document the procedures for issuing reports within Forensic DNA Analysis.

To document workflows leading to the releasing of information via Exhibit Reports to the Queensland Police Service.

2 Scope

This standard operating procedure relates to all statements or reports issued by case analysts to clients using AUSLAB as the LIMS.

3 Definitions

DRMU – DNA Results Management Unit (QPS)
EB – Extraction Batch
EXH – Exhibit Report
FSS – Forensic and Scientific Services
GSI – Generic System Interface (interface between AUSLAB and QPS Forensic Register)
LR – Likelihood Ratio
P+ - Profiler® Plus DNA amplification kit
PP21 - PowerPlex® 21 DNA amplification kit
QIS – 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 Actions

4.1 Presumptive Exhibit Reports

The formats of the accepted EXH comments are located in QIS 23008.

A Presumptive EXH should include the following information:

4.1.1 Overall Status

This should reflect the result. This only applies to EXRs, and does not apply to EXHs.

Negative (Forensic Value) – Used for items that are examined but not submitted for testing.
Negative (Not examined) – Used for items that are received but not examined
Not Received at FSS – Used for items that are not received at FSS
Positive (Forensic Value) – Any sample submitted for DNA testing will have this status result.

4.1.2 Lab Number:

The results are reported under the individual sub-sample. Refer to Appendix 8 for specific guidelines.

4.1.3 Result Status

All result options are available using the F1 lookup function. The results status should reflect any presumptive & confirmatory tests that were conducted and include whether the sample was submitted for DNA testing.

Example 1: If a TMB test was performed that was negative and the swab was submitted as cells but also had a hair attached which was observed under microscopy as not suitable for DNA testing the following lines would be entered:

234967280 Presumptive blood test neg. Submitted as cells.
234967280 Hair located. Not suitable for analysis

Example 2: If different testing was performed on two sub-samples with a positive TMB test recorded for the first which was submitted and both an AP pos and the presence of spermatozoa detected by microscopic examination on the second the following lines would be entered:

234967280 Presumptive blood test pos, submitted – results pending
234967281 Presump sem fluid test pos, submitted – results pending.
234967281 Micro positive for sperm. Submitted – results pending.

NB. Linked No and Warm Link name are not required for presumptive EXHs

4.2 Final Exhibit Reports

The formats of the accepted EXH comments are located in QIS 23008.

4.2.1 Quality Checking:

Final EXHs can only be interpreted and released after the GMID-x batch has been read and Quality Flag checked (and Extraction Batch (EB) checked where appropriate) – refer Appendices 12-13. When flags are raised, Quality Flag checking is usually performed by a Senior Scientist, EB checking is usually performed by a case manager. When flags are not raised, batches can be completed by plate readers or management team members.

For urgent batches (ie. containing urgent (P1) samples), emails are sent by the plate reader or management team members when batches are complete to all case managers alerting them that P1 samples are ready for interpretation.

Incorrect Results

If at statement or Likelihood Ratio calculation stage (ie. when comparing to scene profiles to Evidence Sample profiles) the profile interpretation is not deemed to be consistent with the most current approaches, this reassessment may mean 'incorrect' EXH lines will need to be sent to QPS. Refer to QIS 17117. At any stage when an 'incorrect' is reviewed in

Not Current

AUSLAB, an email must accompany the EXH line. The generic QPS email address of [redacted] should be used. See Appendix 5.

If the result change is such that a formerly reported link or LR is reassessed to an interpretation without links or LRs, or a less discriminatory LR, this should be verified by a Team Leader and personally communicated to QPS Senior Sergeant DRMU. Details should be recorded in AUSLAB and advice should be sought on steps forward eg. correction of links, retraction of statement request.

A Final EXH should include the following information (refer to Appendix 4-5):

4.2.2 Lab Number:

The sub-sample no. of the results being reported. This should include the results for all sub-samples that have been entered into the EXH as presumptive EXHs lines. Any further different results should also be added to the EXH. If there are no sub-samples, the EXH of the Item should be entered.

4.2.3 Result/Status:

A description of the result (eg 9 loci, partial, no DNA profile). All result options are available using the F1 lookup function. There may be more than one EXH line which is suitable however the EXH must fully describe the result. For example if there is a major and minor profile an EXH line must be entered for both the major and minor profiles.

Example 1:

234967280	Mixed DNA Profile. Major component uploaded to NCIDD	UKM1
234967280	Mixed profile, minor component insuff for NCIDD matching	UKM2

4.2.4 Linked Number Field:

<u>If the Crime Scene profile matches an Evidence Sample profile</u>: The barcode no. of the evidence sample is added to the Linked No. field.

<u>If the Crime Scene profile does not match an Evidence Sample profile</u>: If there are no matches to evidence sample profiles, then the profile will be 'unknown'. The designations of 'UK' should be used for unknowns with 'F' (female) or 'M' (male) used to provide further information and 'UKP' should be used if the sex of the DNA profile is unable to be determined. '1' should be used to denote the first male, female or person profile obtained.

Example 1: Three different male profiles would each be reported on a different line with UKM1, UKM2 & UKM3 used to distinguish between the contributors.

Example 2: A single (1) unknown male would be reported as UKM1.

NB: If an unknown profile is reported to QPS and an evidence sample is subsequently received that matches the unknown profile, any further unknown profiles continue sequentially eg. If UKM1 matches John SMITH, then the next unknown male in the case is designated UKM2 (it does not replace the UKM1).

Not Current

4.2.5 Warm Link Name:

The name of the evidence sample the profile matches to is entered into this field. This column is not visible to QPS and is useful at case management to determine who has been compared to the crime scene profiles.

4.3 Suspect Checks:

Suspect checks are useful when a profile is insufficient for NCIDD upload and a permanent barcode/profile exists for a suspect. They are also useful with PowerPlex® 21 mixed DNA profiles where profiles may not be deconvoluted for NCIDD but are suitable for comparison to reference samples and LR calculation.

Suspect checks are usually nominated by the QPS through SSLU. This information may be found in the UR notes (this must always contain the barcode).

It is not a necessity that names are entered in the Warm Link field of the EXH for suspect checks.

For PowerPlex® 21 DNA profiles, these are reported in the EXH using an appropriate EXH line (see QIS 23008). This includes the appropriate Likelihood Ratio EXH lines.

For Profiler® Plus DNA profiles, these are only reported in a final EXH if they do not match. For profiles sufficient for NCIDD, the matches are reported via LKRs (QIS 23890 Uploading and Actioning Samples on NCIDD and QIS 22619 Creating and Reviewing Links). For Intelligence Report templates, see QIS 24015 Procedure for Intelligence Reports and Interstate/Interpol Requests.

If there is a suspect check match and the DNA profile is less than the stringency for searching on NCIDD, an Intelligence Report should be issued to QPS DRMU.

For Profiler® Plus interpretations, if the DNA profile is ‘complex’ or ‘no major/minor’ and the suspect check is performed resulting in a ‘cannot exclude’ interpretation, an Intelligence Report should be issued to QPS.

Intelligence samples may be received by Forensic DNA Analysis associated to particular cases. These samples need to be compared to the case. If the crime scene profile is on NCIDD and the Intel sample is ‘Unlimited Purpose’, a match will be reported to QPS DRMU as a cold link. If the Intel sample is ‘Limited Purpose’, the match needs to be reported in an Intelligence Report (Profiler® Plus) or via EXH (PowerPlex® 21). If the Intel sample does not match a crime scene profile, the non-match does not need to be reported in an EXH (Profiler® Plus) but can be reported via EXH for PowerPlex® 21. If the crime scene profile is Single Source and matches someone other than the profile for the Intel sample, then an EXH line is not required.

If an Intelligence sample/suspect check was profiled with Profiler® Plus and the crime scene profiles are all PowerPlex® 21, if the case is high profile, it is preferable to rework the sample to enable a full comparison of the profiles to be reported. Before the rework is ordered, it is important to intuitively assess the crime scene profile to determine if the reference profile is excluded. If clearly excluded, there is no benefit in reworking the sample with PowerPlex® 21. Refer to QIS 17117 for details on billing and reworking.

Not Current

4.4 Interstate/International Requests – Refer to QIS 24015

4.5 Urgent (Priority 1) Requests

4.5.1 Routine Urgent Requests:

The requests for urgent processing will come via Inspector of DNA Results Management Unit (or higher), and are forwarded to the Managing Scientist and Team Leaders. A phonecall 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 Property Point supervisor where appropriate. The case will be allocated by the Reporting Supervising Scientists and all Management staff informed.

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 dependant 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 EXH line 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 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 in AUSLAB for client requested and internally-raised urgent processing. If internally-raised, approval from Supervising Scientist/Team Leader is required.

4.5.2 Urgent Result Communication on Fridays (only).

Regarding Priority 1 urgent samples as requested by QPS, if results are likely to be available on Fridays, email DRMU ([redacted] in the morning with the relevant barcodes and expected time of release. Aim to release prior to the 3pm GSI transfer and call DRMU if the results are likely to be released later than 3pm.

When results are reviewed, email DRMU that results have been released and if in the 3pm transfer, 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.

4.5.3 Streamlining to Reporting Urgent samples

Not Current

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 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 Results Management Unit, or S/Sgt DNA Results Management Unit.

4.6 Statements and Certificates

4.6.1 AUSLAB Template

For the layout of a Statement of Witness, refer to Appendix 1.

There is a footer on each page that includes the NATA endorsement, the page number and total number of pages, the case reference number, date, name and signature of Reporting Scientist authorising the statement.

Allows the inclusion of a version of the statement Appendix that lists test methodologies (refer to Appendix 2).

Includes a Justice's Declaration Act (refer to Appendix 3) at the end of the Appendix.

The AUSLAB template is the same as the offline templates available in QIS (refer to QIS 29010).

The AUSLAB template pulls in the case details, including the reference and crime scene sample receipt details, Reporting Scientist details, Defendant and Complainant, Appendix and Justice's Act.

The person who presses F6 on the statement page in AUSLAB will have their details pulled into the statement.

Not Current

NB. Prior to statement release, ensure that all EXHs have 'Rev-Ack' in the Peer Review column of the relevant EXH with the exception of 'low support' or 'non-contribution' EXH lines. If an 'incorrect' EXH line was sent to QPS, ensure the status is 'INR-Ack' before statement release.

4.6.2 Statement Requirements (AUSLAB Test Code: FBSOW):

Statements will contain the following information (see Appendix 1):

- Declaration & Details of the Reporting Scientist (eg. Name, State)

- Place of Employment and position (eg. Scientist within Forensic DNA Analysis)

- Qualifications held by the Reporting Scientist (eg. B.Sc.)

- ANZFSS Code of Ethics (if applicable)

- Peer review and Date of issue stamp on top left corner. It is ideal to have these dates to be the same, and the same as the dates on the bottom of each page and on the Justice's Act thus demonstrating the peer review was conducted prior to statement issue. Having a later Date of Issue is acceptable, but not preferable.

- Offence details including Defendant and Complainant details. If there is a deceased involved, the complainant is Regina.

- Details relating to the receipt of items & reference samples including the date of receipt, and the delivery officer (including Australia Post). A list of the barcoded items received.

- Summaries/ Preambles are added by the Reporting Scientist and may include some, all or slight variations of the following depending on case and profile types (see Appendices 9-11):

- The Role of a Forensic Biologist
- Examinations (if performed by another analyst)
- DNA Profiling
- Mixed DNA Profiles
- Blood Stains
- Seminal Stains
- Saliva
- Semen Staining on Items
- Persistence of Semen in the Vagina
- Statistics

- A summary of test results of the Reference Samples, and the type of sample (eg. Blood, Mouth/Buccal, Hair)

- Description and results of each of the Items:

- If Items were examined by QPS, or by QPS and QHFSS, it should be made clear which category the Items fit into.
- Description of the Item including barcode information e.g. 123456789. Receipt sub-numbering e.g. 987654321-002 is optional.
- Condition of the Item (if examined by QHFSS)

Not Current

- Area of staining (if examined by QHFSS)
- Areas submitted for testing (if examined by QHFSS)
- Results obtained eg. Results of comparison to reference DNA profiles and statistical interpretations where appropriate.
- Where relevant, opinions, explanations for opinions and interpretations or summary. A statement of uncertainty where relevant. Reference to other information which may be relevant to the validity or application of the results, e.g. in support of an opinion, explanation or statement of uncertainty.

Note: If a summary of results is required, it should be included at the beginning of the result section of the statement.

Note: It is recommended that the Items are grouped per Receipt. Within each receipt, the similar results are recommended to be grouped together, and then group items examined at QHFSS and QPS, and then to group like results.

- All items received but not tested are listed (listed under each receipt).

- Appendix including information about:

- Accreditation
- Chain of Custody
- DNA Profiling
- Interpreting DNA Profiles
- Use of statistics

- Justices Act 1886 – Signature of Reporting Scientist required. The Justices Act must not be on a page by itself. The number of pages to be written within the Justice's Act should be the same as the number of pages for the whole statement.

4.6.3 Subsequent/ Alternative Statements:

4.6.3.1 Further Versions (AUSLAB Test Code: FBSOW):

AUSLAB has the ability for further versions of statements to be produced under the same testcode. This is useful for replacing statements.

4.6.3.2 Addendum Statement (AUSLAB Test Code: FBADDE):

If a subsequent statement is issued (this may be due to additional exhibits being delivered or an additional request for further interpretation), it must be clearly marked as an addendum to the original statement. This test code is also used for pre-AUSLAB cases and other cases that feature manual receipts.

APPVER testcode should be ordered at the same time as FBADDE to enable the Appendix field to be edited and the FBADDE to be used as a standalone statement (on its own barcode). If on a standalone barcode, an FBSOW needs to be ordered as well to enable the original completed date to populate. The date in this FBSOW needs to be in the same format as the way the date is typed into the FBADDE eg. DDMMYY or DD/MM/YYYY.

Not Current

4.6.3.3 Amended Statement (AUSLAB Test Code: FBAMEN):

If, after the issue of a statement, an error is detected, the original statement shall be withdrawn and, where necessary replaced by one which is clearly indicated as being a replacement statement. This testcode is rarely used since AUSLAB is able to create new versions (see 'a.' above).

4.6.3.4 Intelligence Reports (AUSLAB Test Code: FBINTL) (refer to QIS 24015):

If there is information that cannot 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. The report is written within AUSLAB where the addressee and reviewer's details can be entered.

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.

The signed report can be included in the case file, except where it relates to linking information from NCIDD. In these situations, the signed report should be held in the Intelligence Team area.

A scanned PDF of the signed intelligence report should be sent via MS Outlook to DRMU [redacted] An unsigned PDF (created after validation and saved from AUSLAB when viewed (Shift Insert)) should be sent with the signed copy to DRMU. Upon issuing, the FBIOLR page must be completed. Alternatively, these two PDF files can be sent via email to [redacted] which is managed by SSLU who then send the files on to QPS. SSLU will then complete the FBIOLR page in AUSLAB.

The generic template to be used for offline Intelligence Reports is available in QIS 29011. The FBAR to record the review of the Intelligence Report can be ordered on the same barcode as the FBINTL, as can the FBIOLR testcode to record the release details.

When completing the Casefile Particulars page of the paper casefile, the relevant section to fill out is the one entitled 'Case File without Report?'.

4.7 DNA Evidentiary Certificates: AUSLAB Test Code: FBEVC)

4.7.1 Certificate Details:

Refer to Section 95A Evidence Act 1977.

Not Current

This is a certificate (in an approved form – see Appendix 15) that must be signed by an authorised DNA Analyst.

Current staff who hold appointments (in accordance with Section 133A of the Evidence Act 1977) as DNA Analysts are held with the Managing Scientist. Refer to QIS 25608 for details on the process to undertake 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.

If an Evidentiary Certificate is requested, a workflow has been devised to assist the checking involved in order to sign the certificate (see Appendix 14).

A checklist should be used to record the information examined by the DNA Analyst (refer to QIS 30799). There are instructions to complete this checklist recorded in a worksheet tab within the actual checklist file.

If the information gathered to be checked prior to issuing the Evidentiary Certificate is to be considered part of the casefile, then an FBAR page needs to be requested in AUSLAB and the pages should be numbered and the case identifier added.

NB. Appendix v4 cannot be used with FBEVC testcode.

4.8 Civil Casework Processing and Reports

Refer to QIS 10629 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.

Not Current

4.8.1 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.

4.8.2 Approval process

The Managing Scientist or Team Leader are to complete the form: 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 all details scanned into AUSLAB.

4.8.3 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.
    - A template in AUSLAB does not exist without the NATA logo; therefore, refer to 29008 and ensure all NATA references are removed.
- The Justices Act 1886 should be removed
- Details of testing processes can be detailed in the report by combining the preamble and Appendices used in Criminal matters. Refer to Appendix 19 for an example – NATA references should be removed if the matter is a civil paternity.
- Include the Uniform Civil Procedure Rules 1999 – Sect 428. See Appendix 20.

Not Current

4.8.4 Issue and invoice

When the work is complete, the report should be issued as per Section 4.15.1 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 FSS [redacted] to ask them to organise issuing the invoice to the requesting party. It is advisable to include the approved quote in this email.

4.9 Other Reports – Crime and Corruption Commission (CCC) or Ethical Standards unit of the QPS.

Due to the confidential nature of these cases, results may not be entered into AUSLAB in either EXH or Statement format (as this information is accessible by QPS and other FSS staff). Barcodes will need to be registered to facilitate analytical processing; a case identifier or SSF may be requested in AUSLAB to facilitate this processing. If a QP number exists, the continued use of the QP number should be checked with the requesting QPS party as it may have security control measures implemented in the QPS system.

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 and in such cases, may request direct results via Intelligence Report or email.

Clarification from the requesting party will need to be sought if any results are ok to send via the GSI to QPS, or if by other means (above).

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. This report shall **NOT** be scanned into AUSLAB. **All results are to be included in the case file only.**

Not Current

4.10 Statements with coronial samples.

Refer to QIS 17117.

To ensure samples delivered by the Coronial Support Unit (CSU) are pulled through correctly into Statements, the receipted items require an FTAR testcode to be requested (and the delivery officer etc to be recorded), and the Specimen type to be changed to FTAE. If it has correct CRISP association in the registration in AUSLAB, the receipt details should then pull into the Statement of Witness.

4.11 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.

4.12 Offline Statements

If a Statement of Witness needs to be written outside of AUSLAB (eg. when AUSLAB is down, or the testcode is corrupted), the templates are available in QIS. Templates exist for Statements of Witness and Intelligence Reports - see the following documents:

29010 – Statement of Witness template – stamp
29008 – Statement of Witness template – address – no NATA endorsement
29009 – Statement of Witness template – blank – no NATA endorsement
29024 – Use of offline Forensic Reporting templates
29011 – Generic report template

This type of statement may be written 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 AUSLAB upon completion.

Alternatively, this particular person may create a barcode in AUSLAB under the same UR number, and request an FBSOW testcode. By pressing F6, their details will pull into the statement.

4.13 Statement/ Report Authorisation

In order to release results to the client in the laboratory (excluding EXHs), QIS 30689 needs to be completed. QIS 26993 describes the overall procedure for releasing results at FSS.

Not Current

Qualified Forensic DNA Analysis Reporting Scientists are authorised to sign statements and reports given that all policy and procedure requirements have been satisfactorily fulfilled.

All Staff are authorised to sign and initial worksheets, reports etc according to their level of competence.

A staff list with signatures and initials of all staff (QIS 17088) is kept for reference. This is located in the Quality cupboard.

DNA Analysts can sign Evidentiary Certificates. To be authorised as a DNA Analyst, the Director-General of the Department of Health approves a Briefing Note authored by the Managing Scientist, cleared by the Senior Director (FSS) and verified by the Chief Executive (HSQ). The Director- General is permitted to appoint a public service officer as a DNA Analyst according to the requirements of Section 133A of the *Evidence Act 1977*, if satisfied that the officer has the necessary qualifications and acquired competencies. The minimum details considered by the Managing Scientist are relevant qualifications, relevant experience in the field, and competence in Reporting DNA casework. When authorised, the DNA Analyst appointment is published in the Qld Government Gazette. Refer to QIS 25608.

Another scientist with the same or greater level of competence can sign as Peer Reviewer. Relevant training modules apply to the elements of technical reviews.

4.14 Further Documentation Requests (eg. Audit Trails)

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 LALU (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, an FBAR page should be requested in AUSLAB and 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. Having said this, it is recommended that this occurs as it is helpful if/when it is referred to in court proceedings.

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.

Not Current

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.

4.15 Release of Reports

4.15.1 Statement of Witness and DNA Evidentiary Certificates

The signed document is copied and stamped as 'copy'. The copied document is included in the casefile and page numbered. The original is scanned and emailed to SMU by SSLU for uploading directly to QPRIME, and is sent by SSLU or Forensic DNA Analysis Administration Team to the Investigating Officer (or delegate, which could include the DPP). Urgent documents could be faxed where appropriate.

There is only one 'original' statement/certificate that can be issued. This is the document mailed to the requesting party, usually the Investigating Officer. If a QPS or legal party member requests a 'second original', then the copy of the original that is retained in the casefile should be copied and sent to the requesting party. Details of any communications should be recorded in AUSLAB.

4.15.2 Intelligence Reports

The Intelligence Report is sent via MS Outlook to DRMU [redacted] as a signed PDF file, and an unsigned PDF that is created by AUSLAB post-validation (see section 4.6.3.4)

4.15.3 Coronial and Disaster Victim Identification (DVI) Reports

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.

4.16 Court Monitoring

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 Court Testimony Monitoring Evaluation Form (QIS 17047) 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.

Not Current

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 '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.

Refer to FSS Court Testimony and Attendance Requirements (QIS 18034) for more information.

5 Records

All Statements of Witness issued must bear a stamp on the front page that lists the date of issue, the case analyst's signature and the signature of the analyst who performed the technical review of the statement. The stamp is automatically added to statements by AUSLAB.

A copy of the statement issued for any test/examination must be retained in the case file. After the statement has been reviewed, F6 to validate will change the statement to PDF format. The person pressing F6 to validate will have their details auto-populated by AUSLAB. This means the Reporting Scientist needs to perform this function. A time and date stamp will appear in the footer.

Further versions can be created of Statements of Witness, Intelligence Reports and Evidentiary Certificates and can be viewed in AUSLAB prior to printing - Press Shift –Insert on the validated statement page (to view PDF Report Table) and F8 to view HTML Report. The original (validated) statement can also be viewed by pressing F5 on this page, or scrolling to the version you wish to view.

If a mistake is made and another version needs to be created, insert an audit entry to explain that a new version was created to correct an error (or similar wording).

6 Associated Documentation

10623 Laboratory report format and content
10629 FSS – Quotation and acceptance of work
16004 AUSLAB Users Manual – Forensic DNA Analysis
17088 Procedure for recording handwriting specimens in Forensic DNA Analysis
17047 Court Testimony Monitoring Evaluation Form
17117 Procedure for Case Management
17137 Procedure for STR fragment analysis using GeneMapper® ID-X software
17142 Examination of Items
18034 FSS Court Testimony and Attendance Requirements
20401 Quotation
22619 Creating and Reviewing Links
23008 Explanations of EXH Results
23602 Environmental Monitoring

Not Current

23890 Uploading and Actioning Samples on NCIDD
23955 Disaster Victim Identification Preliminary DNA Reports
23968 Forensic DNA Analysis Communications Procedure
24015 Procedure for Intelligence Reports and Interstate/Interpol Requests
25608 Appointment and Cancellation of State Analysts
26993 Procedure for authorising staff to release results
29008 Statement of Witness template – address – no NATA endorsement
29009 Statement of Witness template – blank – no NATA endorsement
29010 Statement of Witness template – stamp
29011 Generic report template
29024 Use of offline Forensic Reporting templates
30799 DNA Evidentiary Certificate Checklist
31389 STR fragment analysis of PowerPlex® 21 profiles using GeneMapper® ID-X software
31523 Use of STRmix™ software

National Association of Testing Authorities (NATA). Forensic Science ISO/IEC 17025 Application Document, July 2015. Refer to NATA website: http://www.nata.com.au

Evidence Act 1977

Supreme Court of Queensland Act 1991: Uniform Civil Procedure Rules 1999.

7 References

Nil

Not Current

8 Amendment History

Version	Date	Author/s	Amendments
	24 Feb 1999	V Ientile	
QIS Edition			
1	8 Oct 2001	V Ientile	
2	23 Jan 2004	L Freney	Changes to references, update appendices
3	11 Mar 2004	V Ientile	No interim unchecked results to be issued
4	10 Aug 2006	M Gardam	Combined with 17158, amended the title and updated statement requirements, included intelligence reports, statement blurbs & Evidential Reports. Added Reference to Communication SOP, Added EXR reporting guidelines.
5	31 May 2007	M Gardam	Sub-numbering is optional when giving a description of the item.
6	April 2008	QIS 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
7	August 2009	J Howes	Updated Forensic Biology to DNA Analysis, added EXH, added complete preambles, added Evidentiary Certificate workflow, Quality flag checking workflow, updated Statement of Witness and Appendices examples, DNA Analyst list removed, relative frequency paragraph removed from Intel letter example and updated with match probability, EXH table improvements and current lines added to examples.
8	June 2010	J Howes	Added EB checking workflow, added to Quality Flag workflow, moved Quality paragraphs to own Appendix, deleted Pathology and Scientific services logo
9	August 2010	J Howes	Changed FIRMU to DRMU, added some more information to paternity preamble
10	April 2011	J Howes	Changed Appendix 3 to include latest version of Justice's Act, changed HP4/HP5 to 'senior' in Evidentiary Certificate workflow, added some suspect check information.
11	05 April 2012	J Howes	Changed DNA Unit to Sample Mgt Unit, changed 'Evidential Reports' to 'Other Reports', added info to Statement and Intel Report field, changed the number/bullet/paragraph systems to be consistent, added new Appendix version (5), added new preambles, added new Statement of Witness template, add ability to create statement versions, added Offline

Not Current

			statement section, removed Appendices 4 and 5 (covered by 24005), added F6 validation to RECORDS, added Release of Reports section, removed Example 6 (multiple items) from Appendix 9, added Coronial/DVI report release section, add Environmental samples to QFLAG workflow, updated QFLAG and EB checking process, added template for Evidentiary Certificates, updated FBSOW for FBSTAT and workflow, added link to Evidentiary Certificate checklist, added Ethical Standards/CMC information, added Court Monitoring information, added information to Intel report section, added Urgent P1 result communication on Fridays, added FTAs associated to the case (under Suspect Check section).
12	29 Nov 2012	J Howes	Added new HSSA Header, removal of FBSHRT reference that was part of Section 3 and the workflow from Appendix, Linked No. field updated to include use of barcodes for unique profiles, FBEVC added, information on who receives Intel reports added, Intelligence Report section re-organised, added information to negotiate timeframe with requesting party re audit trails, Appendix 6 for statements added to Appendix 2 in this document, added APPVER to workflow for FBADDE and to Section 3, added Appendix 17, added Reference Sample section to Appendices 9-11 to be used where appropriate, Tho1 changed to TH01, Appendix 14 workflow changed to not include AUSLAB matches, added Profiler® Plus for 'cannot exclude' interpretation for suspect check,
13	07 July 2014	J Howes	Reformatted according to Procedures template, added information relating to PowerPlex® 21 and XPLEX, added information from Comments on previous version, re-formatted the Appendices, added 26993 to associated docs, workflow for QFLAGs with PowerPlex® 21, re-ordered Appendices, updated preambles, added Appendix 18 – suggested statement wording, changed HSSA to HSQ, added information to Urgent Processing, changed release of Intel reports to include by Outlook, replaced Appv5 for Appv7 in 9.2, added NATA details, changed Appendix 13 to reflect all carried out in the one spreadsheet, added XPLEX drop down for

Not Current

			Quality Flags to Appendix 13.
14	16 Feb 2016	J Howes	Added to new template and revised numbering, removed Appendix 12 (Quality Paragraphs), added new Appendix 1 screenshot, removed 26874 as associated document, amended rounding examples and added LR less than 10, added 25608 to associated docs and made reference in section 4.7, added macro location to Appendix 14, removed Digital Data Store reference in App 12 and added Environmental sample QFLAG matches details to same Appendix, added info to 4.2.2 regarding QFLAGs, added date of issue details to 4.6.2, added ® and ™ where applicable throughout, added 10629, 20401 and updated NATA details and Uniform Civil Procedure Rules to associated docs, added section 4.8, added Appendices 19 and 20, added information to 4.2.1 regarding incorrects and P1 QFLAG checking, added info to 4.3 regarding LRs for mixtures, added generic QPS DRMU email address, removed 4.2.2 (in previous version), changed wording in 4.2.5, added 'spitting' to App 9 and 10.
15	28 Nov 2017	J Howes	Minor revision due to new SOP relating to Forensic Register implementation. 4.6.3.4: added fill out case file without report section; removed 'cumulative' from Appendix 14, added 'AUSLAB' to the scope

Not Current

9 Appendices

1 An example of the layout of the front page of a Statement of Witness

2 Procedural overview and test methodology (Statement Appendices 6 and 7).

3 Example of the Justice's Declaration Act.

4 Completing Exhibit Reports in AUSLAB

5 Review of Exhibit Reports in AUSLAB

6 Creating an Addendum Statement in AUSLAB

7 Creating a Statement with Receipt Details in AUSLAB

8 EXH Reporting (Sub-Sample No. Rules)

9 Complete Casework Preamble – Examinations by QHFSS

10 Complete Casework Preamble – Examinations by QPS and QHFSS

11 Complete Paternity Preamble

12 Quality Flag Checking Workflow

13 Extraction Batch Checking Workflow

14 General DNA Evidentiary Certificate Workflow

15 DNA Evidentiary Certificate template (and Appendix v5)

16 DNA Evidentiary Certificate Workflow in AUSLAB

17 Suggested PowerPlex® 21 and STRmix™ statement wording

18 QFLAG workflow for Quality Team (when a possible match is identified)

19 Example of combined preamble and Appendix for Civil casework report

20 Uniform Civil Procedure Rules 1999 – Sect 428

Not Current

9.1 An example of the layout of the front page of a Statement of Witness

Queensland Government

Forensic and Scientific Services
HealthSupport Queensland

STATEMENT OF WITNESS

Peer Reviewed .....Yes/No Client Reference : ASUF000999

Case Analyst .....

Peer Analyst .....

Date Issued .....

QUEENSLAND)
TO WIT)

I, Justin Anthony HOWES, of Brisbane in the State of Queensland, do solemnly and sincerely declare that:-

1. I am employed by Queensland Health Forensic and Scientific Services (QHFSS) at Coopers Plains, Brisbane.
2. I hold the position of Senior Scientist in the DNA Analysis Unit of QHFSS.
3. I was awarded a Bachelor of Science from University of Queensland.

   I was awarded a Bachelor of Arts from University of Queensland.

   I was awarded a Master of Science (Forensic Science) from Griffith University.
4. I am a member of the Australian and New Zealand Forensic Science Society.
5. This is my statement in relation to the alleged offence that Occurrence Number: QP1234567890 refers. The defendant in this matter is DEFT. The complainant in this matter is Regina.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025.

Justin Howes ..... 4 January 2016

The results relate solely to the item(s) and/or sample(s) as received.

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone (+61 7) 3274 9000
Fax (+61 7) 3000 9628
Email Forensics@health.qld.gov.au

Page: 1 of 1

9.2 Procedural overview and test methodology (Statement Appendices 6 and 7).

APPENDIX (version 6)

Procedural overview for DNA Analysis,
Forensic and Scientific Services (FSS), Health Services Support Agency

Examinations

Unless otherwise stated, the examinations of items for biological material were conducted by officers within the Queensland Police Service (QPS). Sub-samples from these items were forwarded to Forensic and Scientific Services (FSS), Health Services Support Agency, for the purposes of conducting DNA analysis.

DNA Analysis operates under the premise that 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 FSS DNA Analysis. 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.

Some items may be submitted to this laboratory for the purposes of both examination and DNA profiling. This occurs at the discretion of the QPS. These examinations are performed in accordance with the SOPs of this laboratory. For these items, notes are made at the time of the examination by the examining scientist and form part of the casefile.

Chain of Custody

All DNA Analysis 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 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 exhibit packaging prior to processing. The packaging and labelling of any exhibit is checked and recorded before the sample undergoes DNA analysis.

Entry into DNA Analysis is restricted to authorised persons only, via electronically encoded proximity access cards. DNA Analysis forms part of a Health Services Support Agency campus site which has access controlled and monitored by a security team. Records of Visitors to DNA Analysis are retained.

Accreditation

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 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

Not Current

- 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.
For details of the current ISO/IEC 17025 Field Application Document, Forensic Science, Supplementary requirements for accreditation, please refer to the NATA website:

http://www.nata.asn.au/publications

Not Current

Technical information relating to DNA profiling at DNA Analysis, Forensic and Scientific Services (FSS), Health Services Support Agency

DNA Profiling

DNA is a complex chemical found in almost all cells in the human body. It carries genetic information which determines the physical and chemical characteristics of a person. The testing system used at DNA Analysis looks at 21 regions of DNA, 20 of which contain highly variable Short Tandem Repeats (STRs). The 21st region gives an indication as to the gender of the donor (for details see Table 1). This technique involves the use of a method known as Polymerase Chain Reaction (PCR), used to amplify these specific regions of the DNA to produce numerous copies. In this way, minimal amounts of DNA isolated from small or degraded samples can be increased to a level where they are able to be detected, profiled and compared with other samples.

The individual components (alleles) of a DNA profile are represented by a series of peaks which are measured and given a designation using standard sizing ladders. A person will have two peaks for each STR, one inherited from their mother and one inherited from their father, unless the same STR is inherited from both parents, in which case only one peak will be seen.

A DNA profile obtained from biological material such as blood, semen, saliva, hair or cells (eg. touch DNA) can be compared with the DNA profile obtained from a reference sample from any person. If there is no indication of a contribution by more than one person, then a DNA profile is described as being “single source”. Conversely, if there are indications of two or more contributors, then a DNA profile is described as a “mixed” DNA profile.

Statistical Analysis of DNA profiles

In order to statistically evaluate DNA profiles, it is necessary to make a reasonable assessment of the possible number of people who may have contributed DNA to that DNA profile, based on the information observed.

<u>DNA profiles assumed to originate from one person (single source)</u>

A person can be excluded as a possible source of the biological material if corresponding regions of the crime-scene DNA profile are different from that person's reference DNA profile. If the corresponding regions of the DNA profiles contain the same information, then that person, together 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 DNA originated from the person of interest;
Proposition 2: the 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 DNA components that make up the DNA profile. Upon request, an internationally accepted verbal scale to describe the support for one proposition over another can be used to offer some non-numerical explanation for the likelihood ratio (see Table 2).

If less than the 21 regions of DNA are seen in a DNA profile (termed an 'incomplete or partial DNA profile') this will be reflected by a smaller likelihood ratio than the likelihood ratio that would be obtained from a full DNA profile. In other words, the more incomplete the DNA profile, the greater the likelihood of obtaining the DNA profile if it came from someone other than, and unrelated to the person of interest.

Not Current

DNA profiles assumed to originate from more than one person (mixed DNA profiles)

In order to assess whether a person could or could not have contributed to a mixed DNA profile, a set of competing propositions (similar to a single source DNA profile) are considered. For example, for a two person mixture:

Proposition 1: the DNA originated from the person of interest and an unknown person unrelated to the person of interest;
Proposition 2: the DNA originated from two unknown people unrelated to the person of interest.

The likelihood ratio provides a statistical assessment of a particular contribution of DNA being contained within the mixed DNA profile.

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 intimate area, then it may be possible to make the reasonable assumption that the donor of the sample 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 known donor, such that the presence of the DNA components corresponding with the donor'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, for example:

Proposition 1: the DNA has originated from the complainant and the person of interest;
Proposition 2: the DNA has originated from the complainant and an unknown individual unrelated to the person of interest.

When it appears that a large number of people could have contributed to a mixed DNA profile, it can be difficult to exclude individuals as potential contributors. It can be equally difficult to determine whether a person could in fact be a contributor to the DNA profile. If it is not possible to determine the number of contributors to a mixed DNA profile, or if there is very limited information available, then a mixed DNA profile may be described as unsuitable for interpretation.

If information is received such that the assumptions made in an interpretation are not accepted, then 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, irrespective of whether the DNA profile is single source or mixed. A correction factor θ (theta) is applied to all statistical calculations in order to correct for the possibility of common ancestry (sharing of DNA components inherited from a common ancestor) between people in the general population. The nationally agreed figures for theta are θ=0.02 for the Australian Caucasian dataset, θ=0.03 for South East Asian dataset, and θ=0.05 for the Australian Aboriginal dataset. Unless otherwise specified, the default dataset used in DNA Analysis is the Australian Caucasian dataset. The other datasets are available upon request.

In addition to theta, the calculation of the likelihood ratio also includes an allowance for the sampling variability of the dataset. In other words, if a new dataset were generated it allows for any difference the new dataset could make to the likelihood ratio.

Often the calculated likelihood ratio produces numbers of hundreds (100s) or even thousands (1000s) of billions. To avoid the use of potentially confusing terminology, a ‘ceiling figure’ for the likelihood ratio of 100 billion has been determined (this is called truncation). For example, a calculated likelihood ratio of “150 000 billion times more likely”, would be reported as “more than, or at least 100 billion times more likely”. The actual calculated figure can be provided upon request.

The above listed values for the 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 random fashion in which DNA from parents combines, the probability that two siblings would share the same 20 STR regions 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 is thought that a close blood relative may have been involved, a more meaningful approach would be to submit the reference sample from the relative in question for analysis and direct comparison to the crime stain DNA profile.

Not Current

Standard DNA (STR) profiling system at DNA Analysis, Forensic and Scientific Services (FSS), Health Services Support Agency

Table 1: PowerPlex® 21 multiplex 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

Table 2: Verbal scale to describe Likelihood Ratios
(adapted from Evett IW and Weir BS 1998 *Interpreting DNA Evidence*. Sinauer, Sunderland, MA)

RANGE OF VALUE	LEVEL OF SUPPORT
>1 million	Extremely Strong
100 000 – 1 million	Very Strong
10 000 – 100 000	Strong
1000 – 10 000	Moderately Strong
100 – 1000	Moderate
10 – 100	Low Level
1 – 10	Slight
1	Inconclusive

Not Current

APPENDIX (version 7)

Procedural overview for Forensic DNA Analysis,
Forensic and Scientific Services (FSS), Health Support Queensland

Examinations

Unless otherwise stated, the examinations of items for biological material were conducted by staff within the Queensland Police Service (QPS). Sub-samples from these items were forwarded to Forensic and Scientific Services (FSS), Health Support Queensland, for the purposes of conducting DNA analysis.

Forensic DNA Analysis operates under the agreement that 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 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, notes are made at the time of the examination by the examining scientist and form part of the casefile.

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 exhibit packaging prior to processing. The packaging and labelling of any exhibit is checked and recorded before the sample undergoes DNA analysis.

Entry into Forensic DNA Analysis is restricted to authorised persons only, via electronically encoded proximity access cards. Forensic DNA Analysis forms part of a Health Support Queensland campus site which has access 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 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

Not Current

- 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.
For details of the current ISO/IEC Standard Application Document for accreditation of testing and calibration facilities and Forensic Science ISO/IEC 17025 Application Document, please refer to the NATA website:

http://www.nata.asn.au/publications

Not Current

Technical information relating to DNA profiling at Forensic DNA Analysis, Forensic and Scientific Services (FSS), Health Support Queensland

DNA Profiling

DNA is a complex chemical found in almost all cells of the human body. It carries genetic information which 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 of DNA, 20 of which contain highly variable Short Tandem Repeats (STRs). The 21st region gives an indication as to the gender 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 they are able to be detected, profiled and compared with other samples.

The individual components (alleles) of a DNA profile are represented by a series of peaks which are measured and given a designation using standard sizing ladders. A person will have two alleles or peaks for each STR, one inherited from their mother and one inherited from their father, unless the same allele is inherited from both parents, in which case only one peak will be seen.

A DNA profile obtained from biological material such as blood, semen, saliva, hair or cells (eg. touch DNA) can be compared with the DNA profile obtained from a reference sample from any person. If there is no indication of a contribution by more than one person, then a DNA profile is described as being “single source”. Conversely, if there are indications of two or more contributors, then a DNA profile is described as a “mixed” DNA profile.

Statistical Analysis of DNA profiles

Forensic DNA Analysis uses the STRmix™ software to assist in the interpretation of DNA profiles and calculation of likelihood ratios for DNA profiles generated using the PowerPlex® 21 system. STRmix™ is an expert system developed and validated in Australia and New Zealand.

In order to statistically evaluate DNA profiles, it is necessary to make a reasonable assessment of the possible number of people who may have contributed DNA to that DNA profile, based on the information observed.

DNA profiles assumed to originate from one person (single source)

A person can be excluded as a possible source of the biological material if corresponding regions of the crime-scene DNA profile are different from that person's reference DNA profile. If the corresponding regions of the DNA profiles contain the same information, then that person, together 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 DNA originated from the person of interest;
Proposition 2: the 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 DNA components that make up the DNA profile.

If less than the 21 regions of DNA are seen in a DNA profile the likelihood ratio will be smaller than the likelihood ratio that would be obtained from a full DNA profile. In other words, the more incomplete a DNA profile is, the greater the likelihood of obtaining that DNA profile if it came 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 DNA originated from the person of interest and an unknown person unrelated to the person of interest;
Proposition 2: the DNA originated from two unknown people unrelated to the person of interest.

The likelihood ratio provides a statistical assessment of a particular contribution of DNA being contained within the mixed DNA profile.

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).

Not Current

In certain circumstances, if the ownership of an item is established or if the sample was collected from an intimate area, then it may be possible to make the reasonable assumption that the donor of the sample 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 known donor, such that the presence of the DNA components corresponding with the donor'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, for example:

Proposition 1: the DNA has originated from the complainant and the person of interest;
Proposition 2: the DNA has originated from the complainant and an unknown individual unrelated to the person of interest.

When it appears that a large number of people could have contributed to a mixed DNA profile, it can be difficult to exclude individuals as potential contributors. It can be equally difficult to determine whether a person could in fact be a contributor to the DNA profile. If it is not possible to determine the number of contributors to a mixed DNA profile, or if there is very limited information available, then a mixed DNA profile may be described as unsuitable for interpretation.

If information is received such that the assumptions made in an interpretation are not accepted, then 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, irrespective of whether the DNA profile is single source or mixed. A correction factor θ (theta) is applied to all statistical calculations in order to correct for the possibility of common ancestry (sharing of DNA components inherited from a common ancestor) between people in the general population. The nationally agreed figures for theta are θ=0.02 for the Australian Caucasian dataset, θ=0.03 for 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 dataset. In other words, if a new dataset were generated, this allowance factors in any difference the new dataset might make to the likelihood ratio.

Often the calculated likelihood ratio produces numbers of hundreds (100s) or even thousands (1000s) of billions. To avoid the use of potentially confusing terminology, a 'ceiling figure' for the likelihood ratio of 100 billion has been determined (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.

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 random fashion in which DNA from parents combines, the probability that two siblings would share the same 20 STR regions 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 is thought that a close blood relative may have been involved, the most meaningful

Not Current

approach to interpretation would be to submit the reference sample from the relative in question for analysis and direct comparison to the crime-scene DNA profile.

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

Not Current

9.3 Example of the Justice's Declaration Act.

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 XXXX, and contained in the pages numbered 1 to _____ 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.

_____

Signature

Signed at BRISBANE on XXXX.

Not Current

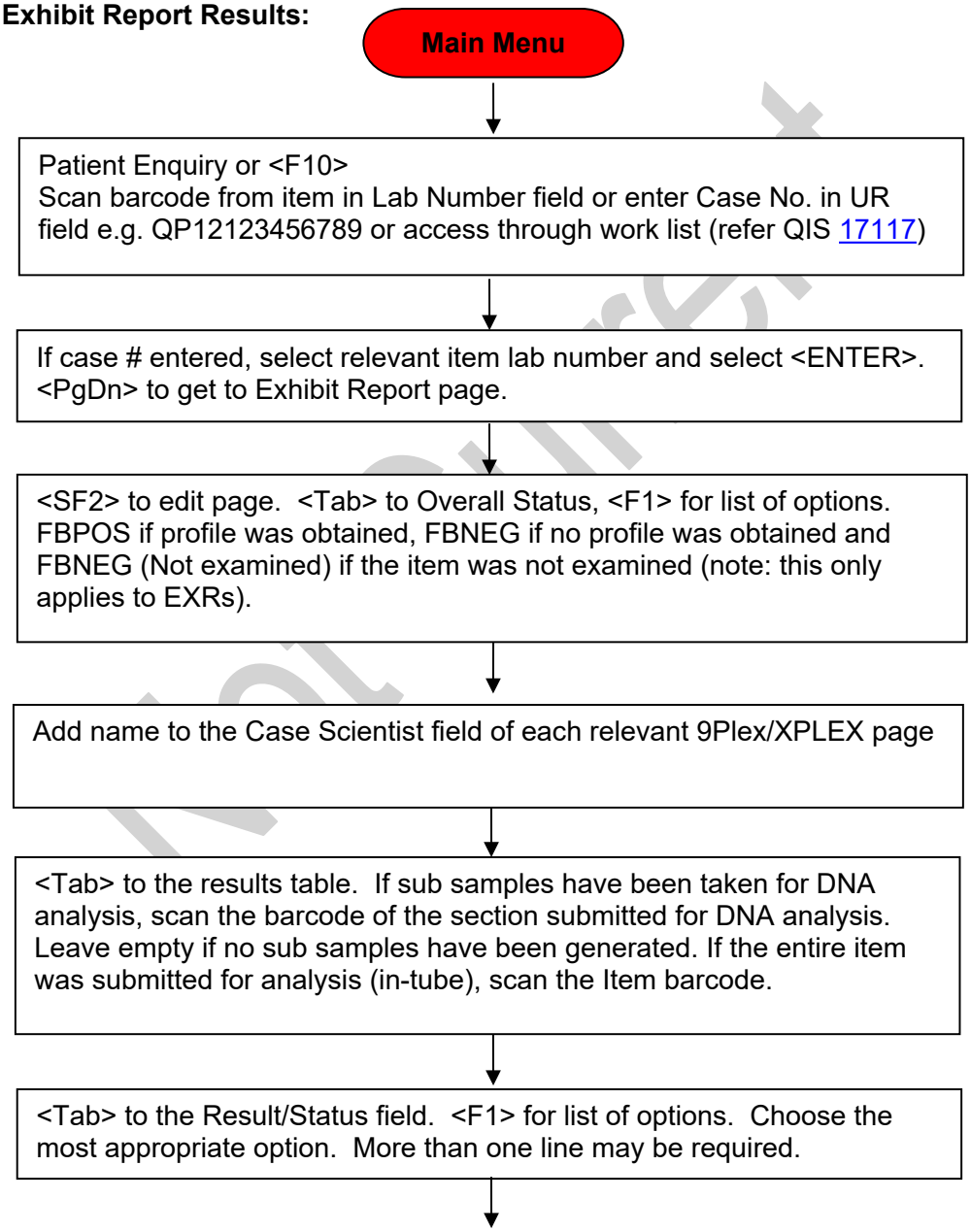
9.4 Completing Exhibit Reports in AUSLAB

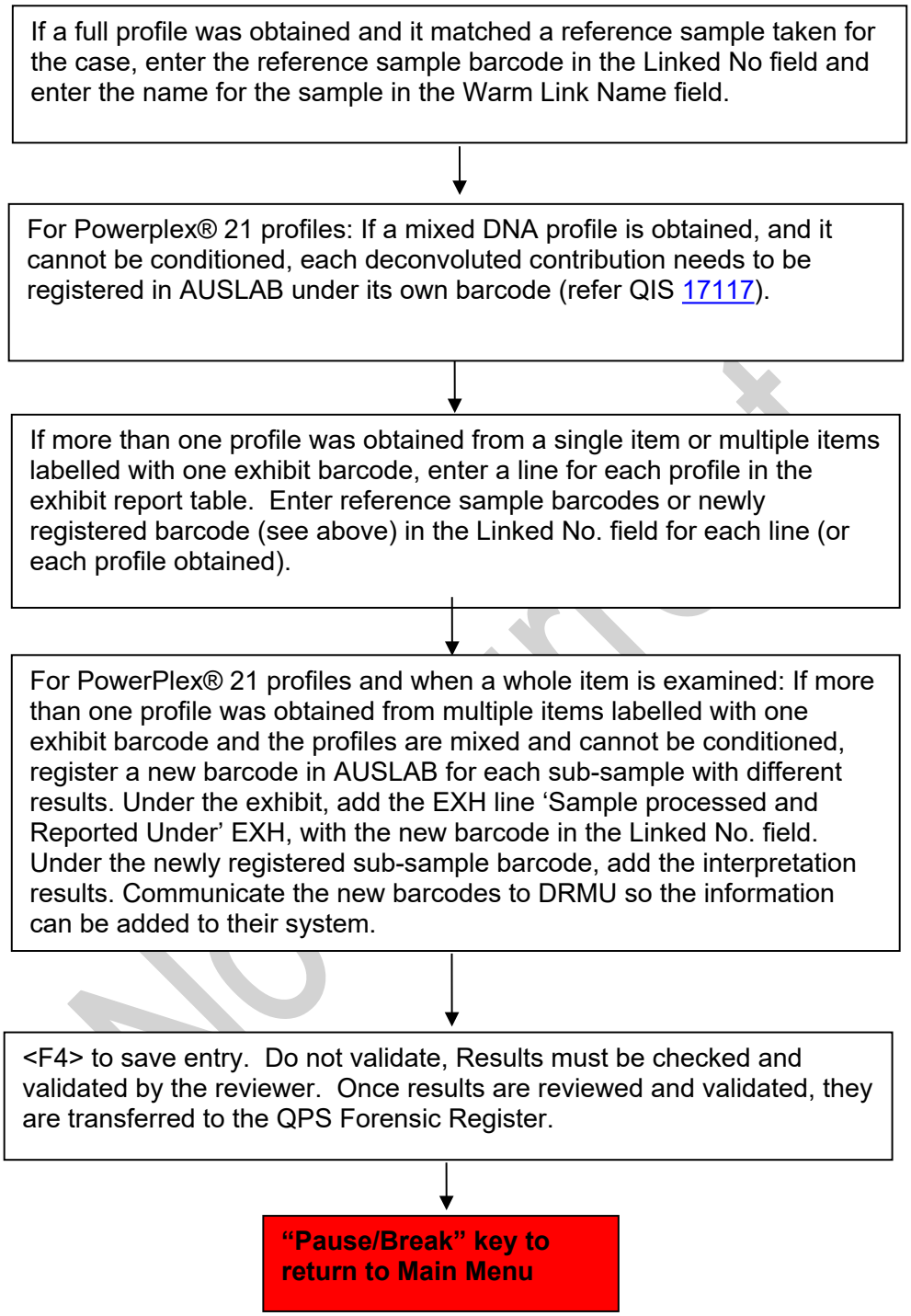
Completing Exhibit Reports

AUSLAB Test Code: EXH

Purpose: Exhibit Reports are a summary of results for each item received. The information stored in the exhibit reports is transferred to the QPS Forensic Register once the results have been checked and validated. Exhibit Reports can contain information about examinations performed, screening test results and DNA profile results. Interim results can be entered and sent to the QPS Forensic Register once they have been validated.

To enter Exhibit Report Results:





NOTE:

- All mixed DNA profiles that can be separated into major/ minor contributions (for Profiler® Plus), should have the designations filled out under the MIXT testcode for 9Plex/ Profiler® Plus, and on the COMIX page for XPLEX/PowerPlex® 21.

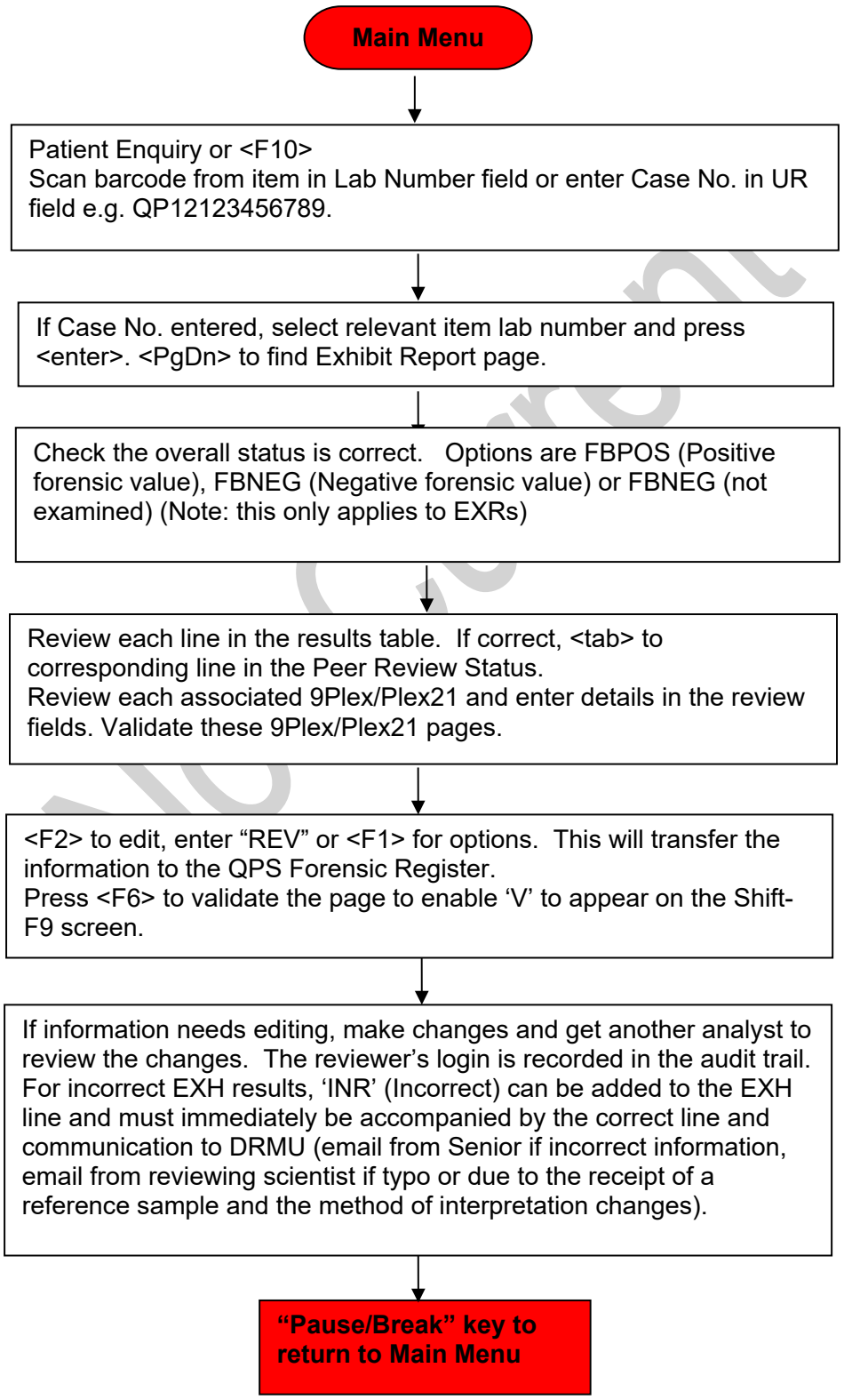
- All mixed DNA profiles that can be ‘conditioned’ should have the designations filled out under the MIXC testcode for 9Plex/ Profiler® Plus, and on the COMIX page for XPLEX/PowerPlex® 21).
- If the interpretation is a conditioned mixture and for intelligence purposes only (eg. conditioned in the absence of a reference sample but using an unknown profile from the same case), this should be made clear in the comments section of the mixture pages.
- If the mixture is major/ minor but the major is mixed and used for POPSTATS purposes, an MIXT testcode should be used and the contributions added to this page. This only applies to 9Plex/ Profiler® Plus profiles.
- If the mixture is major/minor and the major is mixed, and a conditioned interpretation is applied to the major, it may be appropriate to use the MIXC testcode and to record the minor components to the specimen notes (and have these peer reviewed). The comments section can also be used to make it clear what actions have occurred. This should only be relevant for 9Plex/ Profiler® Plus profiles.

Not Current

9.5 Review of Exhibit Reports in AUSLAB

Purpose: An Exhibit report is created for each item as a way of transferring results back to the QPS Forensic Register. Each line of an exhibit report must be reviewed before it can be released and sent to the QPS Forensic Register.

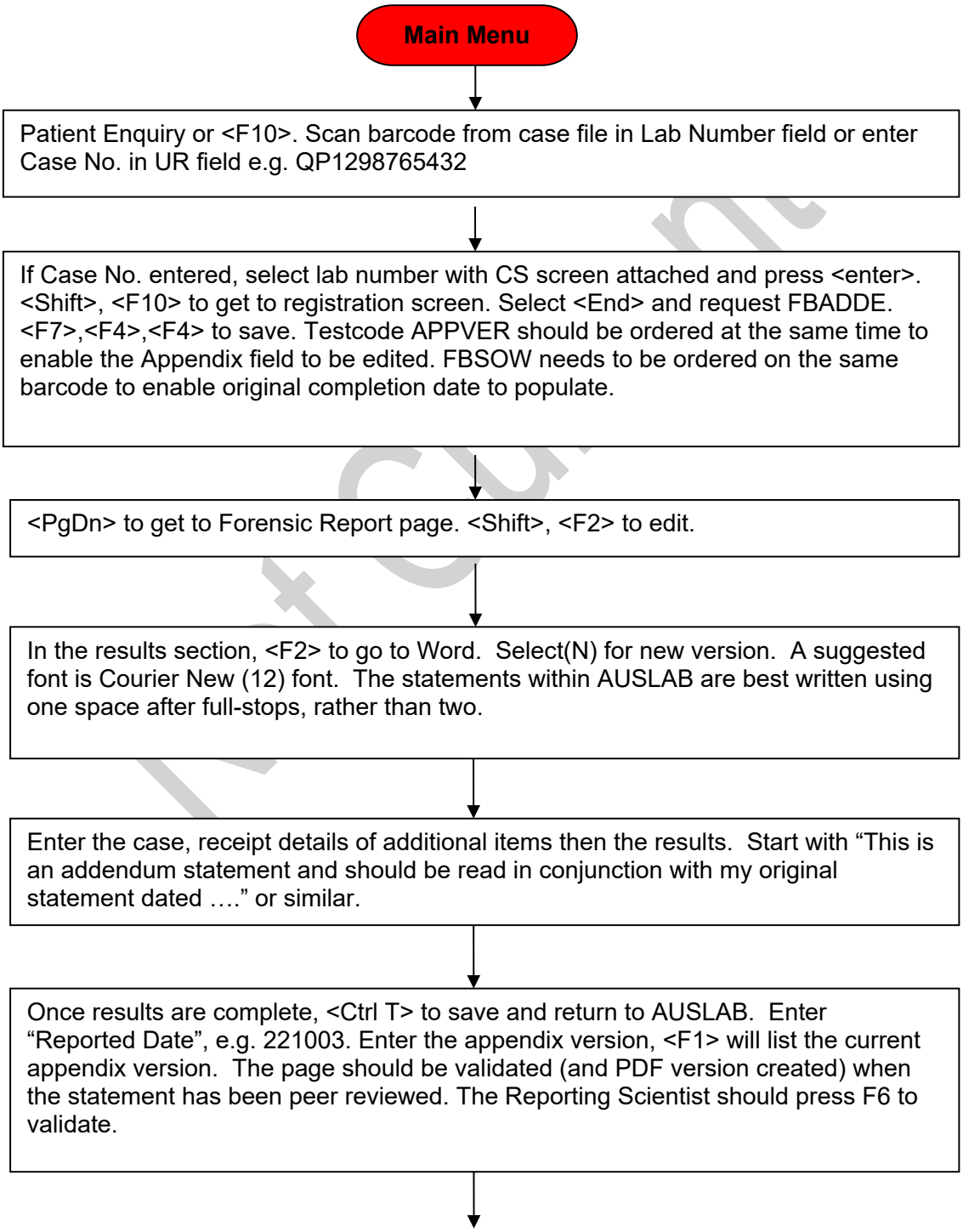
To review an exhibit report:



9.6 Creating an Addendum Statement in AUSLAB

Purpose: The test code FBADDE creates a statement without the receipt details automatically entered. All statement test codes include the scientist's details, and appendix details. This format is used for cases where an additional statement is being written.

To create an addendum statement:



If the FBADDE is a on a standalone barcode, in the ordered FBSOW, add the completed date in the same format as the FBADDE completed date (eg. DD/MM/YY or DDMMYY)

↓

To view statement, <Shift> <Insert>. To print, <Ctrl> <F11> and direct to a printer.

↓

NB. A new barcode should be requested in AUSLAB to record the review and release of the report (FBAR, FBTR and FBIOLR testcodes). The appropriate fields on the Case file Particulars form should be completed.

↓

NB. When an Addendum statement is being written, the Case Status should be changed to REACTIVATED. The status should change to SENT TO PEER, RETURNED FROM PEER and REPORT ISSUED as it progresses through review.

↓

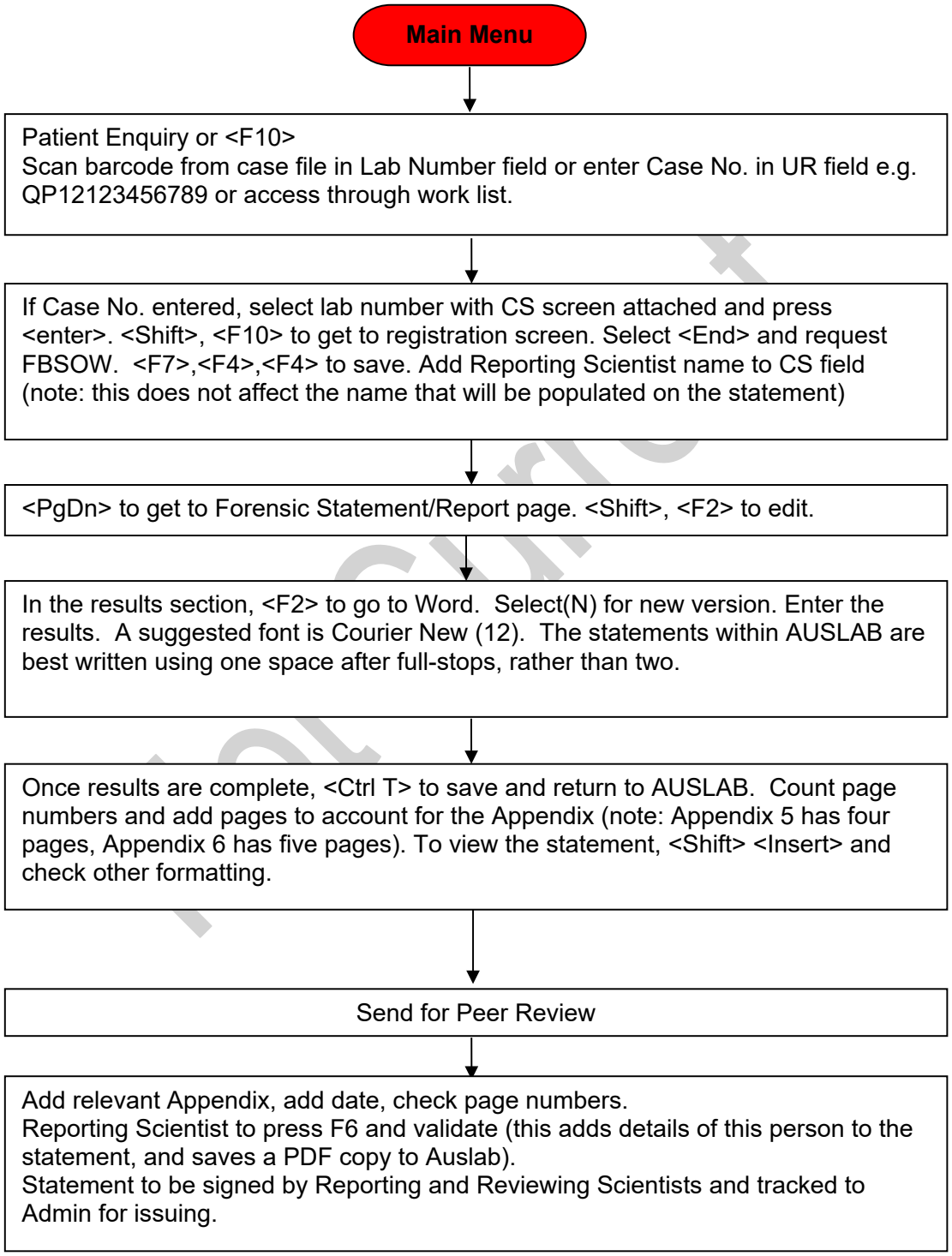
"Pause/Break" key to return to Main Menu

Not Current

9.7 Creating a Statement with Receipt Details in AUSLAB

Purpose: The test code FBSOW creates a statement with the receipt details automatically entered.

To create a statement with receipt details:



9.8 EXH Reporting (Sub-Sample No. Rules)

This appendix is for the process of reporting back results via EXHs, to the QPS DRMU for individual items. Note, the examples provided are relevant to Profiler® Plus interpretations and EXH lines. See 23008 Explanations of EXH Results for the complete list of EXHs relevant for Profiler® Plus and PowerPlex® 21 in conjunction with the use of STRmix™

- Since 1 July 2008, the bulk of the examinations have been performed by QPS. After their examinations, samples are received by Forensic DNA Analysis in-tubes. The barcode on the tubes relate to an EXH barcode and as such, the presumptive and final results are reported back on the single barcode.

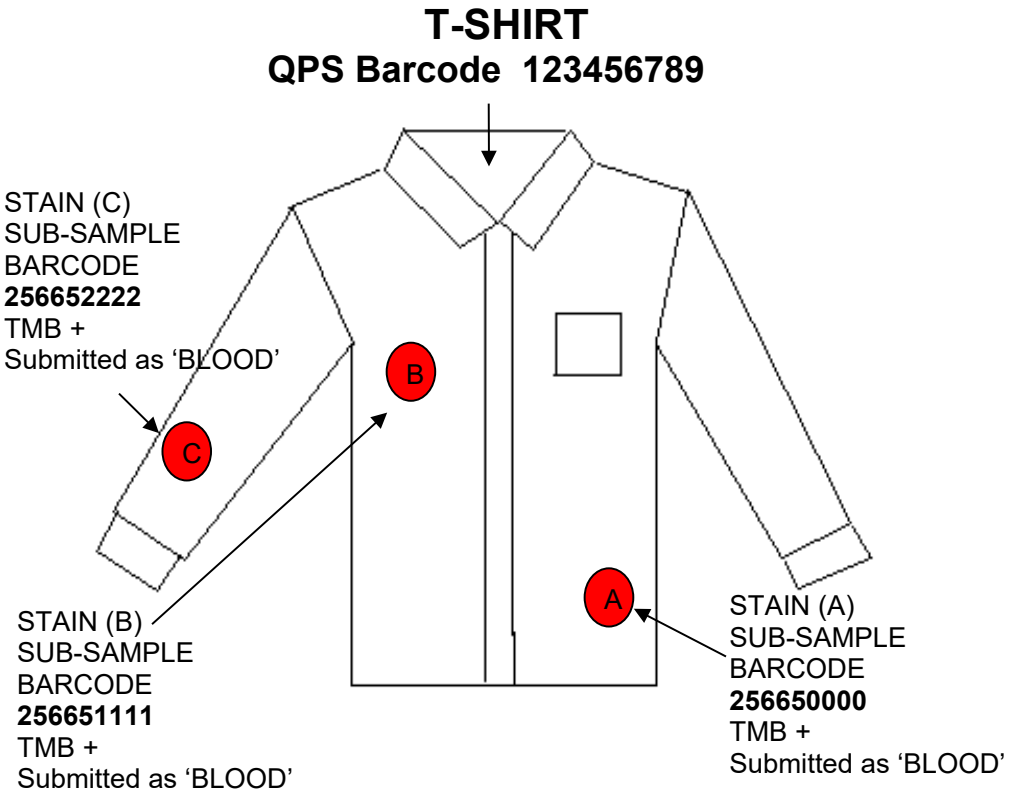
- Different scenarios have been included in examples given in the following pages. These scenarios relate to reporting of non-in tube cases, and the table format is as per EXH pages (excluding the 'Peer Review' column). For more information, refer to QIS 17142.

- Examples of different scenarios are depicted below. Some of these examples use Profiler® Plus interpretations (eg. '9Loci DNA profile'):

1. **One whole Item – multiple stains** - same presumptive result and only one type of extraction requested.
2. **One whole Item – multiple stains** - different presumptive results and two types of extractions requested.
3. **One whole Item – multiple stains** - different presumptive results (but with same extraction request) as well as three differing types of extractions requested.
4. **Swabs** – where no sub-sample barcode is required
5. **Cigarette Butts** – where no sub-sample barcode is required
6. **Sexual Assault Investigation Kits** (SAIK) & clothing
7. **Sexual Assault investigation Kits** (SAIK) – negative results.

Not Current

EXAMPLE 1.



EXH TEST CODE is **registered under 123456789 (T-SHIRT)**

Only sub-samples are used to report back presumptive tests & final results

Not Co

PRESUMPTIVE RESULTS

LAB NO.	Result/Status	Linked No.	Warm Linked Name
256650000	Presumptive blood test pos. Submitted – results pending		

Note as all three stains were TMB positive, only one presumptive test result needs to be entered. (Any one of the three sub-samples for the stains can be entered)

FINAL RESULTS

If all three DNA profiles are the same, then only one result needs to be reported back. If this is the case, then use the same sub-sample as used to originally report back the presumptive test results.

LAB NO.	Result/Status	Linked No.	Warm Linked Name
256650000	Presumptive blood test pos. Submitted – results pending		

256650000	9 loci DNA profile	20076738	COOPER

OR

If the sub-sample originally used is not the best profile, you still need to report back on it – but you will also need to add the sub-sample number which does give you the best profile.

LAB NO.	Result/Status	Linked No.	Warm Linked Name
256650000	Presumptive blood test pos. Submitted – results pending		
256650000	Partial DNA profile	20076738	COOPER
256651111	9 loci DNA profile	20076738	COOPER

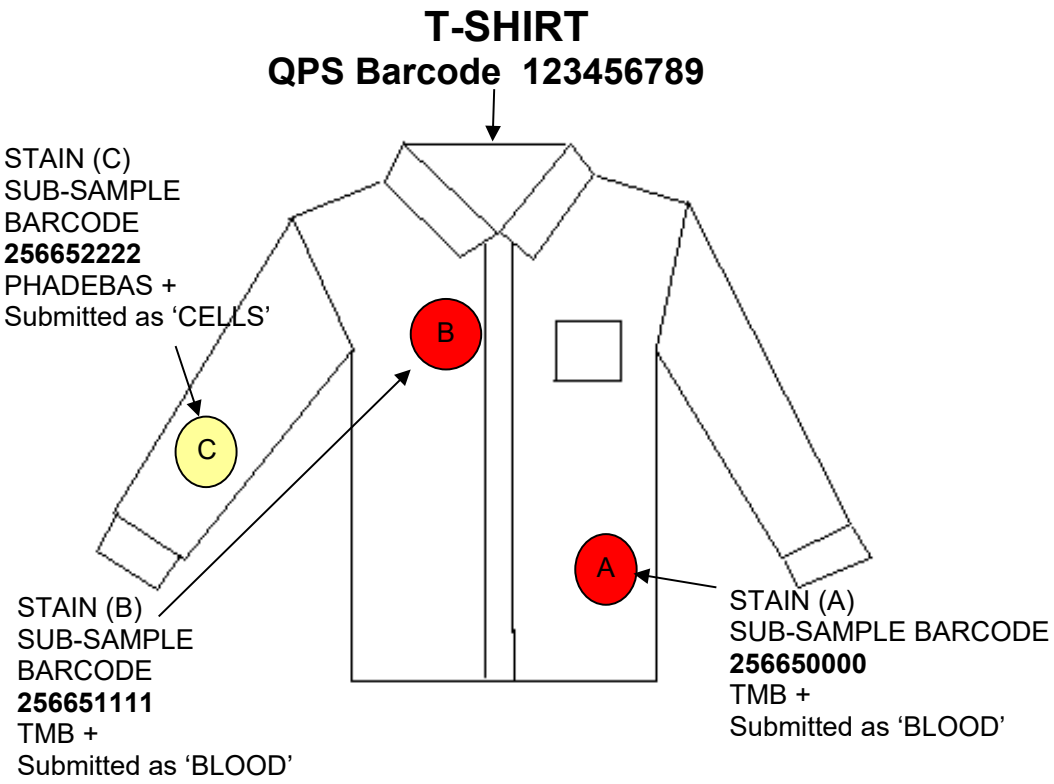
OR

If there are two or three differing DNA profiles resulting from the three stains submitted for analysis, then **report back all differing profiles** using their sub-sample barcodes (as above).

LAB NO.	Result/Status	Linked No.	Warm Linked Name
256650000	Presumptive blood test pos. Submitted – results pending		
256650000	9 loci DNA profile	20076738	COOPER
256651111	9 loci profile. Uploaded to NCIDD	UKM1	
256652222	9 loci profile. Uploaded to NCIDD	UKM2	

Not Current

EXAMPLE 2.



EXH TEST CODE is **registered under 123456789 (T-SHIRT)**

Only sub-samples are used to report back presumptive tests & final results.

PRESUMPTIVE RESULTS

LAB NO.	Result/Status	Linked No.	Warm Linked Name
256650000	Presumptive blood test pos. Submitted – results pending		
256652222	Presumptive saliva positive. Submitted – results pending		

Note as two stains were TMB positive, only one TMB+ presumptive test result is to be sent back to QPS DRMU for this item. Any one of the two sub-samples for the TMB+ stains can be entered (as above). A second presumptive result is sent back for the Phadebas + result as well.

FINAL RESULTS

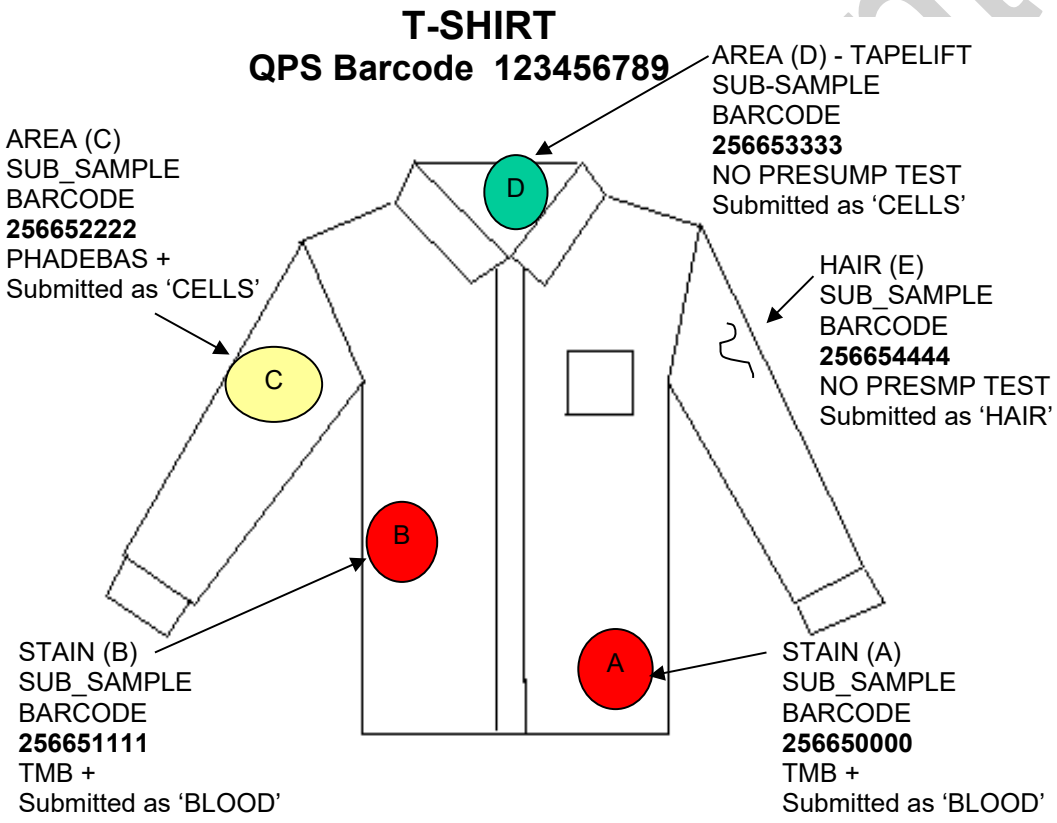
LAB NO.	Result/Status	Linked No.	Warm Linked Name
256650000	Presumptive blood test pos. Submitted – results pending		
256652222	Presumptive saliva positive. Submitted – results pending		

256650000	9 loci profile. Uploaded to NCIDD	03091930	ELLIS
256652222	9 loci profile	03091930	ELLIS
266651111	9 loci profile. Uploaded to NCIDD	05101929	JEFFREY

As two presumptive results were sent to DRMU initially, both the final results from these sub-samples need to be reported back – regardless if these profile end up being from the same source. By doing this DRMU can associate the resulting profiles to a possible cell source.

If the two samples submitted for the blood extraction result in the same DNA profile, then only one result needs to be reported back – use the same sub-sample as reported in the presumptive test results. If the profiles differ then both are reported back via their sub-samples.

EXAMPLE 3



EXH TEST CODE is **registered under 12345-6789 (T-SHIRT)**

PRESUMPTIVE RESULTS

LAB NO.	Result/Status	Linked No.	Warm Linked Name
256650000	Presumptive blood test pos. Submitted – results pending		

256652222	Presumptive saliva positive. Submitted – results pending		
256654444	Hair located. Submitted – results pending		

FINAL RESULTS

LAB NO.	Result/Status	Linked No.	Warm Linked Name
256650000	Presumptive blood test pos. Submitted – results pending		
256652222	Presumptive saliva positive. Submitted – results pending		
256654444	Hair located. Submitted – results pending		
256650000	9 loci DNA profile. Uploaded to NCIDD	2021958	GUGIO
256652222	Partial DNA profile	2021958	GUGIO
256654444	No DNA Profile		
256651111	9 loci DNA profile. Uploaded to NCIDD	UKF1	

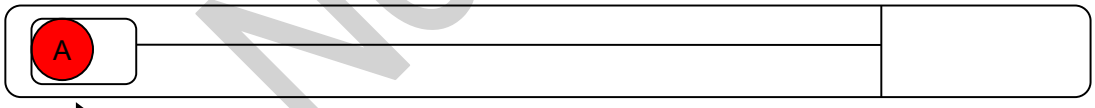
As three presumptive results were sent to DRMU initially, all three final results from these sub-samples need to be reported back – regardless if these profile end up being from the same source. By doing this DRMU can associate the resulting profiles to a possible cell source.

If the two samples submitted for the blood extraction result in the same DNA profile, then only one result needs to be reported back – use the same sub-sample as reported in the presumptive test results.

If the profiles differ then both are reported back via their sub-samples (as shown above).

EXAMPLE 4.

SWAB - QPS BARCODE 123456789



STAIN (A)
NO SUB NUMBER BARCODE GIVEN
TMB +
Submitted as 'BLOOD'

No sub-numbering required for this item as the entire sample is exhausted

PRESUMPTIVE AND FINAL EXH ON SWAB EXH BARCODE

LAB NO.	Result/Status	Linked No.	Warm Linked Name
123456789	Presumptive blood test pos. Submitted – results pending		

Not Current

123456789	9 loci DNA profile. Uploaded to NCIDD	16031989	ANDREW

EXAMPLE 5.

CIG BUTT - QPS BARCODE 12345-9999

AREA (A)
NO SUB NUMBER
BARCODE GIVEN
NO PRESUMPTIVE
TEST
Submitted as 'CELLS'

No sub-numbering required for this item

PRESUMPTIVE AND FINAL EXH ON CIGERETTE BUTT EXH BARCODE

LAB NO.	Result/Status	Linked No.	Warm Linked Name
123459999	Submitted results pending		
123459999	9 loci DNA profile. Uploaded to NCIDD	20071994	RON

EXAMPLE 6.

SAIK = QPS BARCODE 12345-6789

SAIK CONTAINS FIVE SWABS and TWO CLOTHING ITEMS (NOT BARCODED BY QPS)

A — SUB-BARCODE – 256650000 — HV SWAB
MICRO POS FOR SPERMATOZOA

B — SUB-BARCODE – 256651111 — LV SWAB
MICRO POS FOR SPERMATOZOA

Not Current

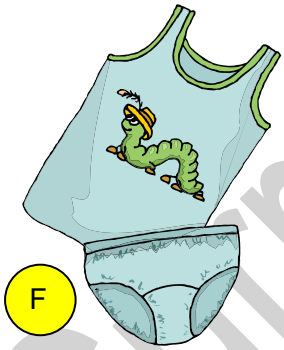
C — SUB-BARCODE – 256652222 — AP NEG MICRO NEGATIVE FOR SPERM — VULVAL SWAB

D — SUB-BARCODE – 256653333 — AP NEG MICRO NEGATIVE FOR SPERM — PERIANAL SWAB

E — SUB-BARCODE – 256654444 — AP NEG MICRO NEGATIVE FOR SPERM — RECTAL SWAB

TWO CLOTHING ITEMS:

SUB-BAROCDE: 256656666
ITEM: UNDERPANTS
AP POSITIVE
MICRO POS FOR SPERM



SUB –BARCODE: 256655555
ITEM: SINGLET TOP
AP NEGATIVE

Reporting back on SAIK via EXH registered under barcode 12345-6789.

PRESUMPTIVE RESULTS

	Result/Status	Linked No.	Warm Linked Name
256650000	Micro positive for sperm. Submitted results pending		
256655555	Semen not detected.		
25665-6666	Micro positive for sperm. Submitted results pending		

Note: only the high vaginal swab is reported back to QPS out of the five swabs submitted in the SAIK. In this example, three swabs share the same positive results and two swabs are negative. The EXH to QPS is reported back on the most probative of all the positive swabs – the high vaginal swab.

There is no need to report back the negative swabs results as these results do not add any information needed by QPS at this stage.

Both items of clothing also have their presumptive results reported back via the same SAIK EXH to QPS. The SAIK and the clothing have their own FBEXAM registered to record the examination details.

When the profile in the Epithelial fraction matches the donor, and is therefore not an unexpected finding, this result is not usually reported in the EXH.

Not Current

FINAL RESULTS

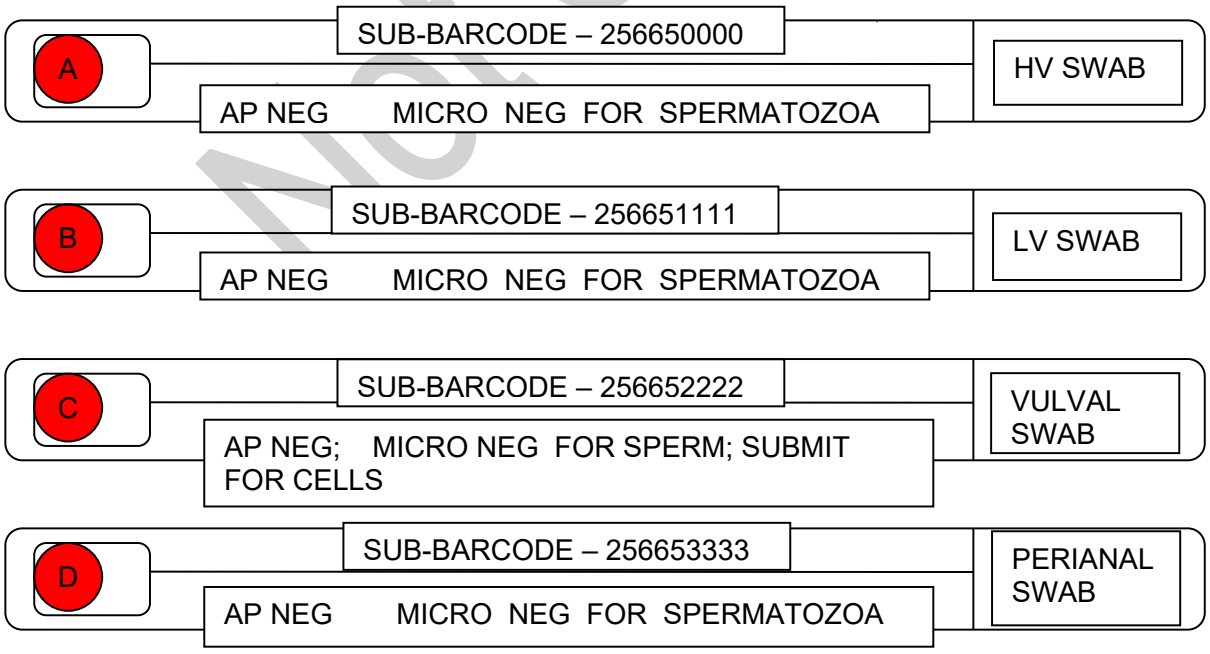
	Result/Status	Linked No.	Warm Linked Name
256650000	**Micro positive for sperm. Submitted results pending**		
256655555	**Semen not detected.**		
256656666	**Micro positive for sperm. Submitted results pending**		
256650000	Mixed profile, major component uploaded to NCIDD.	195000101	DEVON
256650000	Mixed profile, partial minor component.	20062654	CHILD
256651111	Mixed DNA profile, conditioned on.	20062654	CHILD
256651111	Mixed DNA profile. Remaining profile after conditioning.	1950000101	DEVON
256656666	Mixed part profile. No major/minor. Unable to load to NCIDD.		

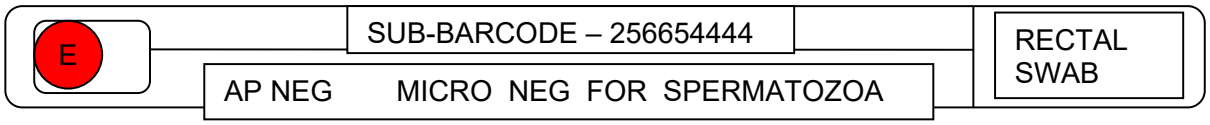
Not Current

EXAMPLE 7.

SAIK = QPS BARCODE 123456789

SAIK CONTAINS FIVE SWABS (NOT BARCODED BY QPS)





PRESUMPTIVE RESULTS

	Result/Status	Linked No.	Warm Linked Name
123456789	Semen not detected.		
256652222	Submitted as cells		

In this example, the five swabs were all negative for AP and microscopy, and the EXH has the parent barcode as the barcode entered to summarise that the whole item did not have semen detected. The two items of clothing are also reported back as negative to QPS. However, even though the vulval swab was also negative to all presumptive testing, it will still be submitted for a 'cell' extraction. DNA analysis is requested for the vulval swab as a last ditch effort, given both the SAIK and clothing are negative for all testing performed.

If QPS request an item for specific testing (eg blood) and the whole item was negative (eg Presump blood test neg), then the EXH will use the item/parent barcode to report back the results.

FINAL RESULTS

	Result/Status	Linked No.	Warm Linked Name
123456789	**Semen not detected.**		
256652222	**Submitted as cells**		
256652222	No DNA profile		

Not Current

9.9 Complete Casework Preamble – Examinations by QHFSS

XX. The following information is provided to assist in the understanding of the contents of this statement.

Forensic Biology

As a forensic biologist, it is my role to report on the examination of items submitted in relation to this 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. Any DNA profiles which are obtained from these samples are then compared with the DNA profiles obtained from an individual's reference sample.

Examinations

The examinations described in this Statement of Witness were carried out by colleagues. The notes, which have been referred to in the preparation of this report, were made at the time of examination. All examinations were performed in accordance with the SOPs of this laboratory.

Forensic DNA Analysis case files 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.

DNA Profiling

Please refer to the Appendix for an overview of DNA profiling.

Reference Samples

One or more reference sample/s provided for this case have been profiled using the PowerPlex®21 system, which tests twenty regions (loci) of DNA containing STRs, and an additional region which provides an indication of gender of the DNA source. All other item/s within this case have been profiled using the Profiler® Plus system (nine regions plus gender). Of the twenty regions of DNA that the PowerPlex®21 system tests, nine of them are the same as those tested using the Profiler® Plus system. Comparisons made between the reference sample/s and all other item/s within the case, and any statistical analyses undertaken, have been made based on the nine regions of DNA common to both systems.

Unknown DNA Profiles

If DNA profiles are obtained which do not match any of the reference DNA profiles associated to the case, they are considered to be of unknown origin. Where possible, these DNA profiles are assessed for gender, and then assigned sequential numerical designations (eg. Unknown Male 1, Unknown Male 2). If it is not possible to assign gender, the term Unknown Person is applied. Please note that numerical designations may be applied prior to the availability of reference DNA profiles. This means that if a reference DNA profile is found to match a DNA profile designated as Unknown Male 1, then Unknown Male 1 will not be referred to in the statement.

Not Current

Mixed DNA profiles *(Profiler® Plus only)*

When more than one person has contributed DNA to a sample, the DNA profile obtained is referred to as a mixed DNA profile. The mixture of DNA can happen in many ways, however the resultant DNA profile can often be explained in terms of the following categories:

Major / minor mixtures – these generally occur when one person contributes more DNA to a sample than another person. It is possible to resolve these mixtures into individual contributions, referred to as major and minor DNA profiles.

Even mixtures – these generally occur when two (or more) people contribute DNA to a sample in approximately equal proportions. It is not possible to determine individual contributions to these mixtures, unless we can assume a contribution of DNA from a particular person (this is referred to as 'conditioning').

Conditioning can be performed on mixed DNA profiles obtained from samples taken from body surfaces, intimate swabs or clothing, where the person / owner is clearly identified through information provided to the laboratory. In these circumstances it is not unexpected to find DNA that could have originated from that person in the sample. Therefore if it is assumed that this person has contributed DNA to the mixed DNA profile, then the components of their DNA profile can be effectively subtracted from the mixture. This may leave a remaining DNA profile which can be used for comparison purposes.

Note: If the relevant information provided to the laboratory changes, for example regarding the ownership of an item of clothing, then the interpretation of the mixture may change in that it may no longer be appropriate to condition the mixture.

Complex mixtures - this is when the DNA profile contains an unknown number of contributors, and / or provides too limited an amount of information for meaningful comparison purposes. In some cases it may be possible to compare the reference DNA profile of a person with the DNA components within these complex mixtures. If it appears that the person's DNA profile is represented within the complex DNA profile, then this person can be described as not being excluded as a potential contributor of DNA. In other cases the mixed DNA profile may be so complex or incomplete that it may not be possible to draw any conclusions as to whether a person may have contributed DNA. In these instances, the complex DNA profile may be deemed unsuitable for comparison purposes.

Note: Additional complexity may arise when interpreting mixed DNA profiles where multiple potential contributors of DNA to the mixture are genetically related. This is due to the increased potential for related individuals to share genetic information.

Touch DNA / Transfer of DNA

When a person touches a surface, it is possible for their cellular material to be transferred onto that surface. This transferred cellular material can often be recovered 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.

The generation of a DNA profile will depend on many factors. These include the amount of cellular material transferred, the nature of the surface being touched and the amount of cellular material a person has available to transfer.

Not Current

The persistence of any transferred cellular material on a surface will depend largely upon the nature of the surface and the conditions under which it has been kept in the time between deposition and recovery of the DNA. For example, cellular material could be lost from the surface by washing or mechanical action such as abrasion.

It therefore follows that the absence of a DNA profile from a touched surface does not necessarily mean that that person has not come into contact with it, as it is possible for a person to come into contact with a surface without a detectable amount of their DNA being transferred or recovered.

Blood stains

Potential blood stains 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

The presence of semen on an item can be indicated by the use of a presumptive chemical test which detects a major constituent of seminal fluid (Acid Phosphatase – AP). This constituent does, however, exist in other body fluids, such as vaginal secretions. Additional presumptive chemical testing (Prostate Specific Antigen – PSA / p30) can be undertaken and a positive reaction to both AP and PSA / p30 makes it highly likely that seminal fluid is present. The presence of semen can be confirmed via the microscopic identification of spermatozoa (sperm heads).

Samples may undergo a differential lysis extraction process which aims to separate spermatozoa and epithelial / cellular 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 intimate female SAIK samples to be stored following a Differential Lysis Extraction process. This is primarily due to the fact that when the vast majority of these fractions are profiled, they are found to match the person from whom the sample was taken. Given the intimate nature of these samples, this finding is not unexpected. These epithelial fractions will be 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. Any semen which 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 likelihood 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.

Not Current

The greater the delay between deposition and sampling, the less chance there is of finding semen. 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 which 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.

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 fluids and anal secretions, although usually at much lower concentration than that found in saliva.

If an area of the body is sucked or licked, saliva may be transferred onto the skin and subsequently onto any items of clothing worn on this area of the body. Saliva may also be transferred by actions such as spitting. Saliva staining, in the form of amylase may then be detected on skin swabs or items of clothing as long as the clothing or skin has not been washed. Cellular material will be shed, to varying degrees, with the saliva and as such it may be possible to obtain a DNA profile from an area of saliva staining.

XX. The results of the scientific examinations conducted in this laboratory are as follows:

Not Current

9.10 Complete Casework Preamble – Examinations by QPS and QHFSS

XX. The following information is provided to assist in the understanding of the contents of this statement.

Forensic Biologist

As a forensic biologist, it is my 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 which are obtained from these samples are then compared with the DNA profiles obtained from an individual's reference sample.

Examinations and DNA Profiling *(PowerPlex® 21 only)*

Please refer to the Appendix for an overview of DNA profiling.

Forensic DNA Analysis case files 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.

Examinations *(Profiler® Plus only)*

Unless otherwise stated, the examinations of items for biological material were conducted by officers within the QPS. Sub-samples from these items were forwarded to Queensland Health Forensic and Scientific Services (QHFSS) for the purposes of conducting DNA analysis.

Samples submitted to QHFSS for DNA analysis may include swabs, tape-lifts or small sections of material cut from an exhibit. Individual samples are typically submitted within small plastic tubes and are referred to as 'in-tube' samples.

It is my understanding that the QPS are responsible for item prioritisation, sample selection, selection of screening / sampling methods, application of anti-contamination and standard operating procedures (SOPs) on work undertaken on the items / samples prior to submission to QHFSS. As such, forensic biologists may not be able to provide information or opinion on the possible biological origin of any 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, notes are made at the time of the examination by the examining scientist and form part of the case file.

Forensic DNA Analysis case files and any samples remaining are available for independent examination and / or testing upon request.

Not Current

As a representative of the laboratory, I am only able to comment on the processes performed within Forensic DNA Analysis.

DNA Profiling ***(Profiler® Plus only)***

Please refer to the Appendix for an overview of DNA profiling.

Reference Samples

One or more reference sample/s provided for this case have been profiled using the PowerPlex®21 system, which tests twenty regions (loci) of DNA containing STRs, and an additional region which provides an indication of gender of the DNA source. All other item/s within this case have been profiled using the Profiler® Plus system (nine regions plus gender). Of the twenty regions of DNA that the PowerPlex®21 system tests, nine of them are the same as those tested using the Profiler® Plus system. Comparisons made between the reference sample/s and all other item/s within the case, and any statistical analyses undertaken, have been made based on the nine regions of DNA common to both systems.

Unknown DNA Profiles

If DNA profiles are obtained which do not match any of the reference DNA profiles associated to the case, they are considered to be of unknown origin. Where possible, these DNA profiles are assessed for gender, and then assigned sequential numerical designations (eg. Unknown Male 1, Unknown Male 2). If it is not possible to assign gender, the term Unknown Person is applied. Please note that numerical designations may be applied prior to the availability of reference DNA profiles. This means that if a reference DNA profile is found to match a DNA profile designated as Unknown Male 1, then Unknown Male 1 will not be referred to in the statement.

Mixed DNA profiles (*Profiler® Plus only)*

When more than one person has contributed DNA to a sample, the DNA profile obtained is referred to as a mixed DNA profile. The mixture of DNA can happen in many ways, however the resultant DNA profile can often be explained in terms of the following categories:

Major / minor mixtures – these generally occur when one person contributes more DNA to a sample than another person. It is possible to resolve these mixtures into individual contributions, referred to as major and minor DNA profiles.

Even mixtures – these generally occur when two (or more) people contribute DNA to a sample in approximately equal proportions. It is not possible to determine individual contributions to these mixtures, unless we can assume a contribution of DNA from a particular person (this is referred to as ‘conditioning’).

Conditioning can be performed on mixed DNA profiles obtained from samples taken from body surfaces, intimate swabs or clothing, where the person / owner is clearly identified through information provided to the laboratory. In these circumstances it is not unexpected to find DNA that could have originated from that person in the sample. Therefore if it is assumed that this person has contributed DNA to the mixed DNA profile, then the components of their DNA profile can be effectively subtracted from the mixture. This may leave a remaining DNA profile which can be used for comparison purposes.

Not Current

Note: If the relevant information provided to the laboratory changes, for example regarding the ownership of an item of clothing, then the interpretation of the mixture may change in that it may no longer be appropriate to condition the mixture.

Complex mixtures - this is when the DNA profile contains an unknown number of contributors, and / or provides too limited an amount of information for meaningful comparison purposes. In some cases it may be possible to compare the reference DNA profile of a person with the DNA components within these complex mixtures. If it appears that the person's DNA profile is represented within the complex DNA profile, then this person can be described as not being excluded as a potential contributor of DNA. In other cases the mixed DNA profile may be so complex or incomplete that it may not be possible to draw any conclusions as to whether a person may have contributed DNA. In these instances, the complex DNA profile may be deemed unsuitable for comparison purposes.

Note: Additional complexity may arise when interpreting mixed DNA profiles where multiple potential contributors of DNA to the mixture are genetically related. This is due to the increased potential for related individuals to share genetic information.

Touch DNA / Transfer of DNA

When a person touches a surface, it is possible for their cellular material to be transferred onto that surface. This transferred cellular material can often be recovered 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.

The generation of a DNA profile will depend on many factors. These include the amount of cellular material transferred, the nature of the surface being touched and the amount of cellular material a person has available to transfer.

The persistence of any transferred cellular material on a surface will depend largely upon the nature of the surface and the conditions under which it has been kept in the time between deposition and recovery of the DNA. For example, cellular material could be lost from the surface by washing or mechanical action such as abrasion.

It therefore follows that the absence of a DNA profile from a touched surface does not necessarily mean that that person has not come into contact with it, as it is possible for a person to come into contact with a surface without a detectable amount of their DNA being transferred or recovered.

Blood stains

Potential blood stains 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

The presence of semen on an item can be indicated by the use of a presumptive chemical test which detects a major constituent of seminal fluid (Acid Phosphatase – AP). This constituent does, however, exist in other body fluids, such as vaginal secretions. Additional presumptive chemical testing (Prostate Specific Antigen – PSA / p30) can be undertaken and a positive reaction to both AP and PSA / p30 makes it highly likely that seminal fluid is present. The presence of semen can be confirmed via the microscopic identification of spermatozoa (sperm heads).

Not Current

Samples may undergo a differential lysis extraction process which aims to separate spermatozoa and epithelial / cellular 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 intimate female SAIK samples to be stored following a Differential Lysis Extraction process. This is primarily due to the fact that when the vast majority of these fractions are profiled, they are found to match the person from whom the sample was taken. Given the intimate nature of these samples, this finding is not unexpected. These epithelial fractions will be 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. Any semen which 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 likelihood 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.

The greater the delay between deposition and sampling, the less chance there is of finding semen. 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 which 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.

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 fluids and anal secretions, although usually at much lower concentration than that found in saliva.

If an area of the body is sucked or licked, saliva may be transferred onto the skin and subsequently onto any items of clothing worn on this area of the body. Saliva may also be transferred by actions such as spitting. Saliva staining, in the form of amylase may then be detected on skin swabs or items of clothing as long as the clothing or skin has not been washed. Cellular material will be shed, to varying degrees, with the saliva and as such it may be possible to obtain a DNA profile from an area of saliva staining.

XX. The results of the scientific examinations conducted in this laboratory are as follows:

Not Current

9.11 Complete Paternity Preamble

XX. The following information is provided to assist in the understanding of the contents of this statement.

Forensic Biology

As a Forensic Biologist, it is my role to report on the examination of items submitted in relation to this 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. Any DNA profiles which are obtained from these samples are then compared with the DNA profiles obtained from an individual's reference sample.

Examinations

The examinations described in this Statement of Witness were carried out by colleagues. The notes, which have been referred to in the preparation of this report, were made at the time of examination. All examinations were carried out in accordance with Standard Operating Procedures.

DNA Profiling

DNA is a complex chemical found in almost all cells in the human body. It carries genetic information which determines the physical and chemical characteristics of a person. The DNA system used at Queensland Health looks at 10 regions of DNA, 9 of which contain Short Tandem Repeats (STRs). The tenth region gives an indication as to the gender of the donor.

Or, if PowerPlex® 21 was used for all samples:

DNA is a complex chemical found in almost all cells in the human body. It carries genetic information which determines the physical and chemical characteristics of a person. The DNA system used at Queensland Health looks at 21 regions of DNA, 20 of which contain Short Tandem Repeats (STRs). The twenty-first region gives an indication as to the gender of the donor.

Two DNA components (alleles) are detected at each region of DNA tested. This total of 18 alleles *(or 40 alleles),* plus gender information, comprises an individual's DNA profile. Of the two alleles detected at each of the regions tested, one is inherited from an individual's biological mother, and the other component is inherited from an individual's biological father.

Reference Samples (NB, Remove if all samples profiled with PowerPlex® 21).

One or more reference sample/s provided for this case have been profiled using the PowerPlex®21 system, which tests twenty regions (loci) of DNA containing STRs, and an additional region which provides an indication of gender of the DNA source. All other item/s within this case have been profiled using the Profiler® Plus system (nine regions plus gender). Of the twenty regions of DNA that the PowerPlex®21 system tests, nine of them are the same as those tested using the Profiler® Plus system. Comparisons made between the reference sample/s and

Not Current

all other item/s within the case, and any statistical analyses undertaken, have been made based on the nine regions of DNA common to both systems.

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 mother is indeed the biological mother of the foetus/child, it is possible to determine which DNA components within the DNA profile of the child could have originated from her. The remaining DNA components within the DNA profile of the foetus/child must have originated from the biological father, and are called *obligate paternal alleles*.

If the DNA profile of a putative father **does not** contain the obligate paternal alleles in at least two of the DNA regions tested, then that person 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 that person is **not excluded** as a potential biological father of the foetus/child. This means that this putative father could indeed be the biological father.

Statistical analysis is then conducted to aid in the understanding of the strength of the evidence. The Paternity Index (PI) is a likelihood of two probabilities conditional upon different competing hypotheses;

1. The alleged father contributed the obligate paternal alleles observed in the DNA profile of the foetus/child

2. Another man chosen at random contributed the obligate paternal alleles observed in the DNA profile of the foetus/child.

The PI reflects how many times more likely it is to see the evidence (ie. Set of alleles) under the first hypothesis compared to the second hypothesis. The generally accepted minimum standard for an inclusion of paternity is a PI of 200 or greater (NATA Paternity Testing Technical Advisory Group, 2004).

(Adapted from Butler, J.M. (2005) Chapter 23, *Kinship and Parentage Testing in* Forensic DNA Typing, Biology, Technology, and Genetics of STR Markers, 2 Ed. Elsevier Academic Press: Burlington, MA 01803, USA.)

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.

Not Current

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.

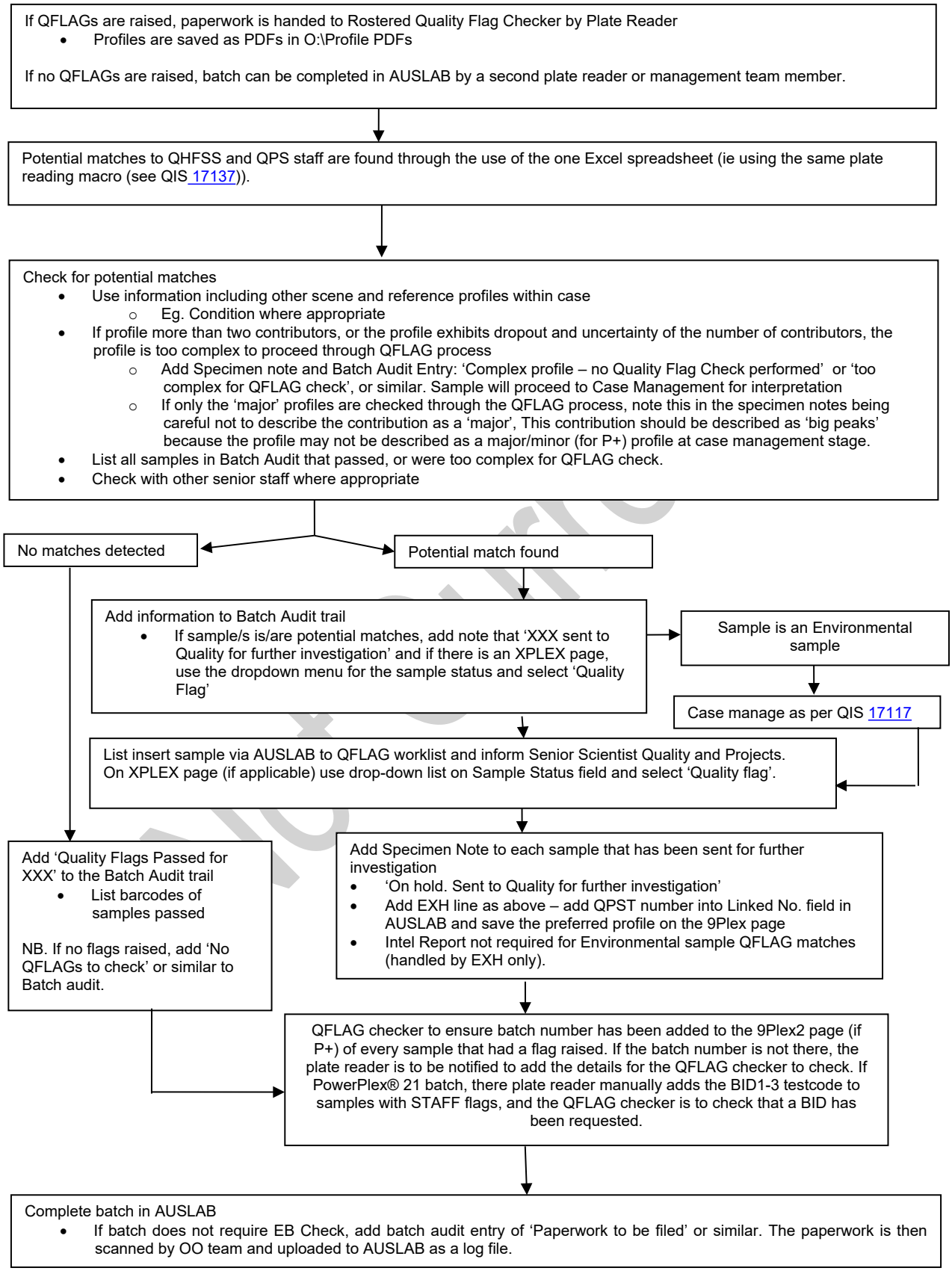
XY possesses all of the obligate paternal alleles. In my opinion, it is possible that XY is the biological father of CC given that XX is the natural mother. The following statistical weighting has been calculated in support of this opinion:

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>.

Not Current

Not Current

9.12 Quality Flag Checking Workflow



Notes on the Quality Flag Checking Process:

- Quality Flag Checking is to detect gross contamination that could have occurred at collection or during processing of the sample.
    - This includes single-source profiles, distinct major or minor profiles, or remaining contributions if the mixed profile has been conditioned.

- Due to the complexity of some DNA profiles, profiles that indicate at least three contributors (and therefore an unknown number of contributors) are generally not suitable for Quality Flag checking for the following reasons:
    - The number of contributors is not known and the often partial nature adds complexity.
    - At most, a person may not be able to be excluded as a potential contributor and this interpretation may not be useful to the client as we cannot evaluate the significance of a possible inclusion by adding statistical weight for Profiler Plus profiles.
    - For PowerPlex® 21 profiles, a STRmix™ evaluation is possible, yet the LR value obtained requires a subjective assessment for QPS to determine likelihood of contributing DNA to the mixture. Caution should be exercised and this can be done by searching and reporting gross contaminations.

- When profiles of at least three contributors are obtained, the Quality Flag Checker should note in the Batch Audit and the Specimen Notes:
    - 'Complex profile – no Quality Flag check performed' or similar wording
    - The profile will then proceed to case management for interpretation with case context.

- It may be possible for the higher RFU peaks (if demonstrating a pattern as such across the profile) to be QFLAG checked.
    - If the peaks pass, write in the Batch Audit and Specimen Notes: 'Big peaks passed QFLAGs. Small peaks too complex for QFLAG checking' or similar wording
    - Refrain from using 'Major/Minor' terminology because the Case Manager may interpret the profile not to be a major/minor profile (vis. PowerPlex® 21 profiles).

- The macro that is applied to detect potential Quality Flags has a stringency of 13 alleles. This means, crime scene profiles with less than 13 alleles detected will not go through the macro and therefore will not be Quality Flag checked.

- If a profile with less than 13 alleles is obtained, this may be checked by the Quality Team as a separate comparison to the QFLAG process. List insert the sample to BQUAL worklist in AUSALB and provide instructions in the Specimen Notes.

- If there are more than 6 alleles at a locus for P+ DNA profiles, there is too much information to be exported from GMID-x and the profile will need further quality checking at case management stage.
    - If the profile is determined to be 'complex unsuitable', then the profile would have been too complex for QFLAG checking.
    - If the profile is 'suitable' for comparison (eg. 'complex cannot exclude'), then a further assessment is made:
        - If there is a 'major' within the first six alleles, then this would have gone through the QFLAG check process – no further work is required.
        - If there are 'major' peaks outside the first six alleles and therefore not captured in the table, this this contribution will need a separate comparison outside the QFLAG process through the Quality Team. List insert the sample to BQUAL and provide instructions in the Specimen Notes in AUSLAB.

- If an EB check is required to check for cross-sample contamination in locked batches (eg. GMPCW…):

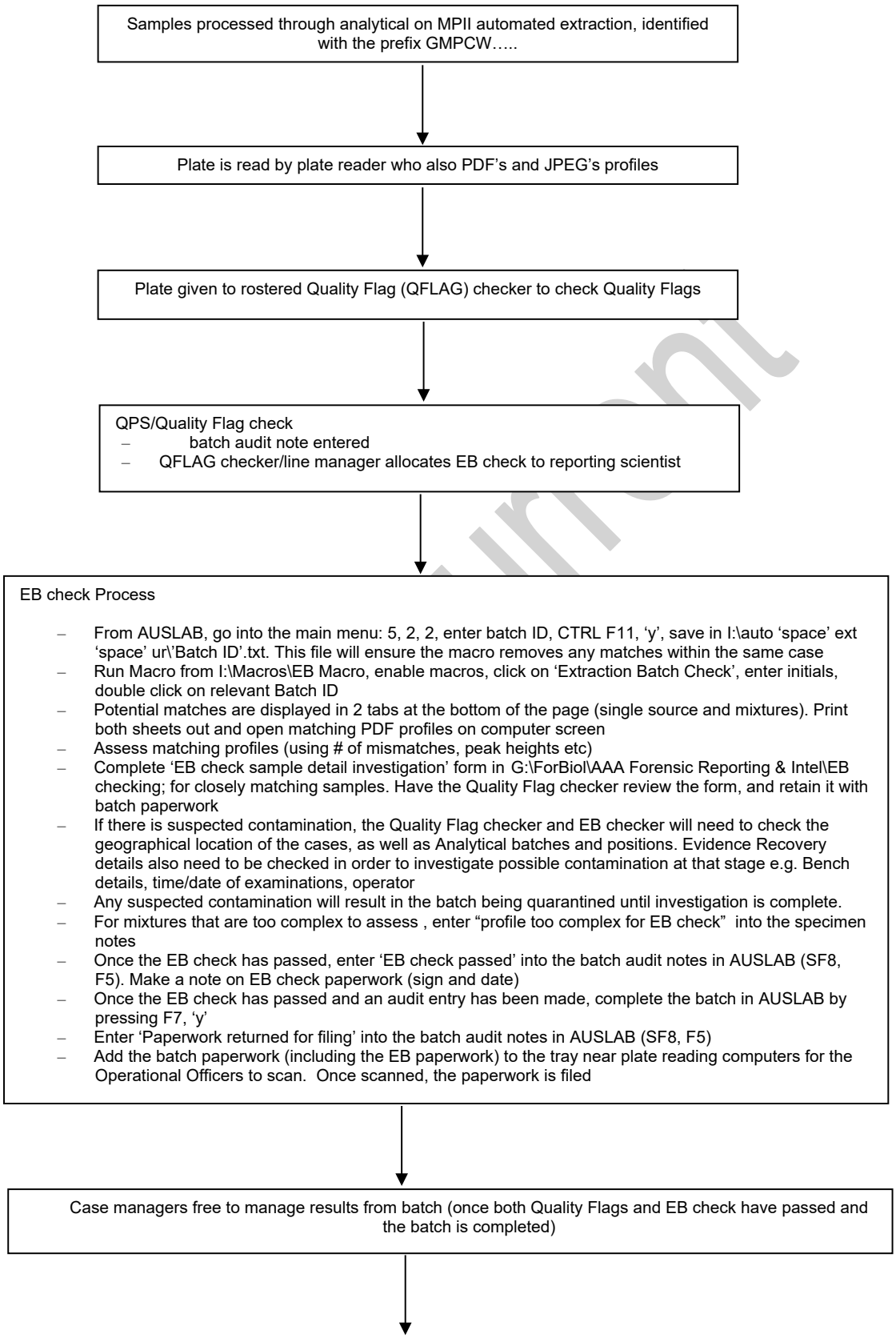
Not Current

- Write ‘Paperwork given to EB Checker/checking team’ or similar, and deliver paperwork to Senior Scientist on the rotation that includes EB Check, or delegate.
- If batch does not require EB Check, add batch audit entry of ‘Paperwork to be filed’ or similar. The paperwork is then scanned by OO team and uploaded to AUSLAB as a log file.

- Once comments from both Quality Flag checker and EB checker have been entered and no remaining flags are to be investigated, the person performing the last of the above tasks is to complete the batch (F7in AUSLAB on batch).

Not Current

9.13 Extraction Batch Checking Workflow (EB Checking)



Case managers to manage rework results (>6 alleles) and perform EB check on samples that were originally extracted on the MPII automated platforms

- access EB Macro
- enter details into fields (sample ID, profile obtained, reader comments) in 'Update and Check from Rework' section
- click on 'Update and check'
- find the original GMPCW 9PLEX batch
- assess updated profile against matches
- if sample passed, enter specimen note 'EB check for rework performed – passed'
- If EB check not completed, enter a specimen note indicating the reason
- file rework EB check paperwork in date order in the blue folder next to the printer

EB Macro Notes:

- The Extraction Batch macro is performed before results are case managed and released to the QPS. It allows for the detection of contamination between samples that we extracted on the same automated MPII extraction batch. These batches are identified by GMPCW…..
- It compares profiles from different cases that have greater than 6 alleles against each other.
- Matches are assessed by the reporting scientist, considering both samples as the potentially contaminating and contaminated profiles.
- The EB macro divides and displays any potential matches into single source and mixtures, in two separate tabs.
- The profile highlighted in white is the profile that the profiles underneath have matched to.
- The macro displays matching loci in different colours: green indicates that there are at least 2 matching alleles, yellow indicates 1 matching allele, light orange indicates a mismatch at the entire loci, and bright orange indicates a mismatch at Amelogenin.
- The EB check can be performed at any desk. The profile highlighted in white is to be printed off, and the profiles matching to it can be displayed on the computer screen so that comparisons can be made.
- Once samples have been reworked, the reworked result needs to be checked against the batch the sample was originally extracted on. If the 9plex result is used as the reported profile; or the rework result is the same, similar, has less information or is too complex, a rework EB check is not necessary. This is assessed by the case manager, and a specimen note added with the reason the EB check was not performed.

Not Current

9.14 General DNA Evidentiary Certificate Workflow

Receive written request and clarify which samples are required to be included.

↓

Ensure that there is adequate time to complete audit trails and issue certificate at least 10 days before court date – negotiate with IO/DPP if required.
Timeframes approx. 4 weeks for Evidentiary Certificate alone, 6 weeks if requested at the same time as a statement.

↓

Create Evidentiary checklist using:
QIS 30799: DNA Evidentiary Certificate Checklist
Follow instructions on Worksheet entitled: 'Instructions'
The minimum requirement is to check the electronic records of samples and batches in AUSLAB.

↓

Work through each sample and the relevant batches, looking at audit trail in AUSLAB to see if any issues have been raised. eg sample removed has not transferred yet, pos control is partial profile, failure of batch due to controls not working/OQI.
If you have examined the records relating to the receipt, storage and testing of the things covered by the Evidentiary Certificate, by 'checking' the boxes, you are confirming that the Quality Assurance Procedures relevant to the above at the time of testing were complied with.

If in examining the records, something needs to be addressed, notify your Senior Scientist and/or Team Leader to co-ordinate a possible investigation.

↓

Check storage audit trail for each sample, noting that there should be two final locations for most samples – one for spin basket and one for final amplified product. Ensure that throughout the audit trail, sample has been added and removed from particular location as it works its way through the process.

↓

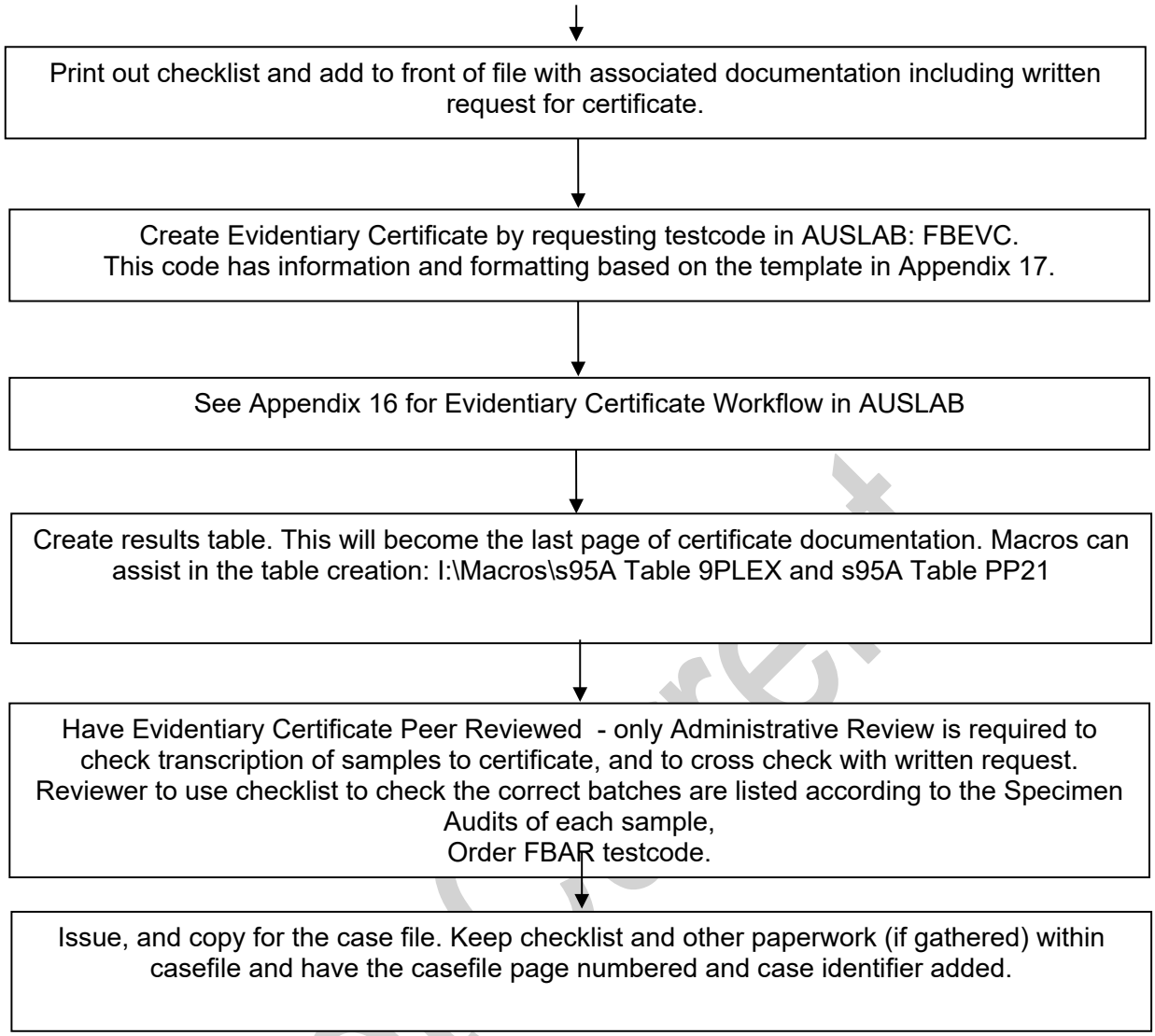
As a minimum, AUSLAB audit trails can be checked for departures from the standard operating procedure. If required, the batch paperwork is scanned into the batches as 'log' files and can be checked by the following:

enter into batch □ Shift F6 ('Files') □ scroll to 'Log' □ Export file to location to be retrieved □ view .PDF

↓

If the paperwork is not complete, get original paperwork correction signed and dated or whatever is required. If this staff member is on holidays, or no longer working in department, get their Senior to sign and date on their behalf.

↓


Print out checklist and add to front of file with associated documentation including written request for certificate.
Create Evidentiary Certificate by requesting testcode in AUSLAB: FBEVC.
This code has information and formatting based on the template in Appendix 17.
See Appendix 16 for Evidentiary Certificate Workflow in AUSLAB
Create results table. This will become the last page of certificate documentation. Macros can assist in the table creation: I:\Macros\s95A Table 9PLEX and s95A Table PP21
Have Evidentiary Certificate Peer Reviewed - only Administrative Review is required to check transcription of samples to certificate, and to cross check with written request.
Reviewer to use checklist to check the correct batches are listed according to the Specimen Audits of each sample,
Order FBAR testcode.
Issue, and copy for the case file. Keep checklist and other paperwork (if gathered) within casefile and have the casefile page numbered and case identifier added.

Not Current

9.15 DNA Evidentiary Certificate (and Appendix v5)

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 …

10. 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.

Not Current

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.

Not Current

APPENDIX 1

Procedural overview for the DNA Analysis Unit, Queensland Health Forensic and Scientific Services (QHFSS)

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.
For details of the current ISO/IEC 17025 Field Application Document, Forensic Science, Supplementary requirements for accreditation, please refer to the NATA website:
http://www.nata.asn.au/publications

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 DNA Analysis Unit of Queensland Health Forensic and Scientific Services (QHFSS)

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.

Not Current

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.

Not Current

DNA (STR) profiling systems available at the DNA Analysis Unit, Queensland Health Forensic and Scientific Services (QHFSS)

Table 1: Profiler® Plus multiplex system, list of loci:

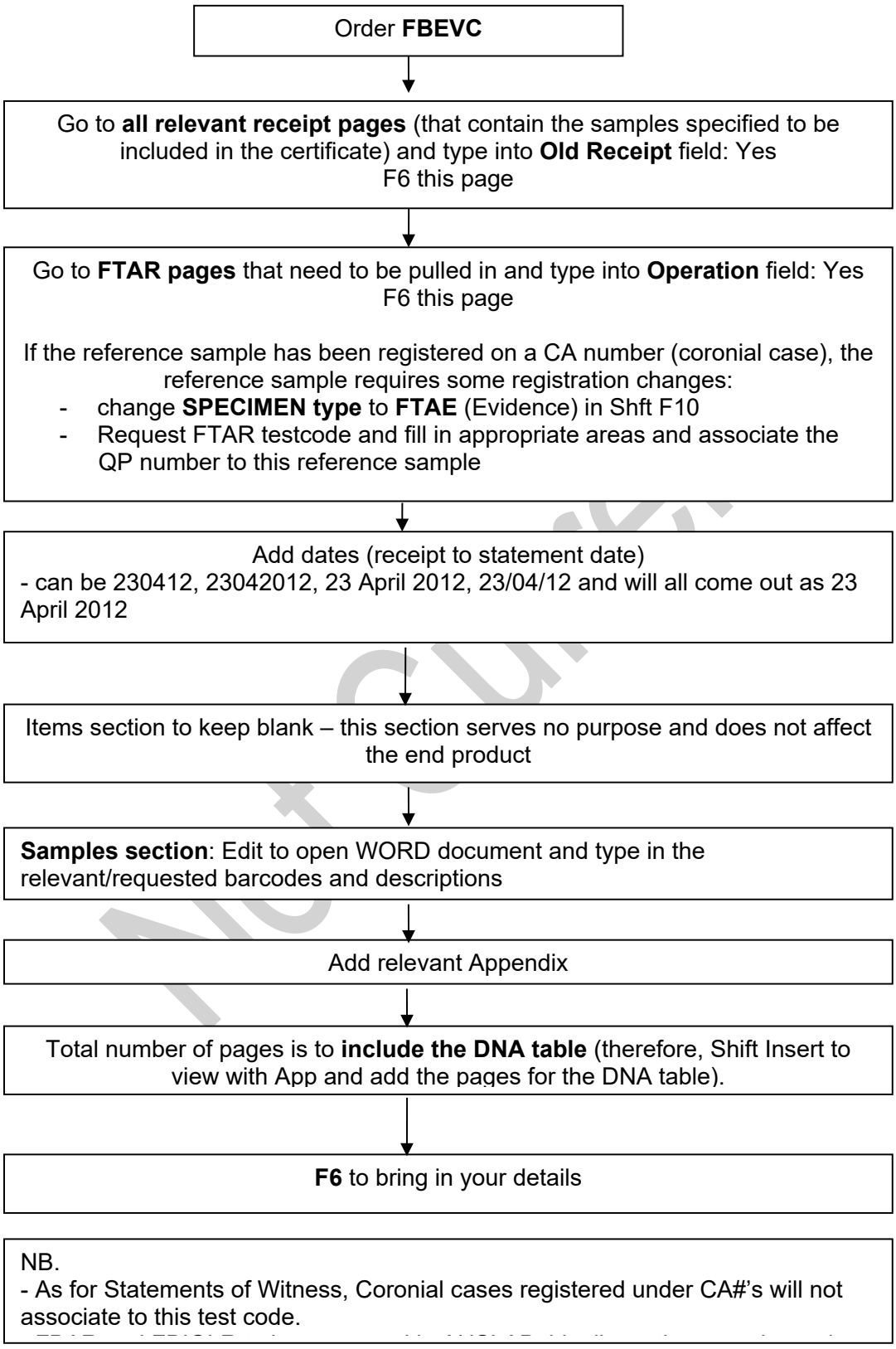
Abbreviated Name	Scientific Name	Chromosomal Name
D3	D3S1358	3
vWA	HUMVWFA31/A	12
FGA	HUMFIBRA	4
Amel	AMELOGENIN	Sex X and Y
D8	D8S1179	8
D21	D21S11	21
D18	D18S51	18
D5	D5S818	5
D13	D13S317	13
D7	D7S820	7

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

Not Current

9.16 DNA Evidentiary Certificate Workflow in AUSLAB



9.17 Suggested PowerPlex® 21 (and STRmix™) statement wording

NOTE 1:
When wording your statements 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	**123456789**	**Swab (A), near rear door**
	123456789	**Swab (D), floor in foyer near charge counter**

Not Current

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

123456789 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

123456789 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

Not Current

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

123456789 Graph 21; swab; pop bottle

This sample contained insufficient DNA to be suitable for analysis and was not tested further.

No DNA Detected

123456789 Graph 9; swab; cot
123456789 Graph 2; swab; flyscreen

DNA was not detected in these samples and therefore they were not tested further.

Complex – no STRmix

Not Current

123456789 Graph 11; swab; right thong
123456789 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

123456789 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.

Not Current

9.18 QFLAG workflow for Quality Team (when a possible match is identified)

Preparing QFLAG Intel Report:

1. Print QFLAG profile and associated “Matching” profile (i.e. QPSTF profile) for visual assessment/evaluation.
2. Using the report template prepare an appropriate Intel report (refer to I:\Quality & Projects\Intelligence reports or Intel report folder - for examples)
3. Complete EXH: Add case manager, save preferred profile, add EXH (eg. QFIH) with QPSTF laboratory number (if applicable) in Link# Field
4. Add “Refer to Specimen Note” in 9PLEX/XPLEX comment, and add specimen note to indicate possible quality issue.
5. Register new barcode AUSLAB [1], [1] FULL Reception Entry with the sample UR number as the QFLAG EXH barcode
a.Specimen type=Case
b. Add FBINTL, FBAR and FBIOLR test codes
6. Enter into newly registered barcode (ensure Microsoft Word is NOT open)
a. On INTEL report page [F2] in word document section to create new word document [E]. (for subsequent drafts save a new version “N”)
b. Paste in word draft of document (ensure at least one carriage return between each paragraph. [Ctl][T] to upload to word file back into AUSLAB
c. Add contact QPS Name and Address (as per previous INTEL reports) and Name of Forensic DNA Analysis peer reviewer and position. DO NOT ADD date of report or date of review until after it has been checked – draft version.
d. Check Intel report using [Shft][Ins]
e. [F6] to validate
f. Print a copy [Shft F11] and provide to reviewer (with profiles).

Review and sending of QFLAG Intel report:

When draft is approved by the reviewer:
1. Add date of report and date of peer review and [F6] to validate. *This creates a PDF of the report – viewable by [Ctl][Ins]. (If further edits are required after review dates are added, delete review dates, edit document then re-add review dates and validates, this creates a new PDF Intel report)
2. Reviewer to validate QFIH EXH, 9PLEX/XPLEX and complete FBAR
3. Print Intel report, and have it signed by quality and reviewer.
4. Completed and signed PDF Intel report to be and scanned and emailed to QPS (by QPS email account only)
5. Add specimen note “Quality Flags noted with sample to QPS Elimination sample. Intel report regarding Quality flags sent to [Insert QPS Staff Name] for action”
6. Complete FBIOLR page with:
a. Posted to: [Insert email recipient]
b. Of: [DNA Management Section]
c. QHSS Officer Posting: [Insert email sender]
d. Date of Posting: [Insert date of sending]
e. [F6] to validate

QPS reply to QFLAG Intel reports:

Not Current

QPS will email back with investigation findings, following actions required:
1. Specimen note detailing QPS investigation findings (eg. “Email received from XXXXXXX, contamination event confirmed – refer to scanned email”)
2. Scan QPS email response to AUSLAB under the relevant barcode
3. Add UR Note if applicable: “Quality Flags noted for XXXXXX refer to specimen notes”
4. If applicable add an additional EXH line (eg. Quality Control failure, refer to QPS) and request the reviewer to validate the additional EXH line.

9.19 Example of combined preamble and Appendix for Civil casework report

XX The following information is provided to assist in the understanding of the contents of this statement.

DNA Profiling
DNA is a complex chemical found in almost all cells in the human body. It carries genetic information which determines the physical and chemical characteristics of a person. The testing system used at DNA Analysis looks at 21 regions of DNA, 20 of which contain highly variable Short Tandem Repeats (STRs). The remaining region gives an indication as to the gender of the donor. This technique involves the use of a method known as Polymerase Chain Reaction (PCR), used to amplify these specific regions of the DNA to produce numerous copies. In this way, minimal amounts of DNA isolated from small or degraded samples can be increased to a level where they are able to be detected, profiled and compared with other samples.

The individual components (alleles) of a DNA profile are represented by a series of peaks which are measured and given a designation using standard sizing ladders. A person will have two peaks for each STR, one inherited from their mother and one inherited from their father, unless the same STR is inherited from both parents, in which case only one peak will be seen.

A DNA profile obtained from biological material can be compared with the DNA profile obtained from a reference sample from any person. If there is no indication of a contribution by more than one person, then a DNA profile is described as being “single source”. Conversely, if there are indications of two or more contributors, then a DNA profile is described as a “mixed” DNA profile.

Touch DNA / Transfer of DNA
When a person touches a surface, it is possible for their cellular material to be transferred onto that surface. This transferred cellular material can often be recovered 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.

The generation of a DNA profile will depend on many factors. These include the amount of cellular material transferred, the nature of the surface being touched and the amount of cellular material a person has available to transfer.

The persistence of any transferred cellular material on a surface will depend largely upon the nature of the surface and the conditions under which it has been kept in the time between deposition and recovery of the DNA. For example, cellular material could be lost from the surface by washing or mechanical action such as abrasion.

Not Current

It therefore follows that the absence of a DNA profile from a touched surface does not necessarily mean that that person has not come into contact with it, as it is possible for a person to come into contact with a surface without a detectable amount of their DNA being transferred or recovered.

Examinations
Unless otherwise stated, the examinations of items for biological material were conducted by officers within the Queensland Police Service (QPS). Sub-samples from these items were forwarded to FSS for the purposes of conducting DNA analysis.

DNA Analysis operates under the premise that 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 FSS DNA Analysis. 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.

Some items may be submitted to this laboratory for the purposes of both examination and DNA profiling. This occurs at the discretion of the QPS. These examinations are performed in accordance with the SOPs of this laboratory. For these items, notes are made at the time of the examination by the examining scientist and form part of the casefile.

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.

Reporting DNA Analyst
It is the role of a reporting scientist to interpret the results obtained from the above processes and includes assessment of possible reworking strategies, if required, to gain further information from a sample. The DNA results are then able to be compared to reference DNA

Not Current

profiles associated to the case, and statistical analysis evaluating the strength of the evidence can be performed.

Statistical Analysis of DNA profiles
In order to statistically evaluate DNA profiles, it is necessary to make a reasonable assessment of the possible number of people who may have contributed DNA to that DNA profile, based on the information observed.

DNA profiles assumed to originate from one person (single source)

A person can be excluded as a possible source of the biological material if corresponding regions of the crime-scene DNA profile are different from that person's reference DNA profile. If the corresponding regions of the DNA profiles contain the same information, then that person, together 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 DNA originated from the person of interest;
Proposition 2: the 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 DNA components that make up the DNA profile.

If less than the 21 regions of DNA are seen in a DNA profile (termed an 'incomplete or partial DNA profile') this will be reflected by a smaller likelihood ratio than the likelihood ratio that would be obtained from a full DNA profile. In other words, the more incomplete the DNA profile, the greater the likelihood of obtaining the DNA profile if it came 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 could or could not have contributed to a mixed DNA profile, a set of competing propositions (similar to a single source DNA profile) are considered. For example, for a two person mixture:

Proposition 1: the DNA originated from the person of interest and an unknown person unrelated to the person of interest;
Proposition 2: the DNA originated from two unknown people unrelated to the person of interest.

The likelihood ratio provides a statistical assessment of a particular contribution of DNA being contained within the mixed DNA profile.

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

Not Current

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 intimate area, then it may be possible to make the reasonable assumption that the donor of the sample 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 known donor, such that the presence of the DNA components corresponding with the donor'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, for example:

Proposition 1: the DNA has originated from the complainant and the person of interest;
Proposition 2: the DNA has originated from the complainant and an unknown individual unrelated to the person of interest.

When it appears that a large number of people could have contributed to a mixed DNA profile, it can be difficult to exclude individuals as potential contributors. It can be equally difficult to determine whether a person could in fact be a contributor to the DNA profile. If it is not possible to determine the number of contributors to a mixed DNA profile, or if there is very limited information available, then a mixed DNA profile may be described as unsuitable for interpretation.

If information is received such that the assumptions made in an interpretation are not accepted, then 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, irrespective of whether the DNA profile is single source or mixed. A correction factor θ (theta) is applied to all statistical calculations in order to correct for the possibility of common ancestry (sharing of DNA components inherited from a common ancestor) between people in the general population. The nationally agreed figures for theta are θ=0.02 for the Australian Caucasian dataset, θ=0.03 for South East Asian dataset, and θ=0.05 for the Australian Aboriginal dataset. Unless otherwise specified, the default dataset used in DNA Analysis is the Australian Caucasian dataset. The other datasets are available upon request.

In addition to theta, the calculation of the likelihood ratio also includes an allowance for the sampling variability of the dataset. In other words, if a new dataset were generated it allows for any difference the new dataset could make to the likelihood ratio.

Often the calculated likelihood ratio produces numbers of hundreds (100s) or even thousands (1000s) of billions. To avoid the use of potentially confusing terminology, a 'ceiling figure' for the likelihood ratio of 100 billion has been determined (this is called truncation). For example, a calculated likelihood ratio of "150 000 billion times more likely", would be reported as "more than, or at least 100 billion times more likely". The actual calculated figure can be provided upon request.

The above listed values for the 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 random fashion in which DNA from parents combines, the probability that two siblings would share the same 20 STR regions 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 is thought that a close blood relative may have been

Not Current

involved, a more meaningful approach would be to submit the reference sample from the relative in question for analysis and direct comparison to the crime stain DNA profile.

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

Chain of Custody

All Forensic DNA Analysis 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 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 exhibit packaging prior to processing. The packaging and labelling of any exhibit is checked and recorded before the sample undergoes DNA analysis.

Entry into Forensic DNA Analysis is restricted to authorised persons only, via electronically encoded proximity access cards. Forensic DNA Analysis forms part of a Health Support Queensland campus site which has access 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 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

Not Current

- 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.
For details of the current ISO/IEC 17025 Field Application Document, Forensic Science, Supplementary requirements for accreditation, please refer to the NATA website:

http://www.nata.asn.au/publications

Not Current

9.20 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

Not Current

Procedure for the Release of Results

1 Purpose

To describe the correct format for statements or reports issued from Forensic DNA Analysis.

To document the procedures for issuing reports within Forensic DNA Analysis.

To document workflows leading to the releasing of information via Exhibit Reports to the Queensland Police Service.

2 Scope

This standard operating procedure relates to all statements or reports issued by case analysts to clients.

3 Definitions

DRMU – DNA Results Management Unit (QPS)
EXH – Exhibit Report
FSS – Forensic and Scientific Services
GSI – Generic System Interface (interface between AUSLAB and QPS Forensic Register)
P+ - Profiler® Plus DNA amplification kit
QIS – Quality Information System version 2
QPS – Queensland Police Service
SMU – Sample Management Unit (QPS)
SSLU – Scientific Services Liaison Unit (FSS)

4 Actions

4.1 Presumptive Exhibit Reports

The formats of the accepted EXH comments are located in QIS **23008**.

A Presumptive EXH should include the following information:

4.1.1 Overall Status:This should reflect the result. *This only applies to EXRs, and does not apply to EXHs.*

Negative (Forensic Value) – Used for items that are examined but not submitted for testing.
Negative (Not examined) – Used for items that are received but not examined
Not Received at FSS – Used for items that are not received at FSS
Positive (Forensic Value) – Any sample submitted for DNA testing will have this status result.

4.1.2 Lab No: The results are reported under the individual sub-sample. Refer to Appendix 11 for specific guidelines.

4.1.3 Result Status – All result options are available using the F1 lookup function. The results status should reflect any presumptive & confirmatory tests that were conducted and include whether the sample was submitted for DNA testing.

Not Current

Example 1: If a TMB test was performed that was negative and the swab was submitted as cells but also had a hair attached which was observed under microscopy as not suitable for DNA testing the following lines would be entered:

234967280	Presumptive blood test neg. Submitted as cells.
234967280	Hair located. Not suitable for analysis

Example 2: If different testing was performed on 2 sub-samples with a positive TMB test recorded for the first which was submitted and both an AP pos and the presence of spermatozoa detected by microscopic examination on the second the following lines would be entered:

234967280	Presumptive blood test pos, submitted – results pending
234967281	Presump sem fluid test pos, submitted – results pending.
234967281	Micro positive for sperm. Submitted – results pending.

NB. Linked No and Warm Link name are not required for presumptive EXHs

4.2 Final Exhibit reports

4.2.1 **Format**: The formats of the accepted EXH comments are located in QIS 23008.

4.2.2 **Quality Checking**: Final EXHs can only be interpreted and released after the GMID-x batch has been read and Quality Flag checked (and Extraction Batch checked where appropriate) – refer Appendices 14-15. Quality Flag checking is usually performed by a Senior Scientist, EB checking is usually performed by a case manager.

4.2.3 **Information**: A Final EXH should include the following information (refer to Appendix 4-5):

4.2.3.1 **Overall Status**: This does not need to be changed from the Overall Status of the Presumptive Exhibit Report. Note, this does not apply to EXHs.

4.2.3.2 **Lab No**: The sub-sample no. of the results being reported. This should include the results for all sub-samples that have been entered into the EXH as presumptive EXHs lines. Any further different results should also be added to the EXH. If there are no sub-samples, the EXH of the Item should be entered.

4.2.3.3 **Result/Status**: A description of the result (eg 9 loci, partial, no DNA profile). All result options are available using the F1 lookup function. There may be more than one EXH line which is suitable however the EXH must fully describe the result. For example if there is a major and minor profile an EXH line must be entered for both the major and minor profiles.

Example 1:

234967280	Mixed DNA Profile. Major component uploaded to NCIDD	UKM1
234967280	Mixed profile, minor component insuff for NCIDD matching	UKM2

4.2.3.4 Linked No. Field:

Not Current

If the Crime Scene profile matches an Evidence Sample: The barcode no. of the evidence sample is added to the Linked No. field.

No Evidence Sample: If there are no evidence samples, then the profile will be unknown. The designations of 'UK' should be used for unknowns with 'F' (female) or 'M' (male) used to provide further information and 'UKP' should be used if the sex of the DNA profile is unable to be determined. 1 should be used to denote the first male, female or person profile obtained.

Example 1: Three different male profiles would each be reported on a different line with UKM1, UKM2 & UKM3 used to distinguish between the contributors.

Example 2: A single (1) unknown male would be reported as UKM1.

NB: If an unknown profile is reported to QPS and an evidence sample is subsequently received that matches the unknown profile, any further unknown profiles continue sequentially eg. If UKM1 matches John SMITH, then the next unknown male in the case is designated UKM2 (it does not replace the UKM1).

4.2.3.5 Warm Link Name: The name of the evidence sample the profile matches to is entered into this field.

4.3 Suspect Checks:

Suspect checks are useful when a profile is insufficient for NCIDD upload and a permanent barcode/profile exists for a suspect. Suspect checks are nominated by the SSLU or SMU. This information may be found in the UR notes (this must always contain the barcode).

It is not a necessity that names are entered in the Warm Link field of the EXH for suspect checks.

For PowerPlex 21 DNA profiles, these are reported in the EXH using an appropriate EXH line (see QIS **23008**). This includes the appropriate Likelihood Ratio EXH lines.

For Profiler® Plus DNA profiles, these are only reported in a final EXH if they do not match. For profiles sufficient for NCIDD, the matches are reported via LKRs (QIS 23890 Uploading and Actioning Samples on NCIDD and QIS 22619 Creating and Reviewing Links). For Intelligence Report templates, see QIS 24015 Procedure for Intelligence Reports and Interstate/Interpol Requests.

If there is a suspect check match and the DNA profile is less than the stringency for searching on NCIDD, an Intelligence Report should be issued to QPS DRMU.

For Profiler® Plus interpretations, if the DNA profile is 'complex' or 'no major/minor' and the suspect check is performed resulting in a 'cannot exclude' interpretation, an Intelligence Report should be issued to QPS.

Intelligence samples may be received by Forensic DNA Analysis associated to particular cases. These samples need to be compared to the case. If the crime scene profile is on NCIDD and the Intel sample is 'Unlimited Purpose', a match will be reported to QPS DRMU as a cold link. If the Intel sample is 'Limited Purpose', the match needs to be reported in an Intelligence Report (Profiler® Plus) or via EXH (PowerPlex 21). If the Intel sample does not

Not Current

match a crime scene profile, the non-match does not need to be reported in an EXH (Profiler® Plus) but can be reported via EXH for PowerPlex 21. If the crime scene profile is Single Source and matches someone other than the profile for the Intel sample, then an EXH line is not required.

If an Intelligence sample was profiled with Profiler® Plus and the crime scene profiles are all PowerPlex 21, if the case is high profile, it is preferable to rework the intelligence sample to enable a full comparison of the profiles to be reported. Before the rework is ordered, it is important to intuitively assess the crime scene profile to determine if the reference profile is excluded. If clearly excluded, there is no benefit in reworking the sample with PowerPlex 21. If a strong Likelihood Ratio (when Profiler® Plus reference is compared to the PowerPlex 21 crime scene profile), a rework is not necessary. If a statistic suggesting 'Low Support' or 'non-contribution' is obtained, rework in PowerPlex 21 to enable all information to be available for comparison.

4.4 Interstate/International Requests – Refer to QIS 24015

4.5 Urgent (Priority 1) Requests

4.5.1 Routine Urgent Requests: The requests for urgent processing will come via Inspector of DNA Results Management Unit (or higher), and are forwarded to the Managing Scientist and Team Leaders. A phonecall 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. The case will be allocated by the Reporting Supervising Scientists and all Management staff informed.

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 dependant 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 EXH line 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 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.

4.5.2 Result communication on Fridays only.

Regarding Priority 1 urgent samples as requested by QPS, if results are likely to be available on Fridays, email DRMU in the morning with the relevant barcodes and expected time of release. Aim to release prior to the 3pm GSI transfer and call DRMU if the results are likely to be released later than 3pm.

When results are reviewed, email DRMU that results have been released and if in the 3pm transfer, alert them whether there are actionable results, or not. Suggested wording is *'the*

Not Current

electronic transfer includes actionable results' or *'the electronic transfer includes non-actionable results'* depending on whether there are results for comparison or not.

4.5.3 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 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 Insp Carstensen, S/Sgt Scott McLaren, and S/Sgt Gerard Simpfendorfer.

4.6 Statements and Certificates

4.6.1 AUSLAB template

For the layout of a Statement of Witness, refer to Appendix 1: Example of 1st page

There is a footer on each page that includes the NATA endorsement, the page number and total number of pages, the case reference number, date, name and signature of Reporting Scientist authorising the statement.

Allows the inclusion of a version of the statement Appendix that lists test methodologies (refer to Appendix 2).

Includes a Justice's Declaration Act (refer to Appendix 3) at the end of the Appendix.

The AUSLAB template is the same as the offline templates available in QIS (refer to QIS 29010).

The AUSLAB template pulls in the case details, including the reference and crime scene sample receipt details, Reporting Scientist details, Defendant and Complainant, Appendix and Justice's Act.

Not Current

The person who presses F6 on the statement page in AUSLAB will have their details pulled into the statement.

4.6.1 Statement Requirements (AUSLAB Test Code: FBSOW):

NB. FBSTAT was the testcode used for statements until the FBSOW was activated in February, 2012.

The Statement will contain the following information:

- Declaration & Details of the Reporting Scientist (eg. Name, State)

- Place of Employment and position (eg. Scientist within Forensic DNA Analysis)
- Qualifications held by the Reporting Scientist (eg. B.Sc.)

- ANZFSS Code of Ethics (if applicable)

- Offence details including Defendant and Complainant details. If there is a deceased involved, the complainant is Regina.

- Details relating to the receipt of items & reference samples including the date of receipt, and the delivery officer (including Australia Post). A list of the barcoded items received.

- Summaries/ Preambles are added by the Reporting Scientist and may include some, all or slight variations of the following depending on case and profile types (see Appendices 9-12):

- The Role of a Forensic Biologist
- Examinations (if performed by another analyst)
- DNA Profiling
- Mixed DNA Profiles
- Blood Stains
- Seminal Stains
- Saliva
- Semen Staining on Items
- Persistence of Semen in the Vagina
- Statistics

- A summary of test results of the Reference Samples, and the type of sample (eg. Blood, Mouth/Buccal, Hair)

- Description and results of each of the Items:

- If Items were examined by QPS, or by QPS and QHFSS, it should be made clear which category the Items fit into.
- Description of the Item including barcode information e.g. 123456789. Receipt sub-numbering e.g. 987654321-002 is optional.
- Condition of the Item (if examined by QHFSS)
- Area of staining (if examined by QHFSS)
- Areas submitted for testing (if examined by QHFSS)
- Results obtained eg. Results of comparison to reference DNA profiles and statistical interpretations where appropriate.
- Where relevant, opinions, explanations for opinions and interpretations or summary. A statement of uncertainty where relevant. Reference to other information which may be relevant to the validity or application of the results, e.g. in support of an opinion, explanation or statement of uncertainty.

Not Current

Note: If a summary of results is required, it should be included at the beginning of the result section of the statement.
Note: It is recommended that the Items are grouped per Receipt. Within each receipt, the similar results are recommended to be grouped together, and then group items examined at QHFSS and QPS, and then to group like results.

- All items received but not tested are listed (listed under each receipt).

- Appendix including information about:

- Accreditation
- Chain of Custody
- DNA Profiling
- Interpreting DNA Profiles
- Use of statistics

- Justices Act 1886 – Signature of Reporting Scientist required. The Justices Act must not be on a page by itself. The number of pages to be written within the Justice's Act should be the same as the number of pages for the whole statement.

4.6.2 Subsequent/ Alternative Statements:

4.6.2.1 Further versions (AUSLAB Test Code: FBSOW) – AUSLAB has the ability for further versions of statements to be produced under the same testcode. This is useful for replacing statements.

4.6.2.2 Addendum Statement (AUSLAB Test Code: FBADDE) - If a subsequent statement is issued (this may be due to additional exhibits being delivered or an additional request for further interpretation), it must be clearly marked as an addendum to the original statement. This test code is also used for pre-AUSLAB cases and other cases that feature manual receipts. APPVER testcode should be ordered at the same time as FBADDE to enable the Appendix field to be edited and the FBADDE to be used as a standalone statement (on its own barcode). If on a standalone barcode, an FBSOW needs to be ordered as well to enable the original completed date to populate. The date in this FBSOW needs to be in the same format as the way the date is typed into the FBADDE eg. DDMMYY or DD/MM/YYYY.

4.6.2.3 Amended Statement (AUSLAB Test Code: FBAMEN) - If, after the issue of a statement, an error is detected, the original statement shall be withdrawn and, where necessary replaced by one which is clearly indicated as being a replacement statement. This testcode is rarely used since AUSLAB is able to create new versions (see 'a.' above).

4.6.2.4 Intelligence Reports (AUSLAB Test Code: FBINTL) (refer to QIS 24015). If there is information that cannot 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. The report is written within AUSLAB where the addressee and reviewer's details can be entered.

Intelligence Reports written regarding Quality issues, should be directed to the Inspector DNA Management Section (QPS). Other Intelligence Reports should be directed to the Senior Sergeant DRMU.

Not Current

Matches on NCIDD that are below our standard match reporting stringency can be reported to DRMU via intelligence reports.

The signed report can be included in the case file, except where it relates to linking information from NCIDD. In these situations, the signed report should be held in the Intelligence Team area.

A scanned PDF of the signed intelligence report should be sent via MS Outlook to DRMU. An unsigned PDF (created after validation and saved from AUSLAB when viewed (Shift Insert)) should be sent with the signed copy to DRMU. Upon issuing, the FBIOLR page must be completed. Alternatively, these two PDF files can be sent via email to [redacted] which is managed by SSLU who then send the files on to QPS. SSLU will then complete the FBIOLR page in AUSLAB.

The template for offline Intelligence Reports is available in QIS 29011. The FBAR to record the review of the Intelligence Report can be ordered on the same barcode as the FBINTL, as can the FBIOLR testcode to record the release details.
The most up-to-date list of QPS DRMU personnel to be included in the email is retained in the Minor Changes spreadsheet (I:\Change Management\ Change Register - Minor Changes).

4.7 DNA Evidentiary Certificates (AUSLAB Test Code: FBEVC) – (Refer to Section 95A Evidence Act 1977)

This is a certificate (in an approved form) that must be signed by an authorised DNA Analyst.

Current staff who hold appointments (in accordance with Section 133A of the Evidence Act 1977) as DNA Analysts are held with the Managing Scientist.

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.

If an Evidentiary Certificate is requested, a workflow has been devised to assist the checking involved in order to sign the certificate (see Appendix 13).

A checklist should be used to record the information examined by the DNA Analyst (refer to QIS 30799). There are instructions to complete this checklist recorded in a worksheet tab within the actual checklist file.

If the information gathered to be checked prior to issuing the Evidentiary Certificate is to be considered part of the casefile, then an FBAR page needs to be requested in AUSLAB and the pages should be numbered and the case identifier added.

Not Current

4.8 Other Reports – Crime and Misconduct Commission (CMC) or Ethical Standards unit of the QPS.

Due to the confidential nature of these cases, results cannot be entered into AUSLAB in either EXH or STATEMENT format (as this information is accessible by QPS and other FSS staff). Barcodes will need to be registered to facilitate analytical processing.

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 Team.

Clarification from the requesting party will need to be sought if any results are ok to send via the GSI to QPS, or if by standard means (above).

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, 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:

1. Receipt details of reference samples and exhibits
2. Blurbs (Role of a Forensic Scientist, DNA Profiling and appropriate blood or semen blurbs)
3. List of Reference Samples (and results)
4. Results of testing for exhibits submitted
5. 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. This report shall **NOT** be scanned into AUSLAB. **All results are to be included in the case file only.**

4.9 Statements including coronial samples.

To ensure samples delivered by the Coronial Support Unit (CSU) are pulled through correctly into Statements, the receipted items require an FTAR testcode to be requested (and the delivery officer etc to be recorded), and the Specimen type to be changed to FTAE. If it has correct CRISP association in the registration in AUSLAB, the receipt details should then pull into the Statement of Witness.

4.10 External Testing (Example Low Copy No. or Mitochondrial DNA) in statements

Not Current

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.

4.11 Offline Statements

If a Statement of Witness needs to be written outside of AUSLAB (eg. when AUSLAB is down, or the testcode is corrupted), the templates are available in QIS. Templates exist for Statements of Witness and Intelligence Reports - see the following documents:

i. 29010 – Statement of Witness template – stamp
ii. 29008 – Statement of Witness template – address – no NATA endorsement
iii. 29009 – Statement of Witness template – blank – no NATA endorsement
iv. 29024 – Use of offline Forensic Reporting templates
v. 29011 – Intelligence report template

This type of statement may be written 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 AUSLAB upon completion.

Alternatively, this particular person may create a barcode in AUSLAB under the same UR number, and request an FBSOW testcode. By pressing F6, their details will pull into the statement.

4.12 Statement/ Report Authorisation

In order to release results to the client in the laboratory (excluding EXHs), QIS 30689 needs to be completed. QIS 26993 describes the overall procedure for releasing results at FSS.

Qualified Forensic DNA Analysis Reporting Scientists are authorised to sign statements and reports given that all policy and procedure requirements have been satisfactorily fulfilled.

All Staff are authorised to sign and initial worksheets, reports etc according to their level of competence.

A staff list with signatures and initials of all staff (QIS 17088) is kept for reference. This is located in the Quality area of the Administration compactus.

DNA Analysts can sign Evidentiary Certificates. To be authorised as a DNA Analyst, the Director-General of the Department of Health approves a Briefing Note authored by the Managing Scientist, cleared by the Senior Director (FSS) and verified by the Chief Executive (HSQ). The Director- General is permitted to appoint a public service officer as a DNA Analyst according to the requirements of Section 133A of the *Evidence Act 1977*, if satisfied that the officer has the necessary qualifications and acquired competencies. The minimum

Not Current

details considered by the Managing Scientist are relevant qualifications, relevant experience in the field, and competence in Reporting DNA casework. When authorised, the DNA Analyst appointment is published in the Qld Government Gazette.

Another scientist with the same or greater level of competence can sign as Peer Reviewer. Relevant training modules apply to the elements of technical reviews.

4.13 Further Documentation Requests (eg. Audit Trails)

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 LALU (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: [redacted] (formerly SSED email account) 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, an FBAR page should be requested in AUSLAB and 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. Having said this, it is recommended that this occurs as it is helpful if/when it is referred to in court proceedings. 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.

4.14 Release of Reports

4.14.1 Statement of Witness and DNA Evidentiary Certificates

The signed document is copied and stamped as ‘copy’. The copied document is included in the casefile and page numbered. The original is scanned and emailed to SMU by SSLU for uploading directly to QPRIME, and is sent by SSLU to the Investigating Officer (or delegate, which could include the DPP). Urgent documents could be faxed where appropriate.

4.14.2 Intelligence Reports

The Intelligence Report is sent via MS Outlook to DRMU as a signed PDF file, and an unsigned PDF that is created by AUSLAB post-validation (see section 4.6.2.4)

Not Current

4.14.3 Coronial and Disaster Victim Identification (DVI) Reports

These 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.

4.15 Court Monitoring

Every Reporting Scientist should have their testimony evaluated every 12 months. The evaluation can be performed by another Reporting Scientist, a court official (DPP or Defence) or QPS Officer.

The first page of the Court Testimony Monitoring Evaluation Form (QIS 17047) 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.

A report of every 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 '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.

Refer to FSS Court Testimony and Attendance Requirements (QIS 18034) for more information.

Not Current

5 Records

All statements issued must bear a stamp on the front page that lists the date of issue, the case analyst's signature and the signature of the analyst who performed the technical review of the statement. The stamp is automatically added to statements by AUSLAB.

A copy of the statement issued for any test/examination must be retained in the case file. After the statement has been reviewed, F6 to validate will change the statement to PDF format. The person pressing F6 to validate will have their details auto-populated by AUSLAB. This means the Reporting Scientist needs to perform this function. A time and date stamp will appear in the footer.

Further versions can be created of statements and can be viewed in AUSLAB prior to printing - Press Shift –Insert on the validated statement page (to view PDF Report Table) and F8 to

view HTML Report. The original (validated) statement can also be viewed by pressing F5 on this page, or scrolling to the version you wish to view.

If a mistake is made and another version needs to be created, insert an audit entry to explain that a new version was created to correct an error (or similar wording).

6 Associated Documentation

10623 FSS – Laboratory Report Format, Content and Handling
16004 AUSLAB Users Manual – DNA Analysis
17088 Procedure for recording handwriting specimens in DNA Analysis
17047 Court Testimony Monitoring Evaluation Form
17117 Procedure for Case Management
17137 Procedure for STR fragment analysis using GeneMapper ID-X software
17142 Examination of Items
18034 FSS Court Testimony and Attendance Requirements
22619 Creating and Reviewing Links
23008 Explanations of EXH Results
23602 Environmental Monitoring
23890 Uploading and Actioning Samples on NCIDD
23955 Disaster Victim Identification Preliminary DNA Reports
23968 DNA Analysis Unit Communications Procedure
24015 Procedure for Intelligence Reports and Interstate/Interpol Requests
26874 Procedure for Paperless Case Management and Review
26993 Procedure for authorising staff to release results
29008 Statement of Witness template – address – no NATA endorsement
29009 Statement of Witness template – blank – no NATA endorsement
29010 Statement of Witness template – stamp
29011 Intelligence report template
29024 Use of offline Forensic Reporting templates
30799 DNA Evidentiary Certificate Checklist
31523 Interpretation and Statistical Analysis of DNA profiles using the STRmix Expert System

National Association of Testing Authorities (2013) ISO/IEC 17025 Standard Application Document for Accreditation of Testing and Calibrations Laboratories July 2013. Australia

National Association of Testing Authorities (2013) Forensic Science ISO/IEC 17025 Application Document July 2013. Australia

National Association of Testing Authorities (2005) AS ISO/IEC 17025-2005 Australian Standard. General requirements for the competence of testing and calibration laboratories. Australia

Evidence Act 1977

7 References

Nil

Not Current

8 Amendment History

Version	Date	Author/s	Amendments
	24 Feb 1999	V Ientile	
QIS Edition			
1	8 Oct 2001	V Ientile	
2	23 Jan 2004	L Freney	Changes to references, update appendices
3	11 Mar 2004	V Ientile	No interim unchecked results to be issued
4	10 Aug 2006	M Gardam	Combined with 17158, amended the title and updated statement requirements, included intelligence reports, statement blurbs & Evidential Reports. Added Reference to Communication SOP, Added EXR reporting guidelines.
5	31 May 2007	M Gardam	Sub-numbering is optional when giving a description of the item.
6	April 2008	QIS 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
7	August 2009	J Howes	Updated Forensic Biology to DNA Analysis, added EXH, added complete preambles, added Evidentiary Certificate workflow, Quality flag checking workflow, updated Statement of Witness and Appendices examples, DNA Analyst list removed, relative frequency paragraph removed from Intel letter example and updated with match probability, EXH table improvements and current lines added to examples.
8	June 2010	J Howes	Added EB checking workflow, added to Quality Flag workflow, moved Quality paragraphs to own Appendix, deleted Pathology and Scientific services logo
9	August 2010	J Howes	Changed FIRMU to DRMU, added some more information to paternity preamble
10	April 2011	J Howes	Changed Appendix 3 to include latest version of Justice's Act, changed HP4/HP5 to 'senior' in Evidentiary Certificate workflow, added some suspect check information.
11	05 April 2012	J Howes	Changed DNA Unit to Sample Mgt Unit, changed 'Evidential Reports' to 'Other Reports', added info to Statement and Intel Report field, changed the number/bullet/paragraph systems to be consistent, added new Appendix version (5), added new preambles, added new Statement of Witness template, add ability to create statement versions, added Offline statement section, removed Appendices 4 and 5 (covered by 24005), added F6 validation to RECORDS, added Release of Reports section, removed Example 6

Not Current

			(multiple items) from Appendix 9, added Coronial/DVI report release section, add Environmental samples to QFLAG workflow, updated QFLAG and EB checking process, added template for Evidentiary Certificates, updated FBSOW for FBSTAT and workflow, added link to Evidentiary Certificate checklist, added Ethical Standards/CMC information, added Court Monitoring information, added information to Intel report section, added Urgent P1 result communication on Fridays, added FTAs associated to the case (under Suspect Check section).
12	29 Nov 2012	J Howes	Added new HSSA Header, removal of FBSHRT reference that was part of Section 3 and the workflow from Appendix, Linked No. field updated to include use of barcodes for unique profiles, FBEVC added, information on who receives Intel reports added, Intelligence Report section re-organised, added information to negotiate timeframe with requesting party re audit trails, Appendix 6 for statements added to Appendix 2 in this document, added APPVER to workflow for FBADDE and to Section 3, added Appendix 17, added Reference Sample section to Appendices 9-11 to be used where appropriate, Tho1 changed to TH01, Appendix 14 workflow changed to not include AUSLAB matches, added Profiler® Plus for 'cannot exclude' interpretation for suspect check,
13	07 July 2014	J Howes	Reformatted according to Procedures template, added information relating to PowerPlex 21 and XPLEX, added information from Comments on previous version, re-formatted the Appendices, added 26993 to associated docs, workflow for QFLAGs with PowerPlex 21, re-ordered Appendices, updated preambles, added Appendix 18 – suggested statement wording, changed HSSA to HSQ, added information to Urgent Processing, changed release of Intel reports to include by Outlook, replaced Appv5 for Appv7 in 9.2, added NATA details, changed Appendix 13 to reflect all carried out in the one spreadsheet, added XPLEX drop down for Quality Flags to Appendix 13.

Not Current

9 Appendices

1 An example of the layout of the front page of a Statement of Witness

2 Procedural overview and test methodology (Appendices 6 and 7).

3 Example of the Justice's Declaration Act.

4 Completing Exhibit Reports in AUSLAB

5 Review of Exhibit Reports in AUSLAB

6 Creating an Addendum Statement in AUSLAB

7 Creating a Statement with Receipt Details in AUSLAB

8 EXH Reporting (Sub-Sample No. Rules)

9 Complete Casework Preamble – Examinations by QHFSS

10 Complete Casework Preamble – Examinations by QPS and QHFSS

11 Complete Paternity Preamble

12 Quality Paragraphs (relating to statements including results of DNAIQ Extractions in period October 2007 – July 2008)

13 Quality Flag Checking Workflow

14 Extraction Batch Checking Workflow

15 General DNA Evidentiary Certificate Workflow

16 DNA Evidentiary Certificate template (and Appendix v5)

17 DNA Evidentiary Certificate Workflow in AUSLAB

18 Suggested PowerPlex 21 and STRmix statement wording

19 QFLAG workflow for Quality Team (when a possible match is identified)

Not Current

9.1 An example of the layout of the front page of a Statement of Witness

Not Current

Queensland Government

CaSS | **Forensic and Scientific Services**
A CLINICAL AND STATEWIDE SERVICE

STATEMENT OF WITNESS

Peer Reviewed .....Yes/No

Client Reference : [redacted]

Case Analyst .....

Peer Analyst .....

Date Issued .....

QUEENSLAND)
TO WIT)

I, Justin Anthony HOWES, of Brisbane in the State of Queensland, do solemnly and sincerely declare that:-

1. I am employed by Queensland Health Forensic and Scientific Services (QHFSS) at Coopers Plains, Brisbane.
2. I hold the position of Senior Scientist in the DNA Analysis Unit of QHFSS.
3. I was awarded a Bachelor of Science from University of Queensland.

   I was awarded a Bachelor of Arts from University of Queensland.

   I was awarded a Master of Science (Forensic Science) from Griffith University.
4. I am a member of the Australian and New Zealand Forensic Science Society.
5. This is my statement in relation to the alleged offence that Occurrence Number: [redacted] refers. The defendant in this matter is defendant. The complainant in this matter is complainant.

9.2 Procedural Overview and Test Methodology (Appendices 6 and 7)

APPENDIX (version 6)

Procedural overview for DNA Analysis,
Forensic and Scientific Services (FSS), Health Services Support Agency

Examinations

Unless otherwise stated, the examinations of items for biological material were conducted by officers within the Queensland Police Service (QPS). Sub-samples from these items were forwarded to Forensic and Scientific Services (FSS), Health Services Support Agency, for the purposes of conducting DNA analysis.

DNA Analysis operates under the premise that 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 FSS DNA Analysis. 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.

Some items may be submitted to this laboratory for the purposes of both examination and DNA profiling. This occurs at the discretion of the QPS. These examinations are performed in accordance with the SOPs of this laboratory. For these items, notes are made at the time of the examination by the examining scientist and form part of the casefile.

Chain of Custody

All DNA Analysis 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 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 exhibit packaging prior to processing. The packaging and labelling of any exhibit is checked and recorded before the sample undergoes DNA analysis.

Entry into DNA Analysis is restricted to authorised persons only, via electronically encoded proximity access cards. DNA Analysis forms part of a Health Services Support Agency campus site which has access controlled and monitored by a security team. Records of Visitors to DNA Analysis are retained.

Accreditation

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 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:

Not Current

- 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.
For details of the current ISO/IEC 17025 Field Application Document, Forensic Science, Supplementary requirements for accreditation, please refer to the NATA website:

http://www.nata.asn.au/publications

Not Current

Technical information relating to DNA profiling at DNA Analysis, Forensic and Scientific Services (FSS), Health Services Support Agency

DNA Profiling

DNA is a complex chemical found in almost all cells in the human body. It carries genetic information which determines the physical and chemical characteristics of a person. The testing system used at DNA Analysis looks at 21 regions of DNA, 20 of which contain highly variable Short Tandem Repeats (STRs). The 21st region gives an indication as to the gender of the donor (for details see Table 1). This technique involves the use of a method known as Polymerase Chain Reaction (PCR), used to amplify these specific regions of the DNA to produce numerous copies. In this way, minimal amounts of DNA isolated from small or degraded samples can be increased to a level where they are able to be detected, profiled and compared with other samples.

The individual components (alleles) of a DNA profile are represented by a series of peaks which are measured and given a designation using standard sizing ladders. A person will have two peaks for each STR, one inherited from their mother and one inherited from their father, unless the same STR is inherited from both parents, in which case only one peak will be seen.

A DNA profile obtained from biological material such as blood, semen, saliva, hair or cells (eg. touch DNA) can be compared with the DNA profile obtained from a reference sample from any person. If there is no indication of a contribution by more than one person, then a DNA profile is described as being “single source”. Conversely, if there are indications of two or more contributors, then a DNA profile is described as a “mixed” DNA profile.

Statistical Analysis of DNA profiles

In order to statistically evaluate DNA profiles, it is necessary to make a reasonable assessment of the possible number of people who may have contributed DNA to that DNA profile, based on the information observed.

DNA profiles assumed to originate from one person (single source)

A person can be excluded as a possible source of the biological material if corresponding regions of the crime-scene DNA profile are different from that person's reference DNA profile. If the corresponding regions of the DNA profiles contain the same information, then that person, together 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 DNA originated from the person of interest;
Proposition 2: the 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 DNA components that make up the DNA profile. Upon request, an internationally accepted verbal scale to describe the support for one proposition over another can be used to offer some non-numerical explanation for the likelihood ratio (see Table 2).

If less than the 21 regions of DNA are seen in a DNA profile (termed an 'incomplete or partial DNA profile') this will be reflected by a smaller likelihood ratio than the likelihood ratio that would be obtained from a full DNA profile. In other words, the more incomplete the DNA profile, the greater the likelihood of obtaining the DNA profile if it came 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 could or could not have contributed to a mixed DNA profile, a set of competing propositions (similar to a single source DNA profile) are considered. For example, for a two person mixture:

Proposition 1: the DNA originated from the person of interest and an unknown person unrelated to the person of interest;
Proposition 2: the DNA originated from two unknown people unrelated to the person of interest.

The likelihood ratio provides a statistical assessment of a particular contribution of DNA being contained within the mixed DNA profile.

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 intimate area, then it may be possible to make the reasonable assumption that the donor of the sample has contributed DNA to the resultant mixed DNA profile. In these cases, a mixed

Not Current

DNA profile can be 'conditioned' on the DNA profile of the known donor, such that the presence of the DNA components corresponding with the donor'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, for example:

Proposition 1: the DNA has originated from the complainant and the person of interest;
Proposition 2: the DNA has originated from the complainant and an unknown individual unrelated to the person of interest.

When it appears that a large number of people could have contributed to a mixed DNA profile, it can be difficult to exclude individuals as potential contributors. It can be equally difficult to determine whether a person could in fact be a contributor to the DNA profile. If it is not possible to determine the number of contributors to a mixed DNA profile, or if there is very limited information available, then a mixed DNA profile may be described as unsuitable for interpretation.

If information is received such that the assumptions made in an interpretation are not accepted, then 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, irrespective of whether the DNA profile is single source or mixed. A correction factor θ (theta) is applied to all statistical calculations in order to correct for the possibility of common ancestry (sharing of DNA components inherited from a common ancestor) between people in the general population. The nationally agreed figures for theta are θ=0.02 for the Australian Caucasian dataset, θ=0.03 for South East Asian dataset, and θ=0.05 for the Australian Aboriginal dataset. Unless otherwise specified, the default dataset used in DNA Analysis is the Australian Caucasian dataset. The other datasets are available upon request.

In addition to theta, the calculation of the likelihood ratio also includes an allowance for the sampling variability of the dataset. In other words, if a new dataset were generated it allows for any difference the new dataset could make to the likelihood ratio.

Often the calculated likelihood ratio produces numbers of hundreds (100s) or even thousands (1000s) of billions. To avoid the use of potentially confusing terminology, a 'ceiling figure' for the likelihood ratio of 100 billion has been determined (this is called truncation). For example, a calculated likelihood ratio of "150 000 billion times more likely", would be reported as "more than, or at least 100 billion times more likely". The actual calculated figure can be provided upon request.

The above listed values for the 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 random fashion in which DNA from parents combines, the probability that two siblings would share the same 20 STR regions 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 is thought that a close blood relative may have been involved, a more meaningful approach would be to submit the reference sample from the relative in question for analysis and direct comparison to the crime stain DNA profile.

Not Current

Standard DNA (STR) profiling system at DNA Analysis, Forensic and Scientific Services (FSS), Health Services Support Agency

Table 1: PowerPlex® 21 multiplex 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

Table 2: Verbal scale to describe Likelihood Ratios
(adapted from Evett IW and Weir BS 1998 *Interpreting DNA Evidence*. Sinauer, Sunderland, MA)

RANGE OF VALUE	LEVEL OF SUPPORT
>1 million	Extremely Strong
100 000 – 1 million	Very Strong
10 000 – 100 000	Strong
1000 – 10 000	Moderately Strong
100 – 1000	Moderate
10 – 100	Low Level
1 – 10	Slight
1	Inconclusive

Not Current

APPENDIX (version 7)

Procedural overview for Forensic DNA Analysis,
Forensic and Scientific Services (FSS), Health Support Queensland

Examinations

Unless otherwise stated, the examinations of items for biological material were conducted by staff within the Queensland Police Service (QPS). Sub-samples from these items were forwarded to Forensic and Scientific Services (FSS), Health Support Queensland, for the purposes of conducting DNA analysis.

Forensic DNA Analysis operates under the agreement that 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 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, notes are made at the time of the examination by the examining scientist and form part of the casefile.

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 exhibit packaging prior to processing. The packaging and labelling of any exhibit is checked and recorded before the sample undergoes DNA analysis.

Entry into Forensic DNA Analysis is restricted to authorised persons only, via electronically encoded proximity access cards. Forensic DNA Analysis forms part of a Health Support Queensland campus site which has access 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 reassessments (every 3 years) and surveillance visits (18 months).

Not Current

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.
For details of the current ISO/IEC Standard Application Document for accreditation of testing and calibration facilities and Forensic Science ISO/IEC 17025 Application Document, please refer to the NATA website:

http://www.nata.asn.au/publications

Not Current

Technical information relating to DNA profiling at Forensic DNA Analysis, Forensic and Scientific Services (FSS), Health Support Queensland

DNA Profiling

DNA is a complex chemical found in almost all cells of the human body. It carries genetic information which 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 of DNA, 20 of which contain highly variable Short Tandem Repeats (STRs). The 21st region gives an indication as to the gender 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 they are able to be detected, profiled and compared with other samples.

The individual components (alleles) of a DNA profile are represented by a series of peaks which are measured and given a designation using standard sizing ladders. A person will have two alleles or peaks for each STR, one inherited from their mother and one inherited from their father, unless the same allele is inherited from both parents, in which case only one peak will be seen.

A DNA profile obtained from biological material such as blood, semen, saliva, hair or cells (eg. touch DNA) can be compared with the DNA profile obtained from a reference sample from any person. If there is no indication of a contribution by more than one person, then a DNA profile is

described as being “single source”. Conversely, if there are indications of two or more contributors, then a DNA profile is described as a “mixed” DNA profile.

Statistical Analysis of DNA profiles

Forensic DNA Analysis uses the STRmix™ software to assist in the interpretation of DNA profiles and calculation of likelihood ratios for DNA profiles generated using the PowerPlex 21® system. STRmix™ is an expert system developed and validated in Australia and New Zealand.

In order to statistically evaluate DNA profiles, it is necessary to make a reasonable assessment of the possible number of people who may have contributed DNA to that DNA profile, based on the information observed.

DNA profiles assumed to originate from one person (single source)

A person can be excluded as a possible source of the biological material if corresponding regions of the crime-scene DNA profile are different from that person’s reference DNA profile. If the corresponding regions of the DNA profiles contain the same information, then that person, together 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 DNA originated from the person of interest;
Proposition 2: the 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 DNA components that make up the DNA profile.

If less than the 21 regions of DNA are seen in a DNA profile the likelihood ratio will be smaller than the likelihood ratio that would be obtained from a full DNA profile. In other words, the more incomplete a DNA profile is, the greater the likelihood of obtaining that DNA profile if it came 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 DNA originated from the person of interest and an unknown person unrelated to the person of interest;
Proposition 2: the DNA originated from two unknown people unrelated to the person of interest.

Not Current

The likelihood ratio provides a statistical assessment of a particular contribution of DNA being contained within the mixed DNA profile.

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 intimate area, then it may be possible to make the reasonable assumption that the donor of the sample 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 known donor, such that the presence of the DNA components corresponding with the donor'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, for example:

Proposition 1: the DNA has originated from the complainant and the person of interest;
Proposition 2: the DNA has originated from the complainant and an unknown individual unrelated to the person of interest.

When it appears that a large number of people could have contributed to a mixed DNA profile, it can be difficult to exclude individuals as potential contributors. It can be equally difficult to determine whether a person could in fact be a contributor to the DNA profile. If it is not possible to determine the number of contributors to a mixed DNA profile, or if there is very limited information available, then a mixed DNA profile may be described as unsuitable for interpretation.

If information is received such that the assumptions made in an interpretation are not accepted, then 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, irrespective of whether the DNA profile is single source or mixed. A correction factor θ (theta) is applied to all statistical calculations in order to correct for the possibility of common ancestry (sharing of DNA components inherited from a common ancestor) between people in the general population. The nationally agreed figures for theta are θ=0.02 for the Australian Caucasian dataset, θ=0.03 for 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 dataset. In other words, if a new dataset were generated, this allowance factors in any difference the new dataset might make to the likelihood ratio.

Often the calculated likelihood ratio produces numbers of hundreds (100s) or even thousands (1000s) of billions. To avoid the use of potentially confusing terminology, a 'ceiling figure' for the likelihood ratio of 100 billion has been determined (this is called truncation). For example, a

Not Current

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.

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 random fashion in which DNA from parents combines, the probability that two siblings would share the same 20 STR regions 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 is thought that a close blood relative may have been involved, the most meaningful approach to interpretation would be to submit the reference sample from the relative in question for analysis and direct comparison to the crime-scene DNA profile.

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

Not Current

Not Current

9.3 Example of the Justice's Declaration Act.

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 XXXX, and contained in the pages numbered 1 to _____ 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.

_____

Signature

Signed at BRISBANE on XXXX.

Not Current

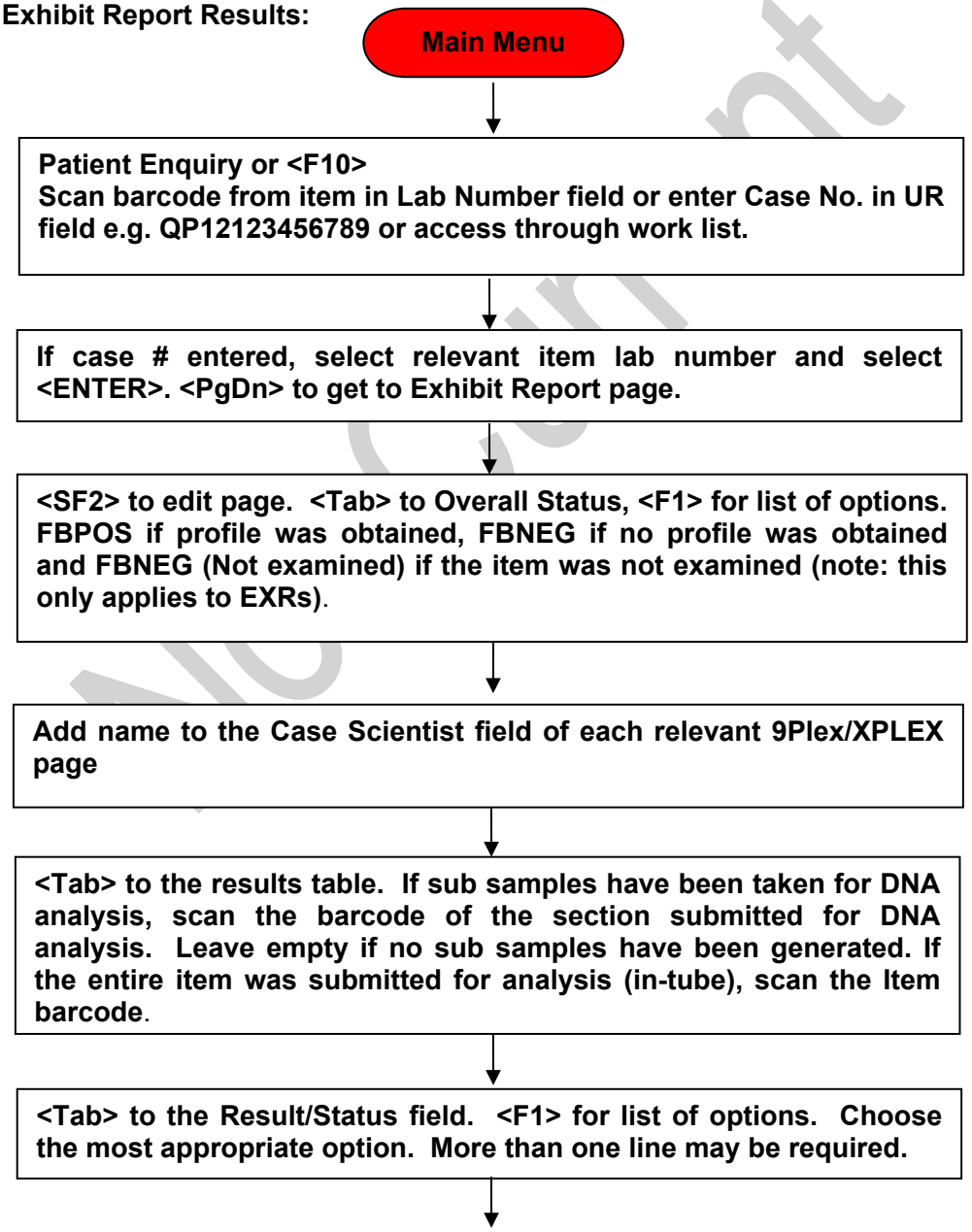
9.4 Completing Exhibit Reports in AUSLAB

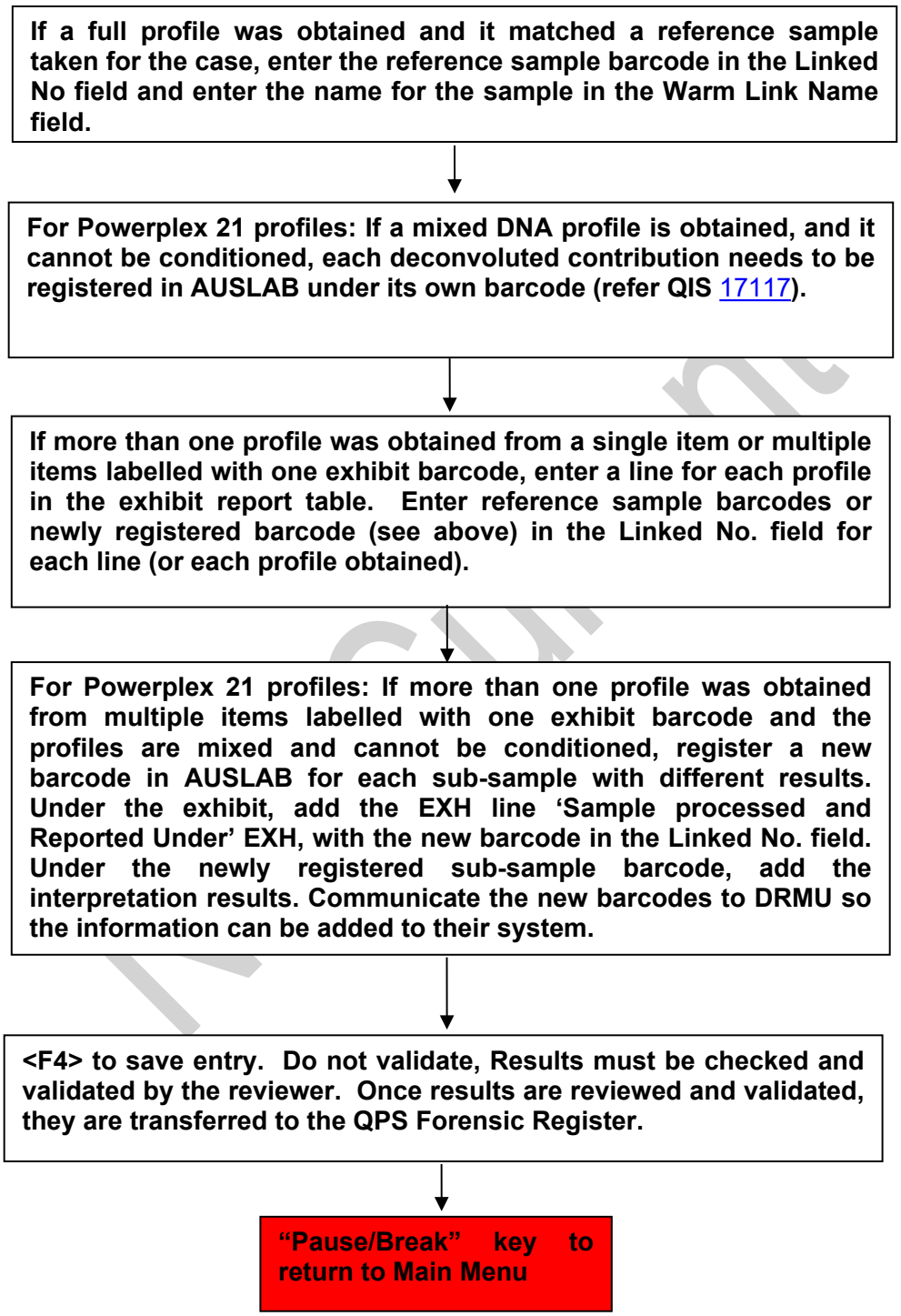
Completing Exhibit Reports

AUSLAB Test Code: EXH

Purpose: Exhibit Reports are a summary of results for each item received. The information stored in the exhibit reports is transferred to the QPS Forensic Register once the results have been checked and validated. Exhibit Reports can contain information about examinations performed, screening test results and DNA profile results. Interim results can be entered and sent to the QPS Forensic Register once they have been validated.

To enter Exhibit Report Results:





NOTE:

- All mixed DNA profiles that can be separated into major/ minor contributions (for Profiler® Plus), should have the designations filled out under the MIXT testcode for 9Plex/ Profiler® Plus, and on the COMIX page for XPLEX/PowerPlex 21.

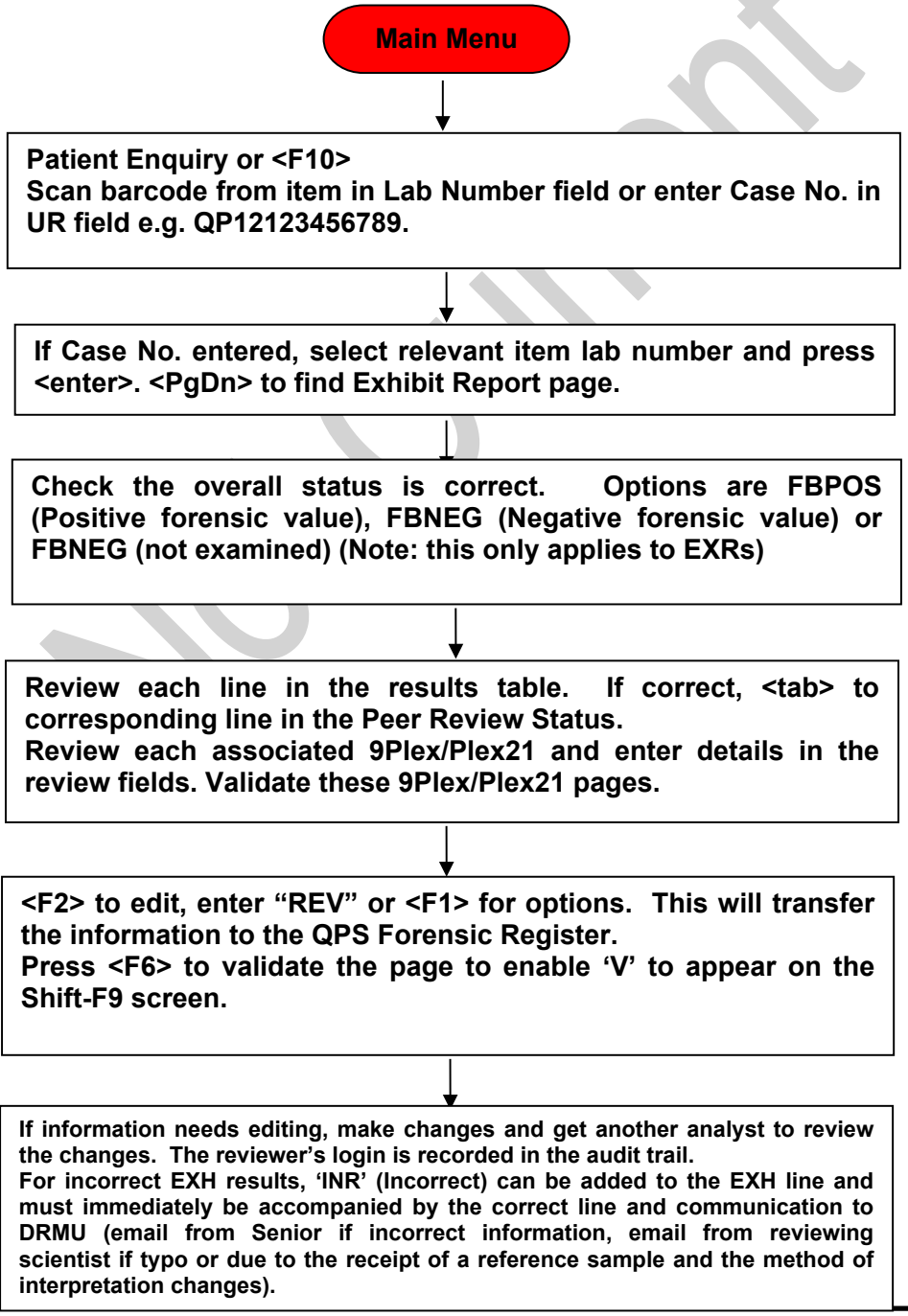
- All mixed DNA profiles that can be 'conditioned' should have the designations filled out under the MIXC testcode for 9Plex/ Profiler® Plus, and on the COMIX page for XPLEX/PowerPlex 21).
- If the interpretation is a conditioned mixture and for intelligence purposes only (eg. conditioned in the absence of a reference sample but using an unknown profile from the same case), this should be made clear in the comments section of the mixture pages.
- If the mixture is major/ minor but the major is mixed and used for POPSTATS purposes, an MIXT testcode should be used and the contributions added to this page. This only applies to 9Plex/ Profiler® Plus profiles.
- If the mixture is major/minor and the major is mixed, and a conditioned interpretation is applied to the major, it may be appropriate to use the MIXC testcode and to record the minor components to the specimen notes (and have these peer reviewed). The comments section can also be used to make it clear what actions have occurred. This should only be relevant for 9Plex/ Profiler® Plus profiles.

Not Current

9.5 Review of Exhibit Reports in AUSLAB

Purpose: An Exhibit report is created for each item as a way of transferring results back to the QPS Forensic Register. Each line of an exhibit report must be reviewed before it can be released and sent to the QPS Forensic Register.

To review an exhibit report:



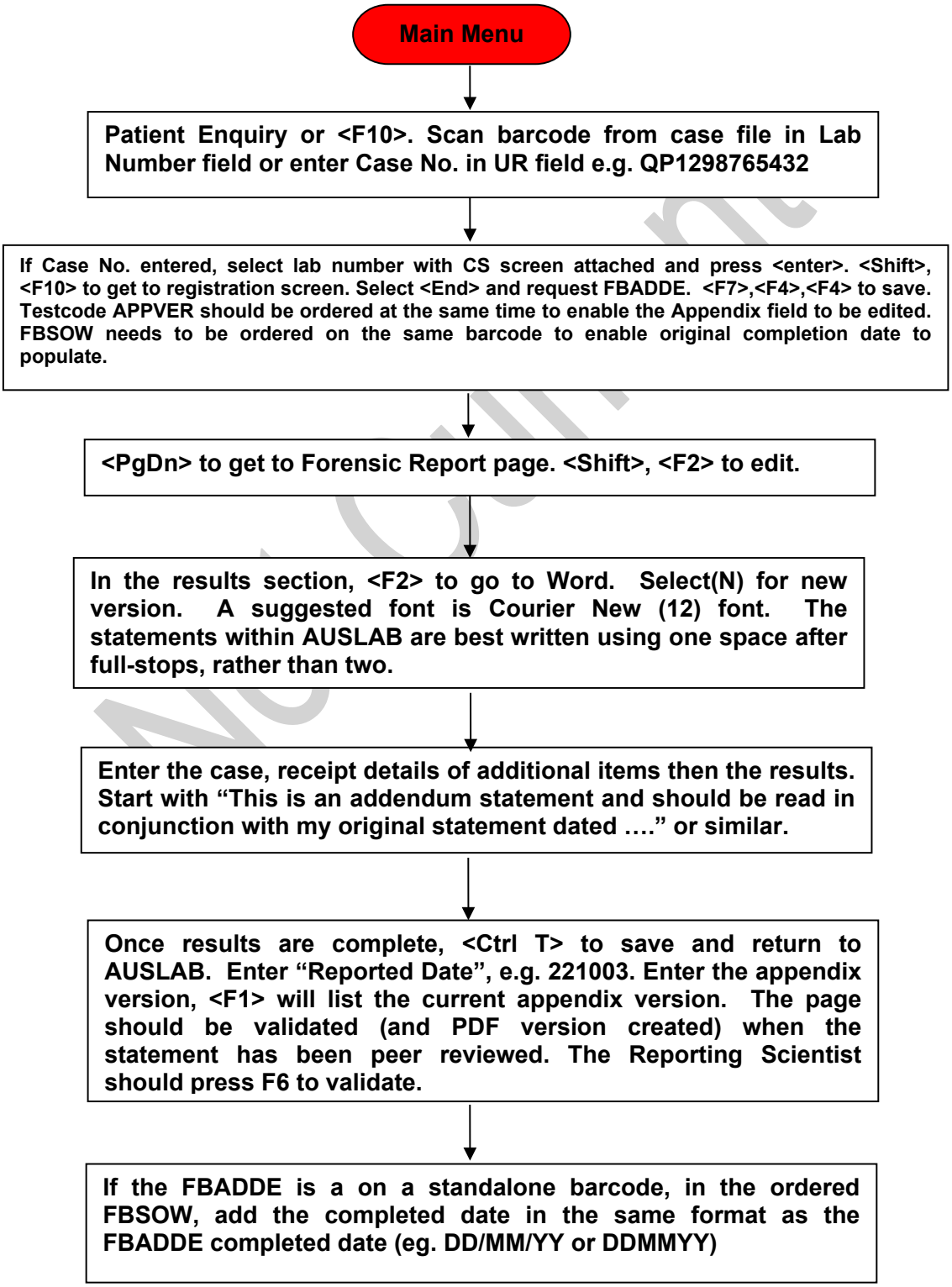
"Pause/Break" key to return to Main Menu

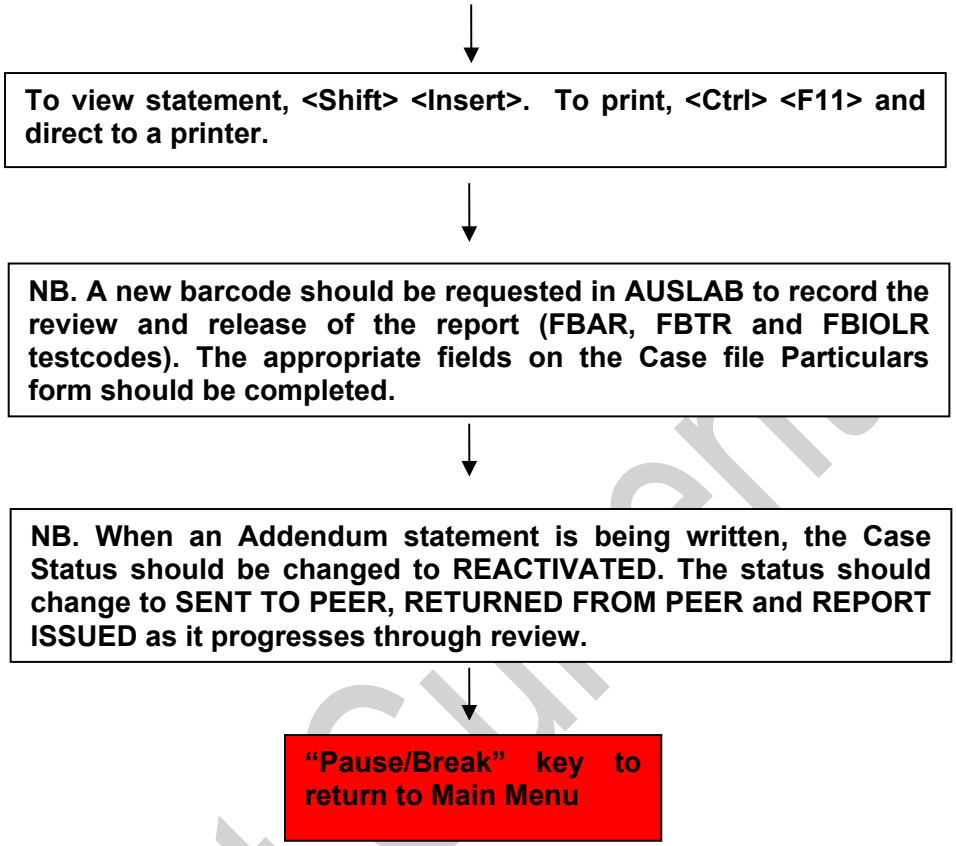
Not Current

9.6 Creating an Addendum Statement in AUSLAB

Purpose: The test code FBADDE creates a statement without the receipt details automatically entered. All statement test codes include the scientist's details, and appendix details. This format is used for cases where an additional statement is being written.

To create an addendum statement:



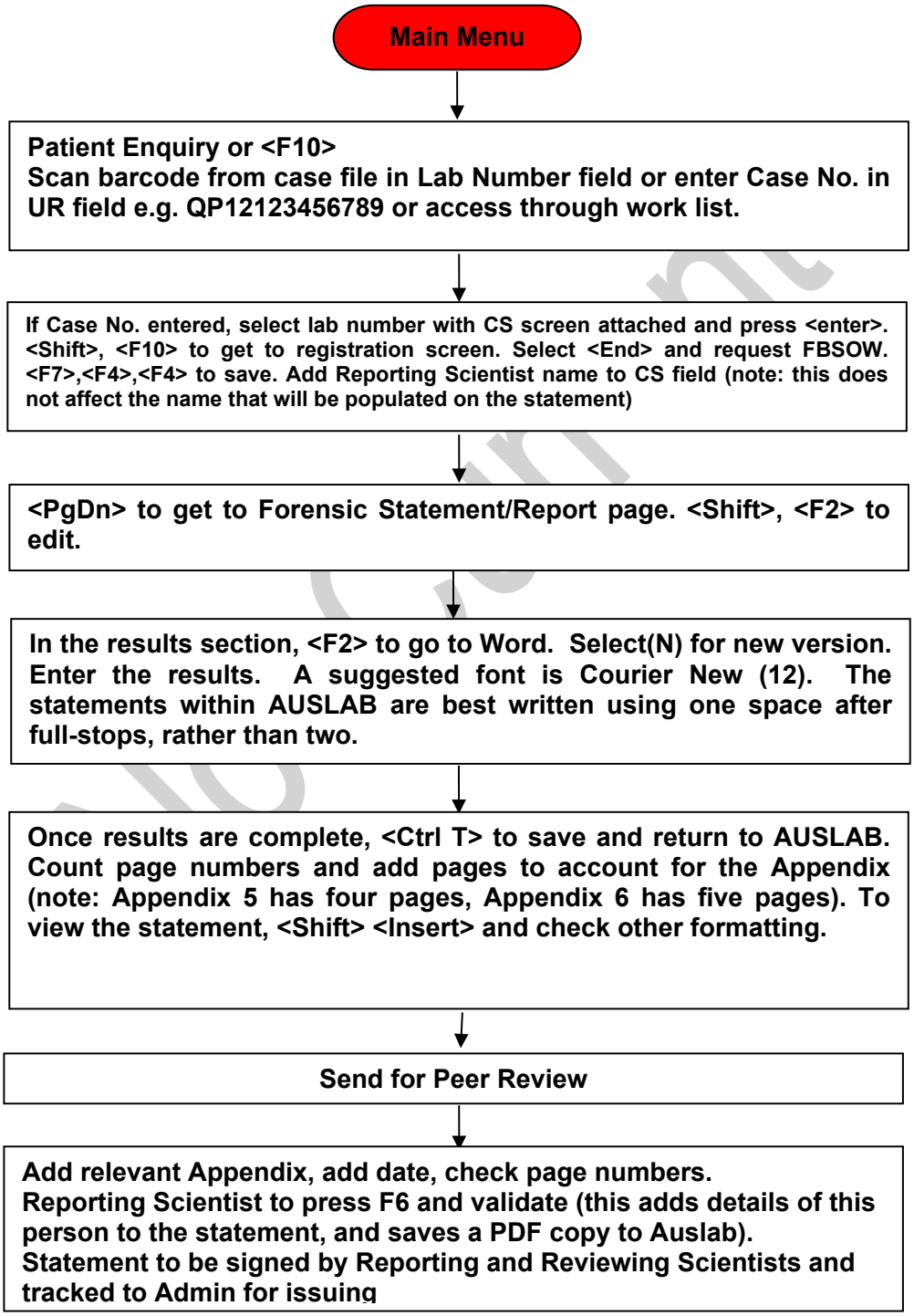

To view statement, <Shift> <Insert>. To print, <Ctrl> <F11> and direct to a printer.
NB. A new barcode should be requested in AUSLAB to record the review and release of the report (FBAR, FBTR and FBIOLR testcodes). The appropriate fields on the Case file Particulars form should be completed.
NB. When an Addendum statement is being written, the Case Status should be changed to REACTIVATED. The status should change to SENT TO PEER, RETURNED FROM PEER and REPORT ISSUED as it progresses through review.
"Pause/Break" key to return to Main Menu

Not Current

9.7 Creating a Statement with Receipt Details in AUSLAB

Purpose: The test code FBSOW creates a statement with the receipt details automatically entered.

To create a statement with receipt details:



9.8 EXH REPORTING (Sub-Sample No. Rules)

This appendix is for the process of reporting back results via EXHs, to the Queensland Police DNA Result Management Unit (DRMU) for individual items by staff of Forensic DNA Analysis. Note, the examples provided are relevant to Profiler® Plus interpretations and EXH lines. See 23008 Explanations of EXH Results for the complete list of EXHs relevant for Profiler® Plus and PowerPlex 21 in conjunction with the use of STRmix™

- Since 1 July 2008, the bulk of the examinations have been performed by QPS. After their examinations, samples are received by Forensic DNA Analysis in-tubes. The barcode on the tubes relate to an EXH barcode and as such, the presumptive and final results are reported back on the single barcode.

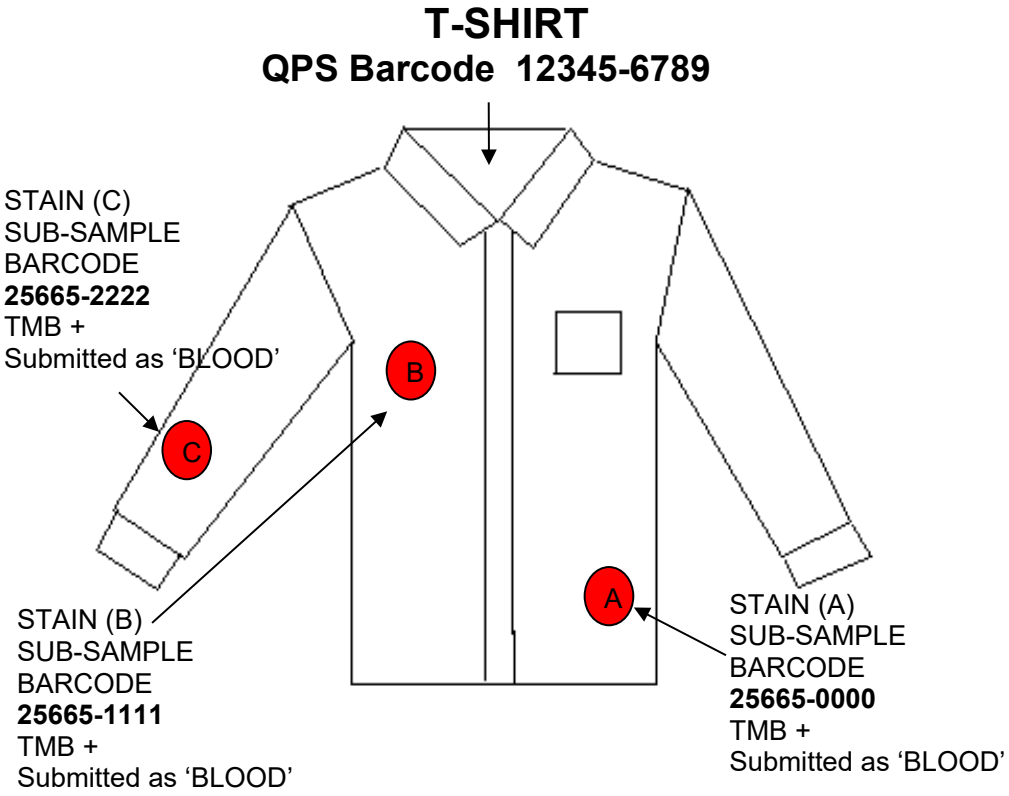
- Different scenarios have been included in examples given in the following pages. These scenarios relate to reporting of non-in tube cases, and the table format is as per EXH pages (excluding the 'Peer Review' column). For more information, refer to QIS 17142.

- Examples of different scenarios are depicted below. Some of these examples use Profiler® Plus interpretations (eg. '9Loci DNA profile'):

1. **One Item – multiple stains** = same presumptive result and only one type of extraction requested.
2. **One Item – multiple stains** = different presumptive results and two types of extractions requested.
3. **One Item – multiple stains** = different presumptive results (but with same extraction request) as well as three differing types of extractions requested.
4. **Swabs** – where no sub-sample barcode is required
5. **Cigarette Butts** – where no sub-sample barcode is required
6. **Sexual Assault Investigation Kits** (SAIK) & clothing
7. **Sexual Assault investigation Kits** (SAIK) – negative results.

Not Current

EXAMPLE 1.



Not C

EXH TEST CODE is **registered under 12345-6789 (T-SHIRT)**

Only sub-samples are used to report back presumptive tests & final results

PRESUMPTIVE RESULTS

LAB NO.	Result/Status	Linked No.	Warm Linked Name
25665-0000	Presumptive blood test pos. Submitted – results pending		

Note as all three stains were TMB positive, only one presumptive test result needs to be entered. (Any one of the three sub-samples for the stains can be entered)

FINAL RESULTS

If all three DNA profiles are the same, then only one result needs to be reported back. If this is the case, then use the same sub-sample as used to originally report back the presumptive test results.

LAB NO.	Result/Status	Linked No.	Warm Linked Name
25665-0000	Presumptive blood test pos. Submitted – results pending		
25665-0000	9 loci DNA profile	[redacted]	

OR

If the sub-sample originally used is not the best profile, you still need to report back on it – but you will also need to add the sub-sample number which does give you the best profile.

LAB NO.	Result/Status	Linked No.	Warm Linked Name
25665-0000	Presumptive blood test pos. Submitted – results pending		
25665-0000	Partial DNA profile	[redacted]	
25665-1111	9 loci DNA profile		

OR

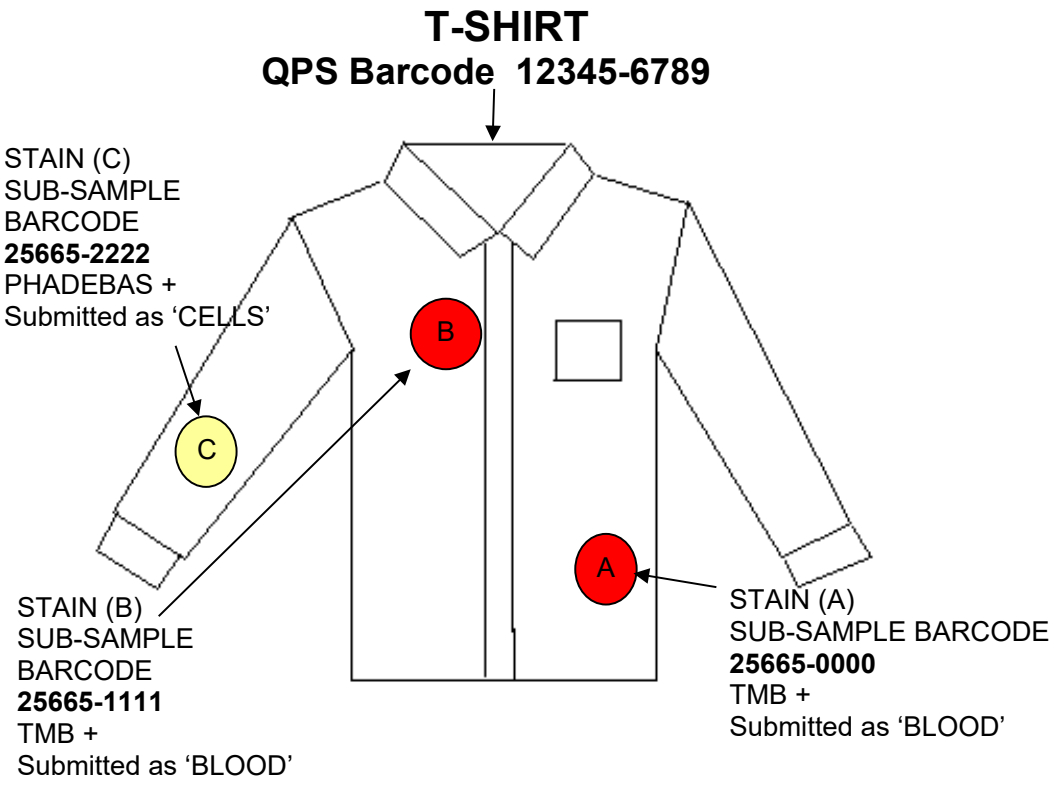
If there are two or three differing DNA profiles resulting from the three stains submitted for analysis, then **report back all differing profiles** using their sub-sample barcodes (as above).

LAB NO.	Result/Status	Linked No.	Warm Linked Name
25665-0000	Presumptive blood test pos. Submitted – results pending		
25665-0000	9 loci DNA profile	[redacted]	

Not Current

25665-1111	9 loci profile. Uploaded to NCIDD	UKM1	
25665-2222	9 loci profile. Uploaded to NCIDD	UKM2	

EXAMPLE 2.



EXH TEST CODE is **registered under 12345-6789 (T-SHIRT)**

Only sub-samples are used to report back presumptive tests & final results.

PRESUMPTIVE RESULTS

LAB NO.	Result/Status	Linked No.	Warm Linked Name
25665-0000	Presumptive blood test pos. Submitted – results pending		
25665-2222	Presumptive saliva positive. Submitted – results pending		

Note as two stains were TMB positive, you only need one TMB+ presumptive test result to be sent back to QPS DRMU for this item. Any one of the two sub-samples for the TMB+ stains can be entered (as above). A second presumptive result is sent back for the Phadebas + result as well.

FINAL RESULTS

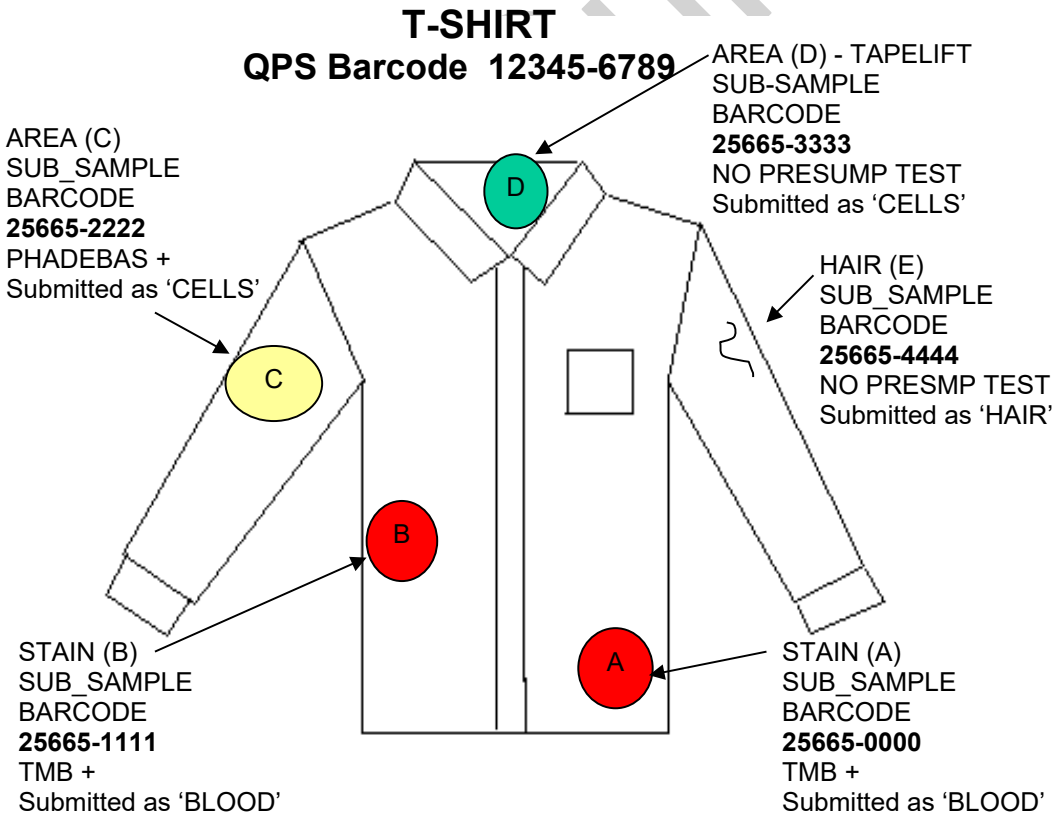
LAB NO.	Result/Status	Linked No.	Warm Linked Name
25665-0000	Presumptive blood test pos. Submitted – results pending		
25665-2222	Presumptive saliva positive. Submitted – results pending		
25665-0000	9 loci profile. Uploaded to NCIDD	[redacted]	
25665-2222	9 loci profile		
26665-1111	9 loci profile. Uploaded to NCIDD		

As two presumptive results were sent to DRMU initially, both the final results from these sub-samples need to be reported back – regardless if these profile end up being from the same source. By doing this DRMU can associate the resulting profiles to a possible cell source.

If the two samples submitted for the blood extraction result in the same DNA profile, then only one result needs to be reported back – use the same sub-sample as reported in the presumptive test results. If the profiles differ then both are reported back via their sub-samples.

Current

EXAMPLE 3



EXH TEST CODE is **registered under 12345-6789 (T-SHIRT)**

PRESUMPTIVE RESULTS

LAB NO.	Result/Status	Linked No.	Warm Linked Name
25665-0000	Presumptive blood test pos. Submitted – results pending		
25665-2222	Presumptive saliva positive. Submitted – results pending		
25665-4444	Hair located. Submitted – results pending		

FINAL RESULTS

LAB NO.	Result/Status	Linked No.	Warm Linked Name
25665-0000	Presumptive blood test pos. Submitted – results pending		
25665-2222	Presumptive saliva positive. Submitted – results pending		
25665-4444	Hair located. Submitted – results pending		
25665-0000	9 loci DNA profile. Uploaded to NCIDD	[redacted]	
25665-2222	Partial DNA profile		
25665-4444	No DNA Profile		
25665-1111	9 loci DNA profile. Uploaded to NCIDD	UKF1	

As three presumptive results were sent to DRMU initially, all three final results from these sub-samples need to be reported back – regardless if these profile end up being from the same source. By doing this DRMU can associate the resulting profiles to a possible cell source.

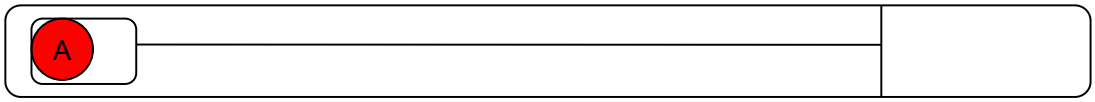
If the two samples submitted for the blood extraction result in the same DNA profile, then only one result needs to be reported back – use the same sub-sample as reported in the presumptive test results.

If the profiles differ then both are reported back via their sub-samples (as shown above).

Not Current

EXAMPLE 4.

SWAB - QPS BARCODE 12345-6789 (-001)



STAIN (A)
NO SUB NUMBER BARCODE GIVEN
TMB +
Submitted as 'BLOOD'

No sub-numbering required for this item as the entire sample is exhausted

PRESUMPTIVE AND FINAL EXH ON SWAB EXH BARCODE

LAB NO.	Result/Status	Linked No.	Warm Linked Name
12345-6789	Presumptive blood test pos. Submitted – results pending		
12345-6789	9 loci DNA profile. Uploaded to NCIDD	[redacted]	

Current

EXAMPLE 5.

CIG BUTT - QPS BARCODE 12345-9999 (-001)

AREA (A)
NO SUB NUMBER BARCODE GIVEN
NO PRESUMPTIVE TEST
Submitted as 'CELLS'

No sub-numbering required for this item

PRESUMPTIVE AND FINAL EXH ON CIGERETTE BUTT EXH BARCODE

LAB NO.	Result/Status	Linked No.	Warm Linked Name
12345-9999	Submitted results pending		

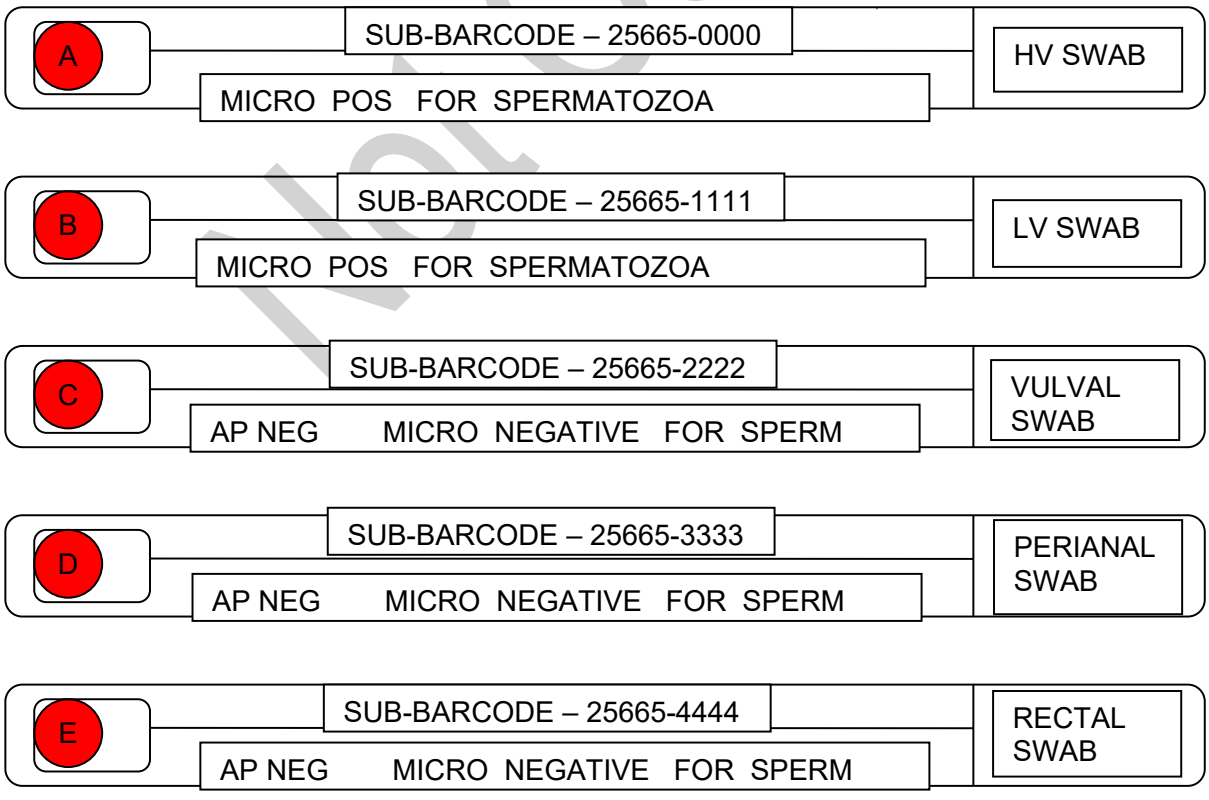
12345-9999	9 loci DNA profile. Uploaded to NCIDD	[redacted]

Not Current

EXAMPLE 6.

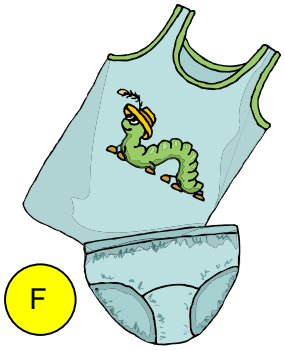
SAIK = QPS BARCODE 12345-6789

SAIK CONTAINS FIVE SWABS and TWO CLOTHING ITEMS (NOT BARCODED BY QPS)



TWO CLOTHING ITEMS:

SUB-BAROCDE: 25665-6666
ITEM: UNDERPANTS
AP POSITIVE
MICRO POS FOR SPERM



SUB –BARCODE: 25665-5555
ITEM: SINGLET TOP
AP NEGATIVE

Reporting back on SAIK via EXH registered under barcode 12345-6789.

PRESUMPTIVE RESULTS

	Result/Status	Linked No.	Warm Linked Name
25665-0000	Micro positive for sperm. Submitted results pending		
25665-5555	Semen not detected.		
25665-6666	Micro positive for sperm. Submitted results pending		

Note: only the high vaginal swab is reported back to QPS out of the five swabs submitted. In this example: three swabs share the same positive results and two swabs are negative. The EXH to QPS is reported back on the most probative of all the positive swabs – the high vaginal swab.

There is no need to report back the negative swabs results as these results do not add any information needed by QPS at this stage.

Both items of clothing also have their presumptive results reported back via the same SAIK EXH to QPS. The SAIK and the clothing have their own FBEXAM registered to record the examination details.

When the profile in the Epithelial fraction matches the donor, and is therefore not an unexpected finding, this result is not usually reported in the EXH.

FINAL RESULTS

	Result/Status	Linked No.	Warm Linked Name
25665-0000	**Micro positive for sperm. Submitted results pending**		
25665-5555	**Semen not detected.**		
25665-6666	**Micro positive for sperm. Submitted results pending**		
25665-0000	Mixed profile, major component uploaded to NCIDD.	[redacted]	
25665-0000	Mixed profile, partial minor component.		

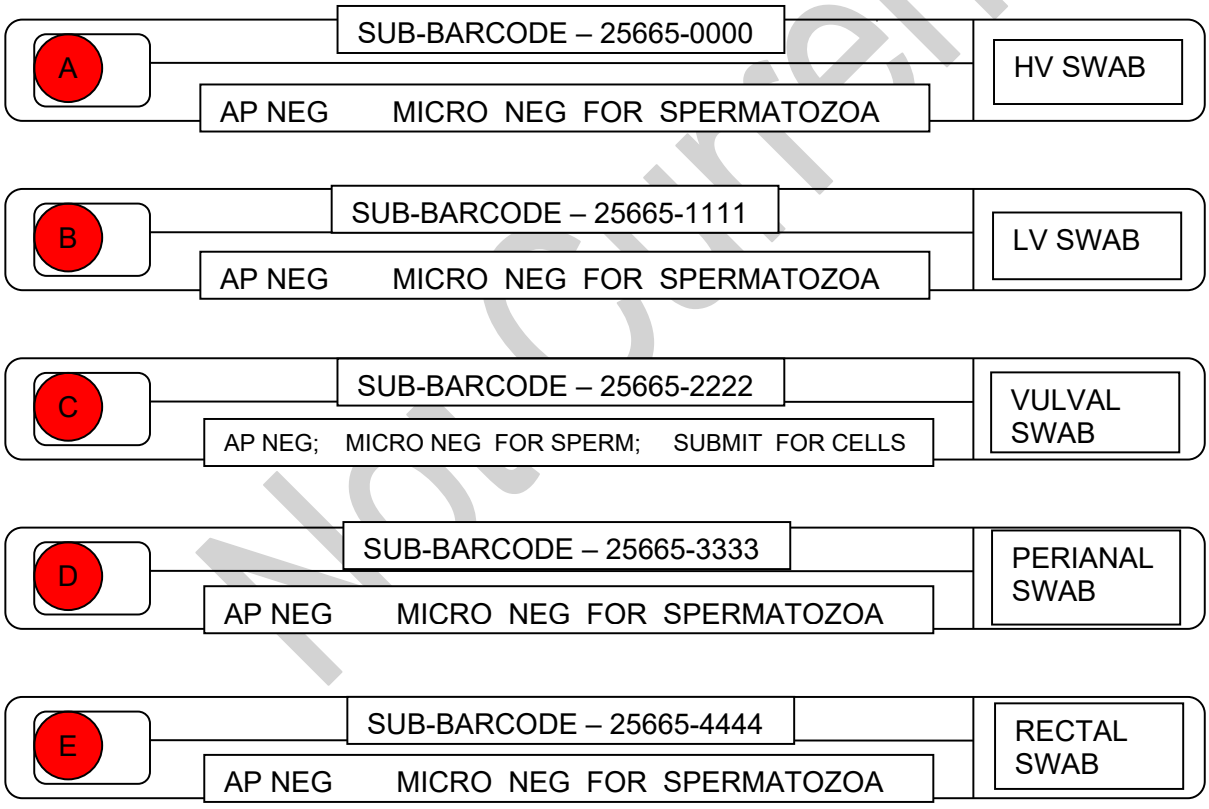
Not Current

25665-1111	Mixed DNA profile, conditioned on.	[redacted]	
25665-1111	Mixed DNA profile. Remaining profile after conditioning.		
25665-6666	Mixed part profile. No major/minor. Unable to load to NCIDD.		

EXAMPLE 7.

SAIK = QPS BARCODE 12345-6789

SAIK CONTAINS FIVE SWABS (NOT BARCODED BY QPS)



Not Current

PRESUMPTIVE RESULTS

	Result/Status	Linked No.	Warm Linked Name
12345-6789	Semen not detected.		
25665-2222	Submitted as cells		

In this example, the five swabs were all negative for AP and microscopy, and the EXH has the parent barcode as the barcode entered to summarise that the whole item did not have semen detected. The two items of clothing are also reported back as negative to QPS. However, even though the vulval swab was also negative to all presumptive testing, it will still be submitted for a 'cell' extraction. DNA analysis is requested for the vulval swab as a last ditch effort, given both the SAIK and clothing are negative for all testing performed.

If QPS request an item for specific testing (eg blood) and the whole item was negative (eg Presump blood test neg), then the EXH will use the item/parent barcode to report back the results.

FINAL RESULTS

	Result/Status	Linked No.	Warm Linked Name
12345-6789	Semen not detected.		
25665-2222	Submitted as cells		
25665-2222	No DNA profile		

Not Current

9.9 COMPLETE CASEWORK PREAMBLE – EXAMINATIONS BY QHFSS

XX. The following information is provided to assist in the understanding of the contents of this statement.

Forensic Biology

As a forensic biologist, it is my role to report on the examination of items submitted in relation to this 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. Any DNA profiles which are obtained from these samples are then compared with the DNA profiles obtained from an individual's reference sample.

Examinations

The examinations described in this Statement of Witness were carried out by colleagues. The notes, which have been referred to in the preparation of this report, were made at the time of examination. All examinations were performed in accordance with the SOPs of this laboratory.

Forensic DNA Analysis case files 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.

DNA Profiling

Please refer to the Appendix for an overview of DNA profiling.

Reference Samples

One or more reference sample/s provided for this case have been profiled using the PowerPlex21 system, which tests twenty regions (loci) of DNA containing STRs, and an additional region which provides an indication of gender of the DNA source. All other item/s within this case have been profiled using the Profiler® Plus system (nine regions plus gender). Of the twenty regions of DNA that the PowerPlex21 system tests, nine of them are the same as those tested using the Profiler® Plus system. Comparisons made between the reference sample/s and all other item/s within the case, and any statistical analyses undertaken, have been made based on the nine regions of DNA common to both systems.

Unknown DNA Profiles

If DNA profiles are obtained which do not match any of the reference DNA profiles associated to the case, they are considered to be of unknown origin. Where possible, these DNA profiles are assessed for gender, and then assigned sequential numerical designations (eg. Unknown Male 1, Unknown Male 2). If it is not possible to assign gender, the term Unknown Person is applied. Please note that numerical designations may be applied prior to the availability of reference DNA profiles. This means that if a reference DNA profile is found to match a DNA profile designated as Unknown Male 1, then Unknown Male 1 will not be referred to in the statement.

Mixed DNA profiles *(Profiler® Plus only)*

When more than one person has contributed DNA to a sample, the DNA profile obtained is referred to as a mixed DNA profile. The mixture of DNA can happen in many ways, however the resultant DNA profile can often be explained in terms of the following categories:

Major / minor mixtures – these generally occur when one person contributes more DNA to a sample than another person. It is possible to resolve these mixtures into individual contributions, referred to as major and minor DNA profiles.

Even mixtures – these generally occur when two (or more) people contribute DNA to a sample in approximately equal proportions. It is not possible to determine individual contributions to these mixtures, unless we can assume a contribution of DNA from a particular person (this is referred to as 'conditioning').

Conditioning can be performed on mixed DNA profiles obtained from samples taken from body surfaces, intimate swabs or clothing, where the person / owner is clearly identified through information provided to the laboratory. In these circumstances it is not unexpected to find DNA that could have originated from that person in the sample. Therefore if it is assumed that this person has contributed DNA to the mixed DNA profile, then the components of their DNA profile can be effectively subtracted from the mixture. This may leave a remaining DNA profile which can be used for comparison purposes.

Not Current

Note: If the relevant information provided to the laboratory changes, for example regarding the ownership of an item of clothing, then the interpretation of the mixture may change in that it may no longer be appropriate to condition the mixture.

Complex mixtures - this is when the DNA profile contains an unknown number of contributors, and / or provides too limited an amount of information for meaningful comparison purposes. In some cases it may be possible to compare the reference DNA profile of a person with the DNA components within these complex mixtures. If it appears that the person's DNA profile is represented within the complex DNA profile, then this person can be described as not being excluded as a potential contributor of DNA. In other cases the mixed DNA profile may be so complex or incomplete that it may not be possible to draw any conclusions as to whether a person may have contributed DNA. In these instances, the complex DNA profile may be deemed unsuitable for comparison purposes.

Note: Additional complexity may arise when interpreting mixed DNA profiles where multiple potential contributors of DNA to the mixture are genetically related. This is due to the increased potential for related individuals to share genetic information.

Touch DNA / Transfer of DNA

When a person touches a surface, it is possible for their cellular material to be transferred onto that surface. This transferred cellular material can often be recovered 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.

The generation of a DNA profile will depend on many factors. These include the amount of cellular material transferred, the nature of the surface being touched and the amount of cellular material a person has available to transfer.

The persistence of any transferred cellular material on a surface will depend largely upon the nature of the surface and the conditions under which it has been kept in the time between deposition and recovery of the DNA. For example, cellular material could be lost from the surface by washing or mechanical action such as abrasion.

It therefore follows that the absence of a DNA profile from a touched surface does not necessarily mean that that person has not come into contact with it, as it is possible for a person to come into contact with a surface without a detectable amount of their DNA being transferred or recovered.

Blood stains

Potential blood stains 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

The presence of semen on an item can be indicated by the use of a presumptive chemical test which detects a major constituent of seminal fluid (Acid Phosphatase – AP). This constituent does, however, exist in other body fluids, such as vaginal secretions. Additional presumptive chemical

Not Current

testing (Prostate Specific Antigen – PSA / p30) can be undertaken and a positive reaction to both AP and PSA / p30 makes it highly likely that seminal fluid is present. The presence of semen can be confirmed via the microscopic identification of spermatozoa (sperm heads).

Samples may undergo a differential lysis extraction process which aims to separate spermatozoa and epithelial / cellular 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 intimate female SAIK samples to be stored following a Differential Lysis Extraction process. This is primarily due to the fact that when the vast majority of these fractions are profiled, they are found to match the person from whom the sample was taken. Given the intimate nature of these samples, this finding is not unexpected. These epithelial fractions will be 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. Any semen which 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 likelihood 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.

The greater the delay between deposition and sampling, the less chance there is of finding semen. 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 which 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.

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 fluids and anal secretions, although usually at much lower concentration than that found in saliva.

If an area of the body is sucked or licked, saliva may be transferred onto the skin and subsequently onto any items of clothing worn on this area of the body. Saliva staining, in the form of amylase may then be detected on skin swabs or items of clothing as long as the clothing or skin has not

Not Current

been washed. Cellular material will be shed, to varying degrees, with the saliva and as such it may be possible to obtain a DNA profile from an area of saliva staining.

12. The results of the scientific examinations conducted in this laboratory are as follows:

Not Current

9.10 COMPLETE CASEWORK PREAMBLE - EXAMINATIONS BY QPS AND QHFSS

XX. The following information is provided to assist in the understanding of the contents of this statement.

Forensic Biologist

As a forensic biologist, it is my 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 which are obtained from these samples are then compared with the DNA profiles obtained from an individual's reference sample.

Examinations and DNA Profiling *(PowerPlex 21 only)*

Please refer to the Appendix for an overview of DNA profiling.

Forensic DNA Analysis case files 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.

Examinations *(Profiler® Plus only)*

Unless otherwise stated, the examinations of items for biological material were conducted by officers within the QPS. Sub-samples from these items were forwarded to Queensland Health Forensic and Scientific Services (QHFSS) for the purposes of conducting DNA analysis.

Samples submitted to QHFSS for DNA analysis may include swabs, tape-lifts or small sections of material cut from an exhibit. Individual samples are typically submitted within small plastic tubes and are referred to as 'in-tube' samples.

It is my understanding that the QPS are responsible for item prioritisation, sample selection, selection of screening / sampling methods, application of anti-contamination and standard operating procedures (SOPs) on work undertaken on the items / samples prior to submission to QHFSS. As such, forensic biologists may not be able to provide information or opinion on the possible biological origin of any 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, notes are made at the time of the examination by the examining scientist and form part of the case file.

Forensic DNA Analysis case files 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.

DNA Profiling *(Profiler® Plus only)*

Please refer to the Appendix for an overview of DNA profiling.

Reference Samples

Not Current

One or more reference sample/s provided for this case have been profiled using the PowerPlex21 system, which tests twenty regions (loci) of DNA containing STRs, and an additional region which provides an indication of gender of the DNA source. All other item/s within this case have been profiled using the Profiler® Plus system (nine regions plus gender). Of the twenty regions of DNA that the PowerPlex21 system tests, nine of them are the same as those tested using the Profiler® Plus system. Comparisons made between the reference sample/s and all other item/s within the case, and any statistical analyses undertaken, have been made based on the nine regions of DNA common to both systems.

Unknown DNA Profiles

If DNA profiles are obtained which do not match any of the reference DNA profiles associated to the case, they are considered to be of unknown origin. Where possible, these DNA profiles are assessed for gender, and then assigned sequential numerical designations (eg. Unknown Male 1, Unknown Male 2). If it is not possible to assign gender, the term Unknown Person is applied. Please note that numerical designations may be applied prior to the availability of reference DNA profiles. This means that if a reference DNA profile is found to match a DNA profile designated as Unknown Male 1, then Unknown Male 1 will not be referred to in the statement.

Mixed DNA profiles (*Profiler® Plus only)*

When more than one person has contributed DNA to a sample, the DNA profile obtained is referred to as a mixed DNA profile. The mixture of DNA can happen in many ways, however the resultant DNA profile can often be explained in terms of the following categories:

Major / minor mixtures – these generally occur when one person contributes more DNA to a sample than another person. It is possible to resolve these mixtures into individual contributions, referred to as major and minor DNA profiles.

Even mixtures – these generally occur when two (or more) people contribute DNA to a sample in approximately equal proportions. It is not possible to determine individual contributions to these mixtures, unless we can assume a contribution of DNA from a particular person (this is referred to as 'conditioning').

Conditioning can be performed on mixed DNA profiles obtained from samples taken from body surfaces, intimate swabs or clothing, where the person / owner is clearly identified through information provided to the laboratory. In these circumstances it is not unexpected to find DNA that could have originated from that person in the sample. Therefore if it is assumed that this person has contributed DNA to the mixed DNA profile, then the components of their DNA profile can be effectively subtracted from the mixture. This may leave a remaining DNA profile which can be used for comparison purposes.

Note: If the relevant information provided to the laboratory changes, for example regarding the ownership of an item of clothing, then the interpretation of the mixture may change in that it may no longer be appropriate to condition the mixture.

Complex mixtures - this is when the DNA profile contains an unknown number of contributors, and / or provides too limited an amount of information for meaningful comparison purposes. In some cases it may be possible to compare the reference DNA profile of a person with the DNA components within these complex mixtures. If it appears that the person's DNA profile is represented within the complex DNA profile, then this person can be described as not being excluded as a potential contributor of DNA. In other cases the mixed DNA profile may be so complex or incomplete that it may not be possible to draw any conclusions as to whether a person

Not Current

may have contributed DNA. In these instances, the complex DNA profile may be deemed unsuitable for comparison purposes.

Note: Additional complexity may arise when interpreting mixed DNA profiles where multiple potential contributors of DNA to the mixture are genetically related. This is due to the increased potential for related individuals to share genetic information.

Touch DNA / Transfer of DNA

When a person touches a surface, it is possible for their cellular material to be transferred onto that surface. This transferred cellular material can often be recovered 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.

The generation of a DNA profile will depend on many factors. These include the amount of cellular material transferred, the nature of the surface being touched and the amount of cellular material a person has available to transfer.

The persistence of any transferred cellular material on a surface will depend largely upon the nature of the surface and the conditions under which it has been kept in the time between deposition and recovery of the DNA. For example, cellular material could be lost from the surface by washing or mechanical action such as abrasion.

It therefore follows that the absence of a DNA profile from a touched surface does not necessarily mean that that person has not come into contact with it, as it is possible for a person to come into contact with a surface without a detectable amount of their DNA being transferred or recovered.

Blood stains

Potential blood stains 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

The presence of semen on an item can be indicated by the use of a presumptive chemical test which detects a major constituent of seminal fluid (Acid Phosphatase – AP). This constituent does, however, exist in other body fluids, such as vaginal secretions. Additional presumptive chemical testing (Prostate Specific Antigen – PSA / p30) can be undertaken and a positive reaction to both AP and PSA / p30 makes it highly likely that seminal fluid is present. The presence of semen can be confirmed via the microscopic identification of spermatozoa (sperm heads).

Samples may undergo a differential lysis extraction process which aims to separate spermatozoa and epithelial / cellular 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 intimate female SAIK samples to be stored following a Differential Lysis Extraction process. This is primarily due to the fact that when the vast majority of these fractions are profiled, they are found to match the person from whom the sample was taken. Given the intimate nature of these samples, this finding is not unexpected. These epithelial fractions will be stored indefinitely, and can be sent for DNA profiling at a future date if required.

Not Current

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. Any semen which 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 likelihood 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.

The greater the delay between deposition and sampling, the less chance there is of finding semen. 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 which 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.

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 fluids and anal secretions, although usually at much lower concentration than that found in saliva.

If an area of the body is sucked or licked, saliva may be transferred onto the skin and subsequently onto any items of clothing worn on this area of the body. Saliva staining, in the form of amylase may then be detected on skin swabs or items of clothing as long as the clothing or skin has not been washed. Cellular material will be shed, to varying degrees, with the saliva and as such it may be possible to obtain a DNA profile from an area of saliva staining.

XX. The results of the scientific examinations conducted in this laboratory are as follows:

9.11 COMPLETE PATERNITY PREAMBLE

XX. The following information is provided to assist in the understanding of the contents of this statement.

Not Current

Forensic Biology

As a Forensic Biologist, it is my role to report on the examination of items submitted in relation to this 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. Any DNA profiles which are obtained from these samples are then compared with the DNA profiles obtained from an individual's reference sample.

Examinations

The examinations described in this Statement of Witness were carried out by colleagues. The notes, which have been referred to in the preparation of this report, were made at the time of examination. All examinations were carried out in accordance with Standard Operating Procedures.

DNA Profiling

DNA is a complex chemical found in almost all cells in the human body. It carries genetic information which determines the physical and chemical characteristics of a person. The DNA system used at Queensland Health looks at 10 regions of DNA, 9 of which contain Short Tandem Repeats (STRs). The tenth region gives an indication as to the gender of the donor.

Or, if PowerPlex 21 was used for all samples:

DNA is a complex chemical found in almost all cells in the human body. It carries genetic information which determines the physical and chemical characteristics of a person. The DNA system used at Queensland Health looks at 21 regions of DNA, 20 of which contain Short Tandem Repeats (STRs). The twenty-first region gives an indication as to the gender of the donor.

Two DNA components (alleles) are detected at each region of DNA tested. This total of 18 alleles *(or 40 alleles),* plus gender information, comprises an individual's DNA profile. Of the two alleles detected at each of the regions tested, one is inherited from an individual's biological mother, and the other component is inherited from an individual's biological father.

Reference Samples (NB, Remove if all samples profiled with PowerPlex 21).

One or more reference sample/s provided for this case have been profiled using the PowerPlex21 system, which tests twenty regions (loci) of DNA containing STRs, and an additional region which provides an indication of gender of the DNA source. All other item/s within this case have been profiled using the Profiler® Plus system (nine regions plus gender). Of the twenty regions of DNA that the PowerPlex21 system tests, nine of them are the same as those tested using the Profiler® Plus system. Comparisons made between the reference sample/s and all other item/s within the case, and any statistical analyses undertaken, have been made based on the nine regions of DNA common to both systems.

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 mother is indeed the biological

Not Current

mother of the foetus/child, it is possible to determine which DNA components within the DNA profile of the child could have originated from her. The remaining DNA components within the DNA profile of the foetus/child must have originated from the biological father, and are called *obligate paternal alleles*.

If the DNA profile of a putative father **does not** contain the obligate paternal alleles in at least two of the DNA regions tested, then that person 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 that person is **not excluded** as a potential biological father of the foetus/child. This means that this putative father could indeed be the biological father.

Statistical analysis is then conducted to aid in the understanding of the strength of the evidence. The Paternity Index (PI) is a likelihood of two probabilities conditional upon different competing hypotheses;

1. The alleged father contributed the obligate paternal alleles observed in the DNA profile of the foetus/child

2. Another man chosen at random contributed the obligate paternal alleles observed in the DNA profile of the foetus/child.

The PI reflects how many times more likely it is to see the evidence (ie. Set of alleles) under the first hypothesis compared to the second hypothesis. The generally accepted minimum standard for an inclusion of paternity is a PI of 200 or greater (NATA Paternity Testing Technical Advisory Group, 2004).

(Adapted from Butler, J.M. (2005) Chapter 23, *Kinship and Parentage Testing in* Forensic DNA Typing, Biology, Technology, and Genetics of STR Markers, 2 Ed. Elsevier Academic Press: Burlington, MA 01803, USA.)

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.

Not Current

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>.

Not Current

9.12 QUALITY PARAGRAPHS

QUALITY PARAGRAPHS

NB. These paragraphs are required to be entered into the preambles of statements containing results from DNAIQ extractions on the Automated Platforms during the period October 2007- July 2008. The particular category will depend on the investigation outcomes of each case.

Quality

Category A

Testing for this case has been conducted in a period where some results were the subject of an adverse event. An adverse event includes a deficient operation or function identified to have occurred within the automated extraction process utilised in testing during the period October 2007 to July 2008. Testing for this case was not the subject of any adverse result. An adverse result is a result which has been affected by an adverse event, whose integrity cannot be verified. This conclusion has been reached by conducting a review of the results and assessing a number of factors, including, but not limited to, the comparison of all other results from samples processed alongside this result, to detect whether the integrity of each sample can be verified. Retesting has been conducted on identified samples which have confirmed information in the original results.

Category B

Testing for this case has been conducted in a period where some results where the subject of adverse events. An adverse event includes a deficient operation or function identified to have occurred within the automated extraction process utilised in testing during the period October 2007 and July 2008. Within this case, the adverse event is demonstrated to have affected a result or results and the integrity cannot be verified. There was no remaining sample for retesting to be conducted. These results have therefore been reported as follows 'these samples did not pass our Quality System requirements at the DNA analysis stage and therefore the DNA profiling results relating to these samples cannot be reported'.

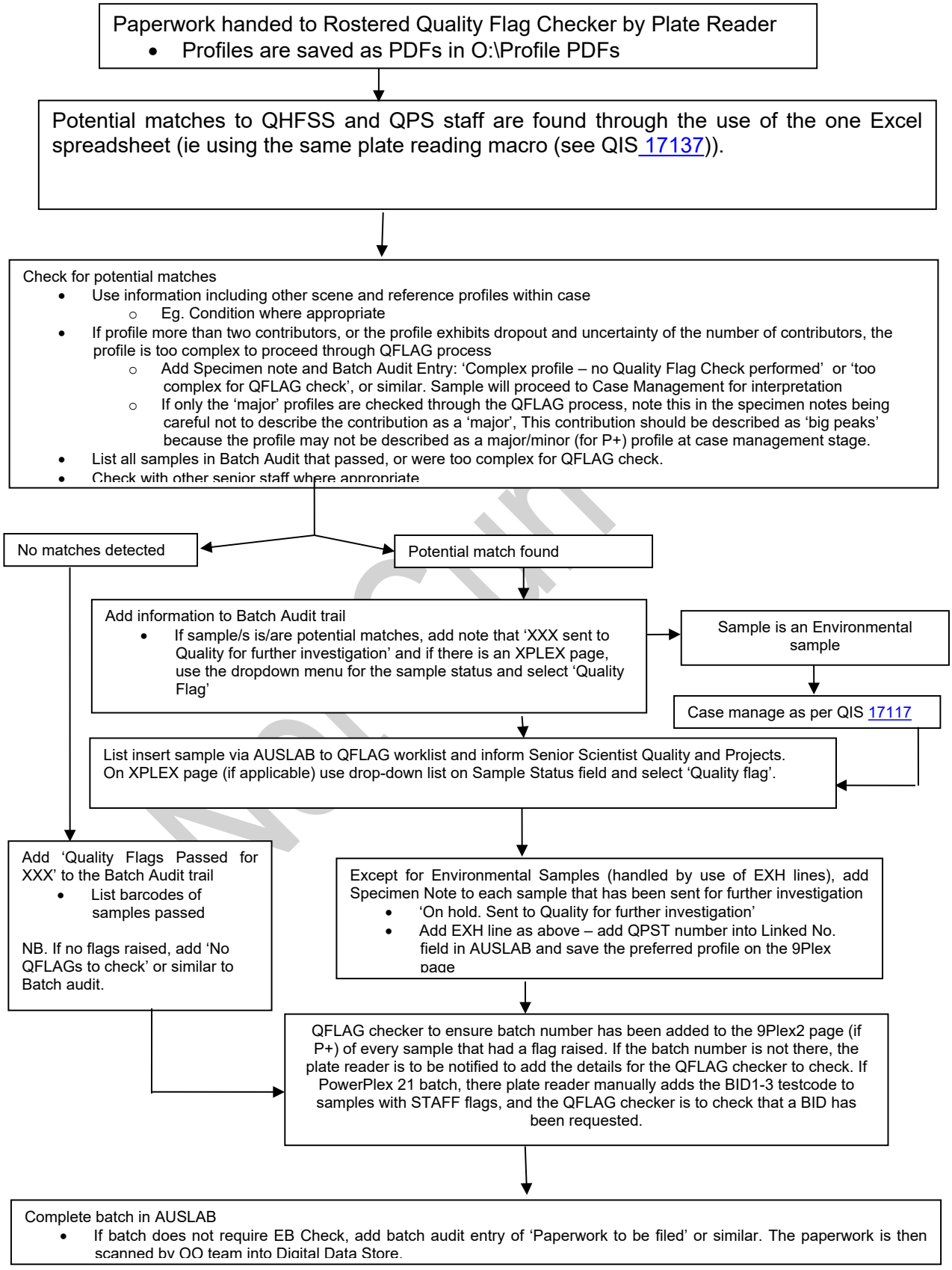
Category C

Testing for this case has been conducted in a period where some results were the subject of adverse events. An adverse event includes a deficient operation or function identified to have occurred within the automated extraction process utilised in testing during the period of October 2007 and July 2008. Testing for some samples within this case has been the subject of an adverse event. The cause of the adverse event was identified to have occurred within the automated extraction process. Portions of the sample remained available for further testing. Retesting has been conducted, using an alternative manual extraction method and all quality assurance checks were satisfactory. These samples have been reported as they have been assessed as no adverse event having been detected and the results have passed all quality assurance checks.

Not Current

9.13 QUALITY FLAG CHECKING WORKFLOW

Not Current


Paperwork handed to Rostered Quality Flag Checker by Plate Reader
• Profiles are saved as PDFs in O:\Profile PDFs
Potential matches to QHFSS and QPS staff are found through the use of the one Excel spreadsheet (ie using the same plate reading macro (see QIS 17137)).
Check for potential matches
• Use information including other scene and reference profiles within case
○ Eg. Condition where appropriate
• If profile more than two contributors, or the profile exhibits dropout and uncertainty of the number of contributors, the profile is too complex to proceed through QFLAG process
○ Add Specimen note and Batch Audit Entry: 'Complex profile – no Quality Flag Check performed' or 'too complex for QFLAG check', or similar. Sample will proceed to Case Management for interpretation
○ If only the 'major' profiles are checked through the QFLAG process, note this in the specimen notes being careful not to describe the contribution as a 'major', This contribution should be described as 'big peaks' because the profile may not be described as a major/minor (for P+) profile at case management stage.
• List all samples in Batch Audit that passed, or were too complex for QFLAG check.
• Check with other senior staff where appropriate
No matches detected
Potential match found
Add information to Batch Audit trail
• If sample/s is/are potential matches, add note that 'XXX sent to Quality for further investigation' and if there is an XPLEX page, use the dropdown menu for the sample status and select 'Quality Flag'
Sample is an Environmental sample
Case manage as per QIS 17117
List insert sample via AUSLAB to QFLAG worklist and inform Senior Scientist Quality and Projects.
On XPLEX page (if applicable) use drop-down list on Sample Status field and select 'Quality flag'.
Add 'Quality Flags Passed for XXX' to the Batch Audit trail
• List barcodes of samples passed
NB. If no flags raised, add 'No QFLAGs to check' or similar to Batch audit.
Except for Environmental Samples (handled by use of EXH lines), add Specimen Note to each sample that has been sent for further investigation
• 'On hold. Sent to Quality for further investigation'
• Add EXH line as above – add QPST number into Linked No. field in AUSLAB and save the preferred profile on the 9Plex page
QFLAG checker to ensure batch number has been added to the 9Plex2 page (if P+) of every sample that had a flag raised. If the batch number is not there, the plate reader is to be notified to add the details for the QFLAG checker to check. If PowerPlex 21 batch, there plate reader manually adds the BID1-3 testcode to samples with STAFF flags, and the QFLAG checker is to check that a BID has been requested.
Complete batch in AUSLAB
• If batch does not require EB Check, add batch audit entry of 'Paperwork to be filed' or similar. The paperwork is then scanned by QQ team into Digital Data Store.

Notes on the Quality Flag Checking Process:

- Quality Flag Checking is to detect gross contamination that could have occurred at collection or during processing of the sample.
  - This includes single-source profiles, distinct major or minor profiles, or remaining contributions if the mixed profile has been conditioned.

- Due to the complexity of some DNA profiles, profiles that indicate at least three contributors (and therefore an unknown number of contributors) are generally not suitable for Quality Flag checking for the following reasons:
  - The number of contributors is not known and the often partial nature adds complexity.
  - At most, a person may not be able to be excluded as a potential contributor and this interpretation may not be useful to the client as we cannot evaluate the significance of a possible inclusion by adding statistical weight for Profiler Plus profiles. For PowerPlex 21 profiles, a STRmix evaluation is possible, yet the LR value obtained requires a subjective assessment for QPS to determine likelihood of contributing DNA to the mixture. Caution should be exercised and this can be done by searching and reporting gross contaminations.

- When profiles of at least three contributors are obtained, the Quality Flag Checker should note in the Batch Audit and the Specimen Notes:
  - 'Complex profile – no Quality Flag check performed' or similar wording
  - The profile will then proceed to case management for interpretation with case context.

- It may be possible for the higher RFU peaks (if demonstrating a pattern as such across the profile) to be QFLAG checked
  - If the peaks pass, write in the Batch Audit and Specimen Notes: 'Big peaks passed QFLAGs. Small peaks too complex for QFLAG checking' or similar wording
  - Refrain from using 'Major/Minor' terminology because the Case Manager may interpret the profile not to be a major/minor profile (vis. PowerPlex 21 profiles).

- The macro that is applied to detect potential Quality Flags has a stringency of 13 alleles. This means, crime scene profiles with less than 13 alleles detected will not go through the macro and therefore will not be Quality Flag checked.
  - When performing the Quality Flag task, the staff match table in AUSLAB is colour coded for ease of interpretation. This table only applies to Profiler Plus batches.
  - The Crime Scene profile is in the column at far left. The QPS Elimination samples are in the next six columns
  - When an allele in the QPS elimination profile matches an allele found in the Crime Scene profile, the allele is coloured yellow.
  - When an allele in the QPS elimination profile is not found in the Crime Scene profile, the allele is coloured green.
  - When there are too many alleles in the Crime Scene profile to fit into the column, the alleles push data across the columns to the right. This is a data fault of the columns in AUSLAB
  - The alleles in the column immediately to the right are part of the profile in the column to the left and the Quality Flag checker should account for this in their comparisons
  - The colouring system is not affected. What this means is that even though the data is pushed into the adjacent column, the match/non-match determination of those alleles with the Crime Scene profile is not affected.

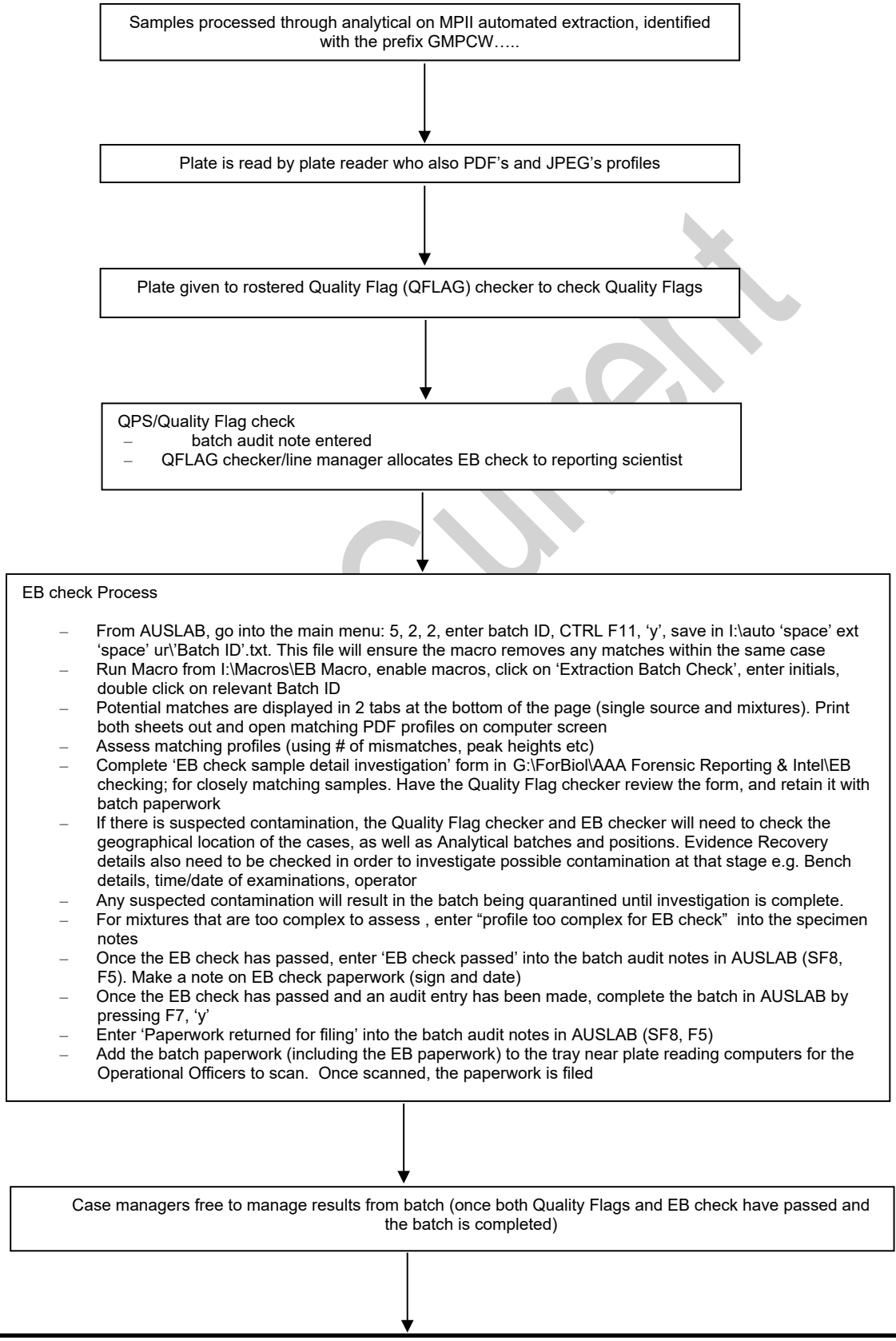
- If an EB check is required to check for cross-sample contamination in locked batches (eg. GMPCW…):
  - Write 'Paperwork given to EB Checker/checking team' or similar, and deliver paperwork to Senior Scientist on the rotation that includes EB Check, or delegate.
  - If batch does not require EB Check, add batch audit entry of 'Paperwork to be filed' or similar. The paperwork is then scanned by OO team into Digital Data Store.

Not Current

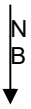
- Once comments from both Quality Flag checker and EB checker have been entered and no remaining flags are to be investigated, the person performing the last of the above tasks is to complete the batch (F7in AUSLAB on batch).

Not Current

9.14 EXTRACTION BATCH CHECKING WORKFLOW (EB Checking)



current



Case managers to manage rework results (>6 alleles) and perform EB check on samples that were originally extracted on the MPII automated platforms

- access EB Macro
- enter details into fields (sample ID, profile obtained, reader comments) in 'Update and Check from Rework' section
- click on 'Update and check'
- find the original GMPCW 9PLEX batch
- assess updated profile against matches
- if sample passed, enter specimen note 'EB check for rework performed – passed'
- If EB check not completed, enter a specimen note indicating the reason
- file rework EB check paperwork in date order in the blue folder next to the printer

EB Macro Notes:

- The Extraction Batch macro is performed before results are case managed and released to the QPS. It allows for the detection of contamination between samples that we extracted on the same automated MPII extraction batch. These batches are identified by GMPCW…..
- It compares profiles from different cases that have greater than 6 alleles against each other.
- Matches are assessed by the reporting scientist, considering both samples as the potentially contaminating and contaminated profiles.
- The EB macro divides and displays any potential matches into single source and mixtures, in two separate tabs.
- The profile highlighted in white is the profile that the profiles underneath have matched to.
- The macro displays matching loci in different colours: green indicates that there are at least 2 matching alleles, yellow indicates 1 matching allele, light orange indicates a mismatch at the entire loci, and bright orange indicates a mismatch at Amelogenin.
- The EB check can be performed at any desk. The profile highlighted in white is to be printed off, and the profiles matching to it can be displayed on the computer screen so that comparisons can be made.
- Once samples have been reworked, the reworked result needs to be checked against the batch the sample was originally extracted on. If the 9plex result is used as the reported profile; or the rework result is the same, similar, has less information or is too complex, a rework EB check is not necessary. This is assessed by the case manager, and a specimen note added with the reason the EB check was not performed.

Not Current

9.15 GENERAL DNA EVIDENTIARY CERTIFICATE WORKFLOW

Not Current

Receive written request and clarify which samples are required to be included.

↓

Ensure that there is adequate time to complete audit trails and issue certificate at least 10 days before court date – negotiate with IO/DPP if required.
Timeframes approx. 4 weeks for Evidentiary Certificate alone, 6 weeks if requested at the same time as a statement.

↓

Create Evidentiary checklist using:
QIS 30799: DNA Evidentiary Certificate Checklist

Follow instructions on Worksheet entitled: 'Instructions'
The minimum requirement is to check the electronic records of samples and batches in AUSLAB.

↓

Work through each sample and the relevant batches, looking at audit trail in AUSLAB to see if any issues have been raised. eg sample removed has not transferred yet, pos control is partial profile, failure of batch due to controls not working/OQI.
If you have examined the records relating to the receipt, storage and testing of the things covered by the Evidentiary Certificate, by 'checking' the boxes, you are confirming that the Quality Assurance Procedures relevant to the above at the time of testing were complied with.

If in examining the records, something needs to be addressed, notify your Senior Scientist and/or Team Leader to co-ordinate a possible investigation.

↓

Check storage audit trail for each sample, noting that there should be two final locations for most samples – one for spin basket and one for final amplified product. Ensure that throughout the audit trail, sample has been added and removed from particular location as it works its way through the process.

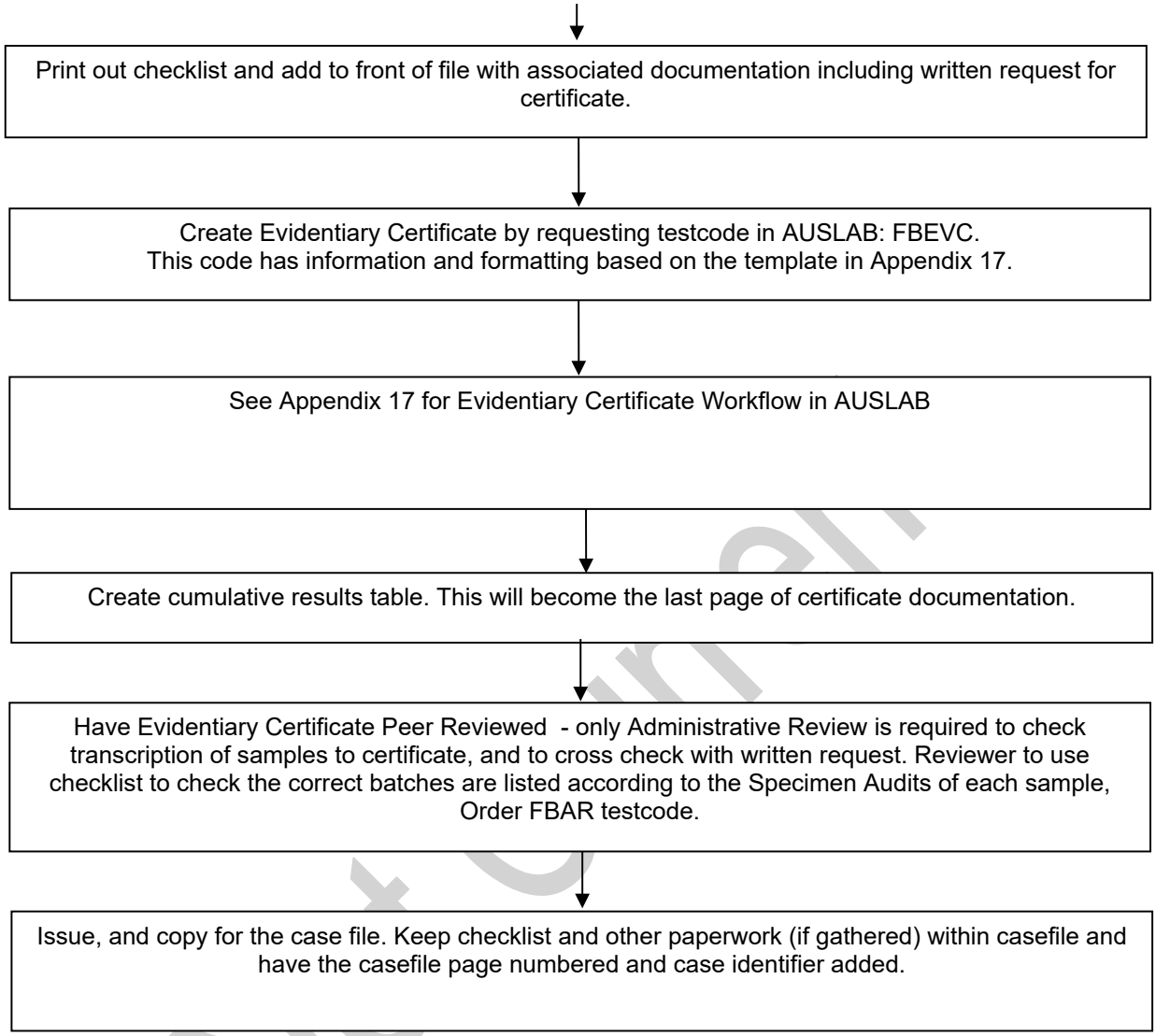
↓

As a minimum, AUSLAB audit trails can be checked for departures from the standard operating procedure. If required, the batch paperwork is scanned into the batches as 'log' files and can be checked by the following:

enter into batch → Shift F6 ('Files') → scroll to 'Log' → Export file to location to be retrieved → view PDF

↓

If the paperwork is not complete, get original paperwork correction signed and dated or whatever is required. If this staff member is on holidays, or no longer working in department, get their Senior to sign and date on their behalf.


Print out checklist and add to front of file with associated documentation including written request for certificate.
Create Evidentiary Certificate by requesting testcode in AUSLAB: FBEVC.
This code has information and formatting based on the template in Appendix 17.
See Appendix 17 for Evidentiary Certificate Workflow in AUSLAB
Create cumulative results table. This will become the last page of certificate documentation.
Have Evidentiary Certificate Peer Reviewed - only Administrative Review is required to check transcription of samples to certificate, and to cross check with written request. Reviewer to use checklist to check the correct batches are listed according to the Specimen Audits of each sample, Order FBAR testcode.
Issue, and copy for the case file. Keep checklist and other paperwork (if gathered) within casefile and have the casefile page numbered and case identifier added.

9.16 DNA EVIDENTIARY CERTIFICATE (and APPENDIX v5)

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 …

10. 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.

Not Current

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.

Not Current

APPENDIX 1

Procedural overview for the DNA Analysis Unit,
Queensland Health Forensic and Scientific Services (QHFSS)

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.

For details of the current ISO/IEC 17025 Field Application Document, Forensic Science, Supplementary requirements for accreditation, please refer to the NATA website:
http://www.nata.asn.au/publications

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.

Not Current

Technical information relating to DNA profiling at the DNA Analysis Unit of Queensland Health Forensic and Scientific Services (QHFSS)

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.

Not Current

DNA (STR) profiling systems available at the DNA Analysis Unit, Queensland Health Forensic and Scientific Services (QHFSS)

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

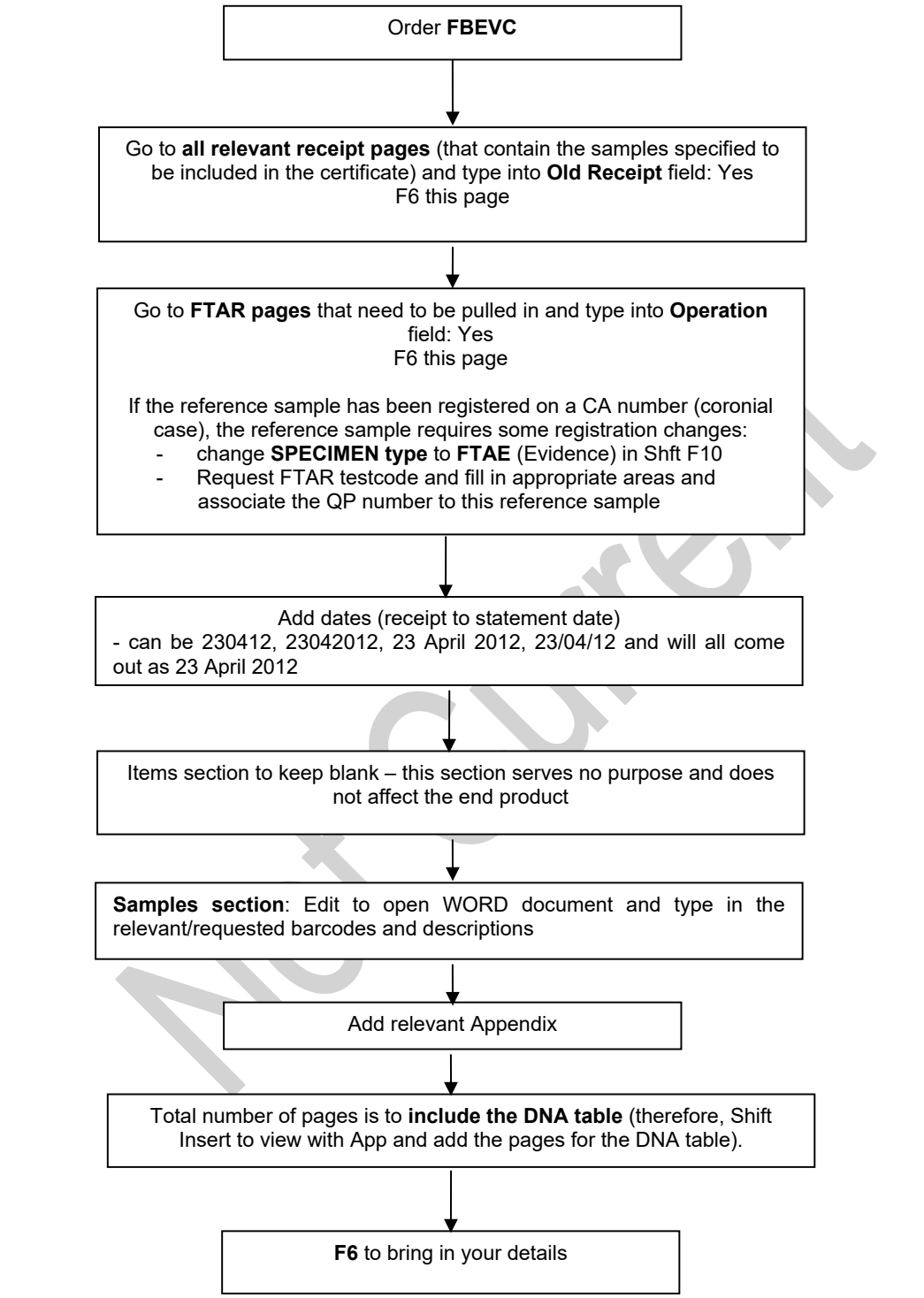
Table 2: COfiler® multiplex system, list of loci:

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

Not Current

9.17 DNA EVIDENTIARY CERTIFICATE WORKFLOW IN AUSLAB

Not Current



Not Current

9.18 Suggested PowerPlex 21 and STRmix statement wording

NOTE 1:
When wording your statements 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, round to LR = 70*
- *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, round to 80.*

Example wording

Unknowns

123456789 Swab (A), near rear door
123456789 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

Not Current

123456789 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

123456789 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.

Not Current

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

123456789 Graph 21; swab; pop bottle

This sample contained insufficient DNA to be suitable for analysis and was not tested further.

No DNA Detected

123456789 Graph 9; swab; cot
123456789 Graph 2; swab; flyscreen

DNA was not detected in these samples and therefore they were not tested further.

Complex – no STRmix

123456789 Graph 11; swab; right thong
123456789 Item 6; tapelift; back of hand

Not Current

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 **123456789 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.

Not Current

9.19 QFLAG workflow for Quality Team (when a possible match is identified)

Preparing QFLAG Intel Report:

1. Print QFLAG profile and associated “Matching” profile (i.e. QPSTF profile) for visual assessment/evaluation.
2. Using the report template prepare an appropriate Intel report (refer to I:\Quality & Projects\Intelligence reports or Intel report folder - for examples)
3. Complete EXH: Add case manager, save preferred profile, add EXH (eg. QFIH) with QPSTF laboratory number (if applicable) in Link# Field
4. Add “Refer to Specimen Note” in 9PLEX/XPLEX comment, and add specimen note to indicate possible quality issue.
5. Register new barcode AUSLAB [1], [1] FULL Reception Entry with the sample UR number as the QFLAG EXH barcode
a.Specimen type=Case
b. Add FBINTL, FBAR and FBIOLR test codes
6. Enter into newly registered barcode (ensure Microsoft Word is NOT open)
a. On INTEL report page [F2] in word document section to create new word document [E]. (for subsequent drafts save a new version “N”)
b. Paste in word draft of document (ensure at least one carriage return between each paragraph. [Ctl][T] to upload to word file back into AUSLAB
c. Add contact QPS Name and Address (as per previous INTEL reports) and Name of Forensic DNA Analysis peer reviewer and position. DO NOT ADD date of report or date of review until after it has been checked – draft version.
d. Check Intel report using [Shft][Ins]
e. [F6] to validate
f. Print a copy [Shft F11] and provide to reviewer (with profiles).

Review and sending of QFLAG Intel report:

When draft is approved by the reviewer:
1. Add date of report and date of peer review and [F6] to validate. *This creates a PDF of the report – viewable by [Ctl][Ins]. (If further edits are required after review dates are added, delete review dates, edit document then re-add review dates and validates, this creates a new PDF Intel report)
2. Reviewer to validate QFIH EXH, 9PLEX/XPLEX and complete FBAR
3. Print Intel report, and have it signed by quality and reviewer.
4. Completed and signed PDF Intel report to be and scanned and emailed to QPS (by QPS email account only)
5. Add specimen note “Quality Flags noted with sample to QPS Elimination sample. Intel report regarding Quality flags sent to [Insert QPS Staff Name] for action”
6. Complete FBIOLR page with:
a. Posted to: [Insert email recipient]
b. Of: [DNA Management Section]
c. QHSS Officer Posting: [Insert email sender]

Not Current

d. Date of Posting: [Insert date of sending]
e. [F6] to validate

QPS reply to QFLAG Intel reports:

QPS will email back with investigation findings, following actions required:
1. Specimen note detailing QPS investigation findings (eg. “Email received from XXXXXXX, contamination event confirmed – refer to scanned email”)
2. Scan QPS email response to AUSLAB under the relevant barcode
3. Add UR Note if applicable: “Quality Flags noted for XXXXXX refer to specimen notes”
4. If applicable add an additional EXH line (eg. Quality Control failure, refer to QPS) and request the reviewer to validate the additional EXH line

Not Current

Queensland Government

Forensic and Scientific Services

HealthSupport Queensland

STATEMENT OF WITNESS

Peer Reviewed.....Yes/ No

Case Analyst.[redacted]....

Peer Analyst.[redacted]

Date Issued.....16.02.2018.....

Client Reference : [redacted]
Report Number : 5257422

QUEENSLAND)
TO WIT)

I, Thomas NURTHEN, of Brisbane in the State of Queensland, do solemnly and sincerely declare that:-

1. I am employed by Queensland Health Forensic and Scientific Services (QHFSS) at Coopers Plains, Brisbane.

2. I hold the position of scientist in the Forensic DNA Analysis laboratory of QHFSS.

3. I was awarded a Bachelor of Science with Honours from the University of Queensland. I am a member of the Australian and New Zealand Forensic Science Society

4. This is my statement in relation to the alleged offence that Occurrence Number [redacted] refers. The defendant in this matter is [redacted] The complainant in this matter is [redacted]

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone [redacted]
Fax
Email forensics@health.qld.gov.au

5. Laboratory records show that on 28 August 2017, [redacted] delivered the following 22 items:

[redacted]

6. Laboratory records show that on 15 August 2017, [redacted] delivered the following reference sample:

[redacted]

7. Laboratory records show that on 1 September 2017, delivered the following reference sample:

[redacted]

8. Laboratory records show that on 10 October 2017, [redacted] delivered the following reference sample:

[redacted]

9. The following information is provided to assist in the understanding of the contents of this statement.

Forensic Biologist

As a forensic biologist, it is my 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 which are obtained from these samples are then compared with the DNA profiles obtained from an individual's reference sample.

Examinations and DNA Profiling

Please refer to the Appendix for an overview of examinations and DNA profiling.

Forensic DNA Analysis case files 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.

Touch DNA / Transfer of DNA

When a person touches a surface, it is possible for their cellular material to be transferred onto that surface. This transferred cellular material can often be recovered 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.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA

PO Box 594 Archerfield QLD 4108 AUSTRALIA

Phone [redacted]
Fax
Email

The generation of a DNA profile will depend on many factors. These include the amount of cellular material transferred, the nature of the surface being touched and the amount of cellular material a person has available to transfer.

The persistence of any transferred cellular material on a surface will depend largely upon the nature of the surface and the conditions under which it has been kept in the time between deposition and recovery of the DNA. For example, cellular material could be lost from the surface by washing or mechanical action such as abrasion.

It therefore follows that the absence of a DNA profile from a touched surface does not necessarily mean that that person has not come into contact with it, as it is possible for a person to come into contact with a surface without a detectable amount of their DNA being transferred or recovered.

Blood stains

Potential blood stains 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

The presence of semen on an item can be indicated by the use of a presumptive chemical test which detects a major constituent of seminal fluid (Acid Phosphatase – AP). This constituent does, however, exist in other body fluids, such as vaginal secretions. Additional presumptive chemical testing (Prostate Specific Antigen – PSA / p30) can be undertaken and a positive reaction to both AP and PSA / p30 makes it highly likely that seminal fluid is present. The presence of semen can be confirmed via the microscopic identification of spermatozoa (sperm heads).

Samples may undergo a differential lysis extraction process which aims to separate spermatozoa and epithelial / cellular fractions. This separation is not always completely effective, and a mixing of fractions can occur. This is often referred to as cellular carryover.

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. Any semen which may have been transferred / deposited can subsequently be lost by actions such as washing.

10. The results of the scientific examinations conducted in the laboratory are as follows:

Reference Samples

[redacted]

DNA profiles were obtained for both reference samples and these DNA profiles are different to each other.

Items received on the 28/08/2017

Items tested by the QPS and Forensic DNA Analysis

[redacted] **- ITEM D1 - AP +IVE FABRIC [FABRIC] excised from the matress [sic] protector**

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA

PO Box 594 Archerfield QLD 4108 AUSTRALIA

Phone Fax Email [redacted]

This item consisted of a beige piece of fabric measuring approximately 55 mm x 105 mm at the widest points. Two marked areas were designated sections 1 & 2 for examination purposes. No staining was observed on either side of the fabric.

Section 1 measured approximately 10 mm x 20 mm.
Section 2 measured approximately 15 mm x 25 mm.

Spermatozoa were microscopically detected in a sample prepared from section 1.

Spermatozoa were not microscopically detected in a sample prepared from section 2. This sample tested negative for the possible presence of seminal fluid.

Each of these samples was submitted separately for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Section 1 - spermatozoa fraction

The DNA profile obtained from this sample indicates the presence of DNA from a single contributor and matches the reference DNA profile of [redacted]

Based on statistical analysis, it is estimated that the DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] has contributed DNA, rather than if he has not.

Section 1 - epithelial fraction

Due to the complex nature of this DNA profile, including uncertainty regarding the number of contributors, in my opinion this DNA profile is not suitable for meaningful interpretation or comparison.

Section 2 - spermatozoa fraction

DNA was not detected in this fraction and therefore it was not tested further.

Section 2 - epithelial fraction

The mixed DNA profile obtained from this fraction indicates the presence of DNA from two contributors. As such, an assumption of two contributors has been made for statistical analysis.

The reference DNA profiles of [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if she has contributed DNA, rather than if she has not.

Excluded

Based on the assumption of two contributors, [redacted] is excluded as a potential contributor of DNA to the mixed DNA profile obtained.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone [redacted]
Fax
Email

[redacted]- ITEM D2 - AP +IVE FABRIC [FABRIC] excised from the mattress protector[redacted]

This item consisted of a beige piece of fabric measuring approximately 105 mm x 175 mm at the widest points. Five marked areas were designated 1 - 5 for examination purposes. No staining was observed on either side of the fabric.

Area 1 measured approximately 5 mm x 10 mm.

Area 2 measured approximately 15 mm x 15 mm.

Area 3 measured approximately 20 mm x 35 mm.

Area 4 measured approximately 15 mm x 15 mm.

Area 5 measured approximately 5 mm x 10 mm.

Spermatozoa were microscopically detected in samples prepared from each of the marked areas.

Each of these fabric samples was submitted separately for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Area 1 - spermatozoa fraction
Area 5 - spermatozoa fraction

DNA was not detected in these fractions and therefore they were not tested further.

Area 1 – epithelial fraction
Area 2 – epithelial fraction
Area 3 – epithelial fraction

Due to the complex nature of these DNA profiles, including uncertainty regarding the number of contributors, in my opinion these DNA profiles are not suitable for meaningful interpretation or comparison.

Area 2 - spermatozoa fraction

The mixed DNA profile obtained from this fraction indicates the presence of DNA from two contributors. As such, an assumption of two contributors has been made for statistical analysis.

The reference DNA profiles of [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if he has contributed DNA, rather than if he has not.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone [redacted]
Fax
Email

Excluded

Based on the assumption of two contributors, [redacted] is excluded as a potential contributor of DNA to the mixed DNA profile obtained.

Area 3 - spermatozoa fraction
Area 4 - spermatozoa fraction

Each of the DNA profiles obtained from these fractions indicate the presence of DNA from a single contributor and match the reference DNA profile of [redacted]

Based on statistical analysis, it is estimated that each of the DNA profiles obtained is greater than 100 billion times more likely to have occurred if [redacted] has contributed DNA, rather than if he has not.

Note: The DNA profiles obtained from each of these fractions indicate the possible presence of additional low level DNA. This possible low level DNA was not used for comparison purposes. In my opinion, this finding does not interfere with the interpretation of the DNA profile obtained for these fractions.

Area 4 – epithelial fraction

The mixed DNA profile obtained from this fraction 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 [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if he has contributed DNA, rather than if he has not.

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if she has contributed DNA, rather than if she has not.

Area 5 – epithelial fraction

The mixed DNA profile obtained from this fraction 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 [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if he has contributed DNA, rather than if he has not.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone [redacted]
Fax
Email

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if she has contributed DNA, rather than if she has not.

[redacted]6 - ITEM D3 - AP +IVE FABRIC [FABRIC] excised from the mattress protector [redacted]

This item consisted of a beige piece of fabric measuring approximately 105 mm x 210 mm at the widest points. Three marked areas were designated sections 1 - 3 for examination purposes. Multiple areas of pale pink staining were observed on the marked side of the fabric. No visible staining was observed on the unmarked side of the fabric.

Section 1 measured approximately 35 mm x 110 mm.

Section 2 measured approximately 10 mm x 20 mm.

Section 3 measured approximately 10 mm x 15 mm.

Spermatozoa were microscopically detected in samples prepared from each of the sections.

Each of these samples was submitted separately for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Section 1 - spermatozoa fraction

The DNA profile obtained from this sample indicates the presence of DNA from a single contributor and matches the reference DNA profile of [redacted]

Based on statistical analysis, it is estimated that the DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] has contributed DNA, rather than if he has not.

Note: The DNA profile obtained from this fraction indicates the possible presence of additional low level DNA. This possible low level DNA was not used for comparison purposes. In my opinion, this finding does not interfere with the interpretation of the DNA profile obtained for this sample.

Section 1 - epithelial fraction
Section 2 - epithelial fraction

Due to the complex nature of these DNA profiles, including uncertainty regarding the number of contributors, in my opinion these DNA profiles are not suitable for meaningful interpretation or comparison.

Section 2 - spermatozoa fraction
Section 3 - spermatozoa fraction

A mixed DNA profile was obtained from each of these fractions and both indicate the presence of DNA from two contributors. As such, an assumption of two contributors has been made for statistical analysis.

The reference DNA profiles of [redacted] and [redacted] have been compared with each of these mixed DNA profiles separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone
Fax
Email [redacted]

In favour of contribution

[redacted] - It is estimated that each of the mixed DNA profiles obtained is greater than 100 billion times more likely to have occurred if he has contributed DNA, rather than if he has not.

Excluded

Based on the assumption of two contributors, [redacted] is excluded as a potential contributor of DNA to each of the mixed DNA profiles obtained.

Section 3 - epithelial fraction

The mixed DNA profile obtained from this fraction 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 [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if she has contributed DNA, rather than if she has not.

[redacted] - It is estimated that the mixed DNA profile obtained is approximately 5.1 million times more likely to have occurred if he has contributed DNA, rather than if he has not.

[redacted] - ITEM D4 - AP +IVE FABRIC [FABRIC] excised from the mattress protector [redacted]

This item consisted of a beige piece of fabric measuring approximately 105 mm x 245 mm at the widest points. Four marked areas were designated 1 - 4 for examination purposes. The entire marked surface appeared dirty with pink staining. No visible staining was observed on the unmarked side of the fabric.

Area 1 measured approximately 20 mm x 35 mm.

Area 2 measured approximately 10 mm x 20 mm.

Area 3 measured approximately 10 mm x 10 mm.

Area 4 measured approximately 15 mm x 15 mm.

Spermatozoa were microscopically detected in samples prepared from each of the marked areas.

Each of these samples was submitted separately for DNA analysis to undergo a differential lysis extraction process.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone [redacted]
Fax
Email

DNA analysis results:

Area 1 - spermatozoa fraction
Area 2 - spermatozoa fraction
Area 3 – epithelial fraction
Area 4 - epithelial fraction

A mixed DNA profile was obtained from each of these fractions that all indicate the presence of DNA from two contributors. As such, an assumption of two contributors has been made for statistical analysis.

The reference DNA profiles of [redacted] and [redacted] have been compared with each of these mixed DNA profiles separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that each of the mixed DNA profiles obtained is greater than 100 billion times more likely to have occurred if he has contributed DNA, rather than if he has not.

Excluded

Based on the assumption of two contributors, in my opinion, [redacted] is excluded as a potential contributor of DNA to each of the mixed DNA profiles obtained.

Area 1 – epithelial fraction

The mixed DNA profile obtained from this fraction indicates the presence of DNA from two contributors. As such, an assumption of two contributors has been made for statistical analysis.

The reference DNA profiles of [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if he has contributed DNA, rather than if he has not.

Excluded

Based on the assumption of two contributors, in my opinion, [redacted] is excluded as a potential contributor of DNA to the mixed DNA profile obtained.

Area 2 – epithelial fraction

Due to the complex nature of this DNA profile, including uncertainty regarding the number of contributors, in my opinion this DNA profile is not suitable for meaningful interpretation or comparison.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone [redacted]
Fax
Email

Area 3 - spermatozoa fraction

The mixed DNA profile obtained from this fraction indicates the presence of DNA from two contributors. As such, an assumption of two contributors has been made for statistical analysis.

The reference DNA profiles of [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if he has contributed DNA, rather than if he has not.

Inconclusive:

[redacted] - It is estimated that the mixed DNA profile obtained is equally likely to have occurred whether or not she has contributed DNA.

Area 4 - spermatozoa fraction

The DNA profile obtained from this sample indicates the presence of DNA from a single contributor and matches the reference DNA profile of [redacted]

Based on statistical analysis, it is estimated that the DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] has contributed DNA, rather than if he has not.

Note: The DNA profile obtained from this fraction indicates the possible presence of additional low level DNA. This possible low level DNA was not used for comparison purposes. In my opinion, this finding does not interfere with the interpretation of the DNA profile obtained for this sample.

[redacted]- ITEM D5 - AP +IVE FABRIC [FABRIC] excised from the mattress protector [redacted]

This item consisted of a beige piece of fabric measuring approximately 75 mm x 125 mm at the widest points. Two marked areas were designated 1 - 2 for examination purposes. Pink staining was observed on the entire marked surface. No visible staining was observed on the unmarked side of the fabric.

Area 1 measured approximately 20 mm x 25 mm.

Area 2 measured approximately 15 mm x 20 mm.

Spermatozoa were not microscopically detected in a sample prepared from Area 1. This sample tested negative for seminal fluid.

Spermatozoa were microscopically detected in a sample prepared from Area 2.

Each of these samples was submitted separately for DNA analysis to undergo a differential lysis extraction process.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA

PO Box 594 Archerfield QLD 4108 AUSTRALIA

Phone [redacted]
Fax
Email

DNA analysis results:

Area 1 - spermatozoa fraction
Area 1 – epithelial fraction
Area 2 – epithelial fraction

Due to the complex nature of these DNA profiles, including uncertainty regarding the number of contributors, in my opinion these DNA profiles are not suitable for meaningful interpretation or comparison.

Area 2 - spermatozoa fraction

The DNA profile obtained from this sample indicates the presence of DNA from a single contributor and matches the reference DNA profile of [redacted]

Based on statistical analysis, it is estimated that the DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] has contributed DNA, rather than if he has not.

Note: The DNA profile obtained from this fraction indicates the possible presence of additional low level DNA. This possible low level DNA was not used for comparison purposes. In my opinion, this finding does not interfere with the interpretation of the DNA profile obtained for this sample.

[redacted] - ITEM D6 - AP +IVE FABRIC [FABRIC] excised from the mattress protector [redacted]

This item consisted of a beige piece of fabric measuring approximately 75 mm x 75 mm. Two marked areas were designated 1 - 2 for examination purposes. A small amount of red/brown staining measuring approximately 25 mm x 30 mm was observed in the middle of the fabric and this stain tested negative for blood.
The entire marked area was dirty.

Area 1 measured approximately 5 mm x 18 mm.

Area 2 measured approximately 20 mm x 25 mm.

Spermatozoa were microscopically detected in samples prepared from both of the marked areas.

Each of these samples was submitted separately for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Area 1 - spermatozoa fraction
Area 2 - spermatozoa fraction

Each of the DNA profiles obtained from these samples indicate the presence of DNA from a single contributor and match the reference DNA profile of [redacted]

Based on statistical analysis, it is estimated that each of the DNA profiles obtained is greater than 100 billion times more likely to have occurred if [redacted] has contributed DNA, rather than if he has not.

Note: The DNA profile obtained from Area 2 spermatozoa fraction indicates the possible presence of additional low level DNA. This possible low level DNA was not used for comparison purposes. In my opinion, this finding does not interfere with the interpretation of the DNA profile obtained for this sample.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone [redacted]
Fax
Email

Area 1 – epithelial fraction

The mixed DNA profile obtained from this fraction 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 [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if he has contributed DNA, rather than if he has not.

[redacted] - It is estimated that the mixed DNA profile obtained is approximately 80 times more likely to have occurred if she has contributed DNA, rather than if she has not.

Area 2 – epithelial fraction

The mixed DNA profile obtained from this fraction 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 [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if he has contributed DNA, rather than if he has not.

[redacted] - It is estimated that the mixed DNA profile obtained is approximately 150 times more likely to have occurred if she has contributed DNA, rather than if she has not.

[redacted]- ITEM D7 - AP +IVE FABRIC [FABRIC] excised from the mattress protector [redacted]

This item consisted of a beige piece of fabric measuring approximately 130 mm x 180 mm. Four marked areas were designated 1 - 4 for examination purposes. The entire marked surface appeared dirty with pink staining. No visible staining was observed on the unmarked side of the fabric.

Area 1 measured approximately 10 mm x 10 mm.

Area 2 measured approximately 15 mm x 30 mm.

Area 3 measured approximately 20 mm x 20 mm.

Area 4 measured approximately 15 mm x 25 mm.

Spermatozoa were microscopically detected in both samples prepared from Area 1 and Area 4.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone
Fax
Email [redacted]

Spermatozoa were not microscopically detected in either sample prepared from Area 2 and Area 3. These samples tested negative for seminal fluid.

Each of these samples was submitted separately for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Area 1 - spermatozoa fraction

The DNA profile obtained from this sample indicates the presence of DNA from a single contributor and matches the reference DNA profile of [redacted]

Based on statistical analysis, it is estimated that the DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] has contributed DNA, rather than if he has not.

Note: The DNA profile obtained from this fraction indicates the possible presence of additional low level DNA. This possible low level DNA was not used for comparison purposes. In my opinion, this finding does not interfere with the interpretation of the DNA profile obtained for this sample.

Area 1 – epithelial fraction

The mixed DNA profile obtained from this fraction 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 [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if he has contributed DNA, rather than if he has not.

[redacted] - It is estimated that the mixed DNA profile obtained is approximately 66 times more likely to have occurred if she has contributed DNA, rather than if she has not.

Area 2 - spermatozoa fraction
Area 3 - spermatozoa fraction

Due to the complex nature of these DNA profiles, including uncertainty regarding the number of contributors, in my opinion these DNA profiles are not suitable for meaningful interpretation or comparison.

Area 2 – epithelial fraction

The mixed DNA profile obtained from this fraction indicates the presence of DNA from two contributors. As such, an assumption of two contributors has been made for statistical analysis.

The reference DNA profiles of [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone Fax Email [redacted]

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if she has contributed DNA, rather than if she has not.

Excluded

Based on the assumption of two contributors, [redacted] is excluded as a potential contributor of DNA to the mixed DNA profile obtained.

Area 3 – epithelial fraction

The mixed DNA profile obtained from this fraction 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 [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if she has contributed DNA, rather than if she has not.

[redacted] - It is estimated that the mixed DNA profile obtained is approximately 500 times more likely to have occurred if he has contributed DNA, rather than if he has not.

Area 4 - spermatozoa fraction

The mixed DNA profile obtained from this fraction indicates the presence of DNA from two contributors. As such, an assumption of two contributors has been made for statistical analysis.

The reference DNA profiles of [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if he has contributed DNA, rather than if he has not.

[redacted] - It is estimated that the mixed DNA profile obtained is approximately 2 times more likely to have occurred if she has contributed DNA, rather than if she has not.

Area 4 – epithelial fraction

The mixed DNA profile obtained from this fraction indicates the presence of DNA from three contributors. As such, an assumption of three contributors has been made for statistical analysis.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone
Fax
Email [redacted]

The reference DNA profiles of [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if he has contributed DNA, rather than if he has not.

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if she has contributed DNA, rather than if she has not.

[redacted] - ITEM D8 - AP +IVE FABRIC [FABRIC] excised from the mattress protector [redacted]

This item consisted of a beige piece of fabric measuring approximately 50 mm x 140 mm. Two marked areas were designated 1 & 2 for examination purposes. Pink staining was observed on the marked surface. No visible staining was observed on the unmarked side of the fabric.

Area 1 measured approximately 10 mm x 15 mm.

Area 2 measured approximately 10 mm x 25 mm.

Spermatozoa were microscopically detected in samples prepared from each of the marked areas.

Each of these samples was submitted separately for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Area 1 - spermatozoa fraction

The DNA profile obtained from this sample indicates the presence of DNA from a single contributor and matches the reference DNA profile of [redacted]

Based on statistical analysis, it is estimated that the DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] has contributed DNA, rather than if he has not.

Area 2 - spermatozoa fraction

The mixed DNA profile obtained from this fraction indicates the presence of DNA from two contributors. As such, an assumption of two contributors has been made for statistical analysis.

The reference DNA profiles of [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if he has contributed DNA, rather than if he has not.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone [redacted]
Fax
Email

Excluded

Based on the assumption of two contributors, [redacted] is excluded as a potential contributor of DNA to the mixed DNA profile obtained.

Area 1 – epithelial fraction
Area 2 – epithelial fraction

Due to the complex nature of these DNA profiles, including uncertainty regarding the number of contributors, in my opinion these DNA profiles are not suitable for meaningful interpretation or comparison.

[redacted] - ITEM D9 - AP +IVE FABRIC [FABRIC] excised from the mattress protector ([redacted]

This item consisted of a beige piece of fabric measuring approximately 50 mm x 70 mm. Pink staining was observed on the marked surface. No visible staining was observed on the unmarked side of the fabric.

One marked area measured approximately 20 mm x 25 mm in size. Spermatozoa were microscopically detected in a sample prepared from the entire marked area and this sample was submitted for DNA analysis to undergo a differential lysis extraction process.

A second area measured approximately 5 mm x 5 mm in size and was delineated by an incomplete line. No further work was performed on this area.

DNA analysis results:

Spermatozoa fraction

The mixed DNA profile obtained from this fraction indicates the presence of DNA from two contributors. As such, an assumption of two contributors has been made for statistical analysis.

The reference DNA profiles of [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if he has contributed DNA, rather than if he has not.

Excluded

Based on the assumption of two contributors, [redacted] is excluded as a potential contributor of DNA to the mixed DNA profile obtained.

Epithelial fraction

The mixed DNA profile obtained from this fraction 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 [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone [redacted]
Fax
Email

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if he has contributed DNA, rather than if he has not.

[redacted] - It is estimated that the mixed DNA profile obtained is approximately 230 thousand times more likely to have occurred if she has contributed DNA, rather than if she has not.

[redacted] - ITEM D10 - AP +IVE FABRIC [FABRIC] excised from the mattress protector [redacted]

This item consisted of a beige piece of fabric measuring approximately 45 mm x 45 mm. The marked area measured approximately 20 mm x 25 mm in size. Pink staining was observed on the marked surface. No visible staining was observed on the unmarked side of the fabric.

Spermatozoa were microscopically detected in a sample prepared from the entire marked area and this sample was submitted for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Spermatozoa fraction

The mixed DNA profile obtained from this fraction indicates the presence of DNA from two contributors. As such, an assumption of two contributors has been made for statistical analysis.

The reference DNA profiles of [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if he has contributed DNA, rather than if he has not.

Excluded

Based on the assumption of two contributors, [redacted] is excluded as a potential contributor of DNA to the mixed DNA profile obtained

Epithelial fraction

Due to the complex nature of this DNA profile, including uncertainty regarding the number of contributors, in my opinion this DNA profile is not suitable for meaningful interpretation or comparison.

[redacted] - BACK SEAT COVER [FABRIC] collected from the back seat on passenger side of [redacted]

This item consisted of an apparent brown patterned piece of fabric with foam backing measuring approximately 90 mm x 100 mm. A marked area on the fabric side measured approximately 65 mm x 70 mm in size. The foam side appeared dirty. No visible staining was observed on the fabric side.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone
Fax
Email [redacted]

Semen was not detected in a sample prepared from the entire marked area and this sample was submitted for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Spermatozoa fraction

DNA was not detected in this fraction and therefore it was not tested further.

Epithelial fraction

Due to the complex nature of this DNA profile, including uncertainty regarding the number of contributors, in my opinion this DNA profile is not suitable for meaningful interpretation or comparison.

[redacted] - BACK SEAT COVER [FABRIC] collected from the back seat on passenger side of [redacted]

This item consisted of an apparent brown patterned piece of fabric with foam backing measuring approximately 65 mm x 80 mm. A marked area on the fabric side measured approximately 30 mm x 55 mm in size. The foam side appeared dirty. No visible staining was observed on the fabric side.

Spermatozoa were microscopically detected in a sample prepared from the entire marked area and this sample was submitted for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Spermatozoa fraction

The DNA profile obtained from this sample indicates the presence of DNA from a single contributor and matches the reference DNA profile of [redacted]

Based on statistical analysis, it is estimated that the DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] has contributed DNA, rather than if he has not.

Note: The DNA profile obtained from this fraction indicates the possible presence of additional low level DNA. This possible low level DNA was not used for comparison purposes. In my opinion, this finding does not interfere with the interpretation of the DNA profile obtained for this sample.

Epithelial fraction

The mixed DNA profile obtained from this fraction indicates the presence of DNA from two contributors. As such, an assumption of two contributors has been made for statistical analysis.

The reference DNA profiles of [redacted] and [redacted] have been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analyses, the results are as follows:

In favour of contribution

[redacted] - It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if she has contributed DNA, rather than if she has not.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone
Fax
Email [redacted]

[redacted] - It is estimated that the mixed DNA profile obtained is approximately 1.8 million times more likely to have occurred if he has contributed DNA, rather than if he has not.

[redacted] **- C1A - AP +IVE FABRIC [FABRIC] collected from the front edge of the left cushion.**

This item consisted of a grey piece of fabric measuring approximately 60 mm x 440 mm at the widest points. Six marked areas were designated sections 1 - 6 for examination purposes. No visible staining was observed on the either side of the fabric.

Spermatozoa were microscopically detected in a sample prepared from section 3.

Semen was not detected in any of samples prepared from sections 1, 2, 4, 5, and 6.

Each of these samples was submitted separately for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Section 1 - spermatozoa fraction
Section 2 - spermatozoa fraction
Section 3 - spermatozoa fraction
Section 4 - spermatozoa fraction
Section 5 - spermatozoa fraction
Section 6 - spermatozoa fraction
Section 4 - epithelial fraction

DNA was not detected in these fractions and therefore they were not tested further.

Section 1 - epithelial fraction
Section 2 - epithelial fraction
Section 3 - epithelial fraction
Section 5 - epithelial fraction
Section 6 - epithelial fraction

Due to the complex nature of these DNA profiles, including uncertainty regarding the number of contributors, in my opinion these DNA profiles are not suitable for meaningful interpretation or comparison.

[redacted] **- C1B - AP +IVE FABRIC [FABRIC] collected from the rear edge of the left cushion.**

This item consisted of a grey piece of fabric measuring approximately 90 mm x 340 mm at the widest points. Six marked areas were designated sections 1 - 6 for examination purposes. No visible staining was observed on the either side of the fabric.

Semen was not detected in any of samples prepared from sections 1 to 6.

Each of these samples was submitted separately for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Section 1 - spermatozoa fraction
Section 2 - spermatozoa fraction
Section 3 - spermatozoa fraction

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone [redacted]
Fax
Email

Section 4 - spermatozoa fraction
Section 5 - spermatozoa fraction
Section 6 - spermatozoa fraction
Section 2 - epithelial fraction
Section 5 - epithelial fraction

DNA was not detected in these fractions and therefore they were not tested further.

Section 3 - epithelial fraction
Section 4 - epithelial fraction
Section 6 - epithelial fraction

Due to the complex nature of these DNA profiles, including uncertainty regarding the number of contributors, in my opinion these DNA profiles are not suitable for meaningful interpretation or comparison.

Section 1 - epithelial fraction

This fraction did not meet the Forensic DNA Analysis quality requirements and therefore was not considered suitable for reporting. Please refer to the QPS for further information if required.

[redacted] - C1C - AP +IVE FABRIC [TLIFT] collected from the rear left section(of side 1) of the left cushion.

This item consisted of an A4 tapelift measuring approximately 105 mm x 110 mm. The tapelift appears dirty with what appeared to be fluff, dirt and fibres attached. Two apparent brown hairs each measuring approximately 25 mm in length, one apparent light brown hair measuring approximately 35 mm in length and one apparent white hair measuring approximately 30 mm in length were located on the tapelift. These hairs were removed from the tapelift and retained. No further processing was performed on the hairs.

Semen was not detected in a sample prepared from the entire surface of the tapelift and this sample was submitted for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Spermatozoa fraction
Epithelial fraction

DNA was not detected in these fractions and therefore they were not tested further.

[redacted] - C1D - AP +IVE FABRIC [TLIFT] collected from the rear right section (of side 1) of the left cushion.

This item consisted of an A4 tapelift measuring approximately 105 mm x 110 mm. The tapelift appears dirty with what appeared to be fluff, dirt and fibres attached. Two apparent brown hairs measuring approximately 5 mm and 20 mm in length were located on the tapelift. These hairs were removed from the tapelift and retained. No further processing was performed on the hairs.

Semen was not detected in a sample prepared from the entire surface of the tapelift and this sample was submitted for DNA analysis to undergo a differential lysis extraction process.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone [redacted]
Fax
Email

DNA analysis results:

Spermatozoa fraction
Epithelial fraction

DNA was not detected in these fractions and therefore they were not tested further.

[redacted] **- C1E - AP +IVE FABRIC [TLIFT] collected from the rear left section (of side 2) of the left cushion.**

This item consisted of an A4 tapelift measuring approximately 110 mm x 110 mm. The tapelift appears dirty with what appeared to be fluff, dirt and fibres attached. One apparent white hair measuring approximately 60 mm in length was located on the tapelift. This hair was removed from the tapelift and retained. No further processing was performed on the hair.

Semen was not detected in a sample prepared from the entire surface of the tapelift and this sample was submitted for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Spermatozoa fraction

DNA was not detected in this fraction and therefore it was not tested further.

Epithelial fraction

Low levels of DNA were detected in this fraction and it was not submitted for further DNA profiling.

[redacted]**- C1F - AP +IVE FABRIC [TLIFT] collected from the rear right section (of side 2) of the left cushion.**

This item consisted of an A4 tapelift measuring approximately 100 mm x 105 mm. The tapelift appears dirty with what appeared to be fluff, dirt and fibres attached. These large fibres were removed from the tapelift and retained. No further processing was performed on the large fibres.

Semen was not detected in a sample prepared from the entire surface of the tapelift and this sample was submitted for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Spermatozoa fraction

DNA was not detected in this fraction and therefore it was not tested further.

Epithelial fraction

Low levels of DNA were detected in this fraction and it was not submitted for further DNA profiling.

[redacted] **- C2A - TAPE LIFT [TLIFT] Collected from the left side of side 1 of the right cushion**

This item consisted of an A4 tapelift measuring approximately 100 mm x 110 mm. The tapelift appears dirty with what appeared to be fluff, dirt and fibres attached. Three apparent brown hairs ranging in length from approximately 5 mm

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone [redacted]
Fax
Email

to 15 mm in length were located on the tapelift. These hairs were removed from the tapelift and retained. No further processing was performed on the hairs.

Semen was not detected in a sample prepared from the entire surface of the tapelift and this sample was submitted for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Spermatozoa fraction
Epithelial fraction

DNA was not detected in these fractions and therefore they were not tested further.

[redacted] **- C2B - TAPE LIFT [TLIFT] Collected from the right side of side 1 of the right cushion**

This item consisted of an A4 tapelift measuring approximately 110 mm x 110 mm. The tapelift appears dirty with what appeared to be fluff, dirt and fibres attached. Five apparent brown hairs ranging from approximately 5 mm to 150 mm in length were located on the tapelift. These hairs were removed from the tapelift and retained. No further processing was performed on the hairs.

Semen was not detected in a sample prepared from the entire surface of the tapelift and this sample was submitted for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Spermatozoa fraction
Epithelial fraction

DNA was not detected in these fractions and therefore they were not tested further.

[redacted] **- C2C - TAPE LIFT [TLIFT] Collected from the left side of side 2 of the right cushion**

This item consisted of an A4 tapelift measuring approximately 90 mm x 110 mm. The tapelift appears dirty with what appeared to be fluff, dirt and fibres attached. Two apparent brown hairs each measuring from approximately 5 mm in length were located on the tapelift. These hairs were removed from the tapelift and retained. No further processing was performed on the hairs.

Semen was not detected in a sample prepared from the entire surface of the tapelift and this sample was submitted for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Spermatozoa fraction
Epithelial fraction

DNA was not detected in these fractions and therefore they were not tested further.

[redacted] **- C2D - TAPE LIFT [TLIFT] Collected from the right side of side 2 of the right cushion**

This item consisted of an A4 tapelift measuring approximately 100 mm x 105 mm. The tapelift appears dirty with what appeared to be fluff, dirt and fibres attached. One apparent brown hair measuring approximately 15 mm in length was

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone [redacted]
Fax
Email

located on the tapelift. This hair was removed from the tapelift and retained. No further processing was performed on the hair.

Semen was not detected in a sample prepared from the entire surface of the tapelift and this sample was submitted for DNA analysis to undergo a differential lysis extraction process.

DNA analysis results:

Spermatozoa fraction
Epithelial fraction

DNA was not detected in these fractions and therefore they were not tested further.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone
Fax
Email [redacted]

APPENDIX

Procedural overview for Forensic DNA Analysis, Forensic and Scientific Services (FSS), Health Support Queensland

Examinations

Unless otherwise stated, the examinations of items for biological material were conducted by staff within the Queensland Police Service (QPS). Sub-samples from these items were forwarded to Forensic and Scientific Services (FSS), Health Support Queensland, for the purposes of conducting DNA analysis.

Forensic DNA Analysis operates under the agreement that 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 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, notes are made at the time of the examination by the examining scientist and form part of the casefile.

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 exhibit packaging prior to processing. The packaging and labelling of any exhibit is checked and recorded before the sample undergoes DNA analysis.

Entry into Forensic DNA Analysis is restricted to authorised persons only, via electronically encoded proximity access cards. Forensic DNA Analysis forms part of a Health Support Queensland campus site which has access 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 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:

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone
Fax
Email [redacted]

- 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.
For details of the current ISO/IEC Standard Application Document for accreditation of testing and calibration facilities and Forensic Science ISO/IEC 17025 Application Document, please refer to the NATA website:

http://www.nata.asn.au/publications

Technical information relating to DNA profiling at Forensic DNA Analysis, Forensic and Scientific Services (FSS), Health Support Queensland

DNA Profiling

DNA is a complex chemical found in almost all cells of the human body. It carries genetic information which 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 of DNA, 20 of which contain highly variable Short Tandem Repeats (STRs). The 21st region gives an indication as to the gender 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 they are able to be detected, profiled and compared with other samples.

The individual components (alleles) of a DNA profile are represented by a series of peaks which are measured and given a designation using standard sizing ladders. A person will have two alleles or peaks for each STR, one inherited from their mother and one inherited from their father, unless the same allele is inherited from both parents, in which case only one peak will be seen.

A DNA profile obtained from biological material such as blood, semen, saliva, hair or cells (eg. touch DNA) can be compared with the DNA profile obtained from a reference sample from any person. If there is no indication of a contribution by more than one person, then a DNA profile is described as being "single source". Conversely, if there are indications of two or more contributors, then a DNA profile is described as a "mixed" DNA profile.

Statistical Analysis of DNA profiles

Forensic DNA Analysis uses the STRmix™ software to assist in the interpretation of DNA profiles and calculation of likelihood ratios for DNA profiles generated using the PowerPlex® 21 system. STRmix™ is an expert system developed and validated in Australia and New Zealand.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone Fax Email [redacted]

In order to statistically evaluate DNA profiles, it is necessary to make a reasonable assessment of the possible number of people who may have contributed DNA to that DNA profile, based on the information observed.

DNA profiles assumed to originate from one person (single source)

A person can be excluded as a possible source of the biological material if corresponding regions of the crime-scene DNA profile are different from that person's reference DNA profile. If the corresponding regions of the DNA profiles contain the same information, then that person, together 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 DNA originated from the person of interest;
Proposition 2: the 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 DNA components that make up the DNA profile.

If less than the 21 regions of DNA are seen in a DNA profile the likelihood ratio will be smaller than the likelihood ratio that would be obtained from a full DNA profile. In other words, the more incomplete a DNA profile is, the greater the likelihood of obtaining that DNA profile if it came 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 DNA originated from the person of interest and an unknown person unrelated to the person of interest;
Proposition 2: the DNA originated from two unknown people unrelated to the person of interest.

The likelihood ratio provides a statistical assessment of a particular contribution of DNA being contained within the mixed DNA profile.

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 intimate area, then it may be possible to make the reasonable assumption that the donor of the sample 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 known donor, such that the presence of the DNA components corresponding with the donor'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, for example:

Proposition 1: the DNA has originated from the complainant and the person of interest;
Proposition 2: the DNA has originated from the complainant and an unknown individual unrelated to the person of interest.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone Fax Email [redacted]

When it appears that a large number of people could have contributed to a mixed DNA profile, it can be difficult to exclude individuals as potential contributors. It can be equally difficult to determine whether a person could in fact be a contributor to the DNA profile. If it is not possible to determine the number of contributors to a mixed DNA profile, or if there is very limited information available, then a mixed DNA profile may be described as unsuitable for interpretation.

If information is received such that the assumptions made in an interpretation are not accepted, then 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, irrespective of whether the DNA profile is single source or mixed. A correction factor θ (theta) is applied to all statistical calculations in order to correct for the possibility of common ancestry (sharing of DNA components inherited from a common ancestor) between people in the general population. The nationally agreed figures for theta are θ=0.02 for the Australian Caucasian dataset, θ=0.03 for 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 dataset. In other words, if a new dataset were generated, this allowance factors in any difference the new dataset might make to the likelihood ratio.

Often the calculated likelihood ratio produces numbers of hundreds (100s) or even thousands (1000s) of billions. To avoid the use of potentially confusing terminology, a 'ceiling figure' for the likelihood ratio of 100 billion has been determined (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.

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 random fashion in which DNA from parents combines, the probability that two siblings would share the same 20 STR regions 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 is thought that a close blood relative may have been involved, the most meaningful approach to interpretation would be to submit the reference sample from the relative in question for analysis and direct comparison to the crime-scene DNA profile.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone
Fax
Email [redacted]

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

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 16 February 2018 and contained in the pages numbered 1 to 28 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.

[redacted]
.....

Thomas NURTHEN

Signed at BRISBANE on 16 February 2018

Justin Howes

From: Justin Howes
Sent: Wednesday, 4 April 2018 4:06 PM
To: Matthew Hunt; Kylie Rika; Sharon Johnstone
Subject: FW: change to statement format

Hi
In addition to the job below that is in VSTS, I think we have a good opportunity to revise the statement wording paragraphs that we developed in 2013 (and subsequently added to the SOP).

I am after your advice on a small working party (2- one from each Reporting Team) to review the wording that automatically adds to the statement template. I have one nomination, Jacqui, to be on the group because of the sheer amount of statements she gets through and also because she has had direct feedback from legal professionals regarding wording and understanding.

Terms of reference:

- Overarching goal – movement towards automatic statement generation and minimal editing

- In scope:
  - automatic wording review
  - identification of profile types where automatic wording does not currently exist (eg. subsamples)
  - format of text – is it better to group similar results (barcode 1, barcode 2…same interp), or keep as it is generated (barcode 1 interp, barcode 2 interp)
  - Grouping of exclusions when multiple refs eg. all other reference profiles are excluded….
  - Free-text examination wording – work with idea that as long as it is not incorrect, it is fine, but a general guideline here would be beneficial

- Out of scope:
  - wording in Appendix, positioning of App in statement
  - use of descriptor as registered in FR

Matthew, please think of an R1 member to work with Jacqui. I will let her know that she is to rep R2.

Timeframe – recommendations to be put to R1 and R2 teams in their separate meeting forums, and to non-Reporting Team Reporting Scientists. Consultation and final version to be with me to add to VSTS by **27 April.**

Thanks
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 | 39 Kessels Road, Coopers Plains, QLD 4108
w | Queensland Health e | [redacted]

HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

From: Justin Howes
Sent: Wednesday, 7 March 2018 4:30 PM
To: Sharon Johnstone; Kylie Rika; Matthew Hunt; Amanda Reeves; Adrian Pippia
Cc: Paula Brisotto
Subject: change to statement format

Hi
I have sought Legal advice on the best place for the Justice's Act to appear in our statements – before or after the Appendix.

The feedback is that it should be before the Appendix. Furthermore, the Appendix should be introduced in the body (prior to Justice's Act) and should be called 'Certificate of Exhibit 'A''. The template to be added to the FR has a point (point 9 in the template) that introduces the 'Certificate….'. I have put a break in before this point so that there is always text on a page with the Justice's Act.

Please note, not having the Justice's Act before the appendix does not affect any of the 1000s of statements we have ever issued.

In I:\Change Management\2014-2015 FR development\Statements\Statement versions_User Story 23_06022018, I have created a few documents and sent on to FR via VSTS:

- Statement template to add to FR
- FR APPENDIX_Decon v1 or v2_LRs v2_06022018
- FR APPENDIX_Decon v1_LRs v1_06022018
- FR APPENDIX_Paternity PP21_06022018
- FR APPENDIX_Profiler Plus_06022018

These Appendices (called 'Certificate….' within the actual file) have all the preambles and technical information paragraphs relevant to our testing. This will mean that we will have no need for any editing of the Appendix to occur, and therefore no formatting issues which I understand to be somewhat frustrating. Adding all paragraphs explaining testing in the laboratory is in line with what other jurisdictions do for their statements as well, and follows on from what we requested during FR development. I have had some staff help with wording and formatting of the template and Appendices which has been great.

One other addition to the appendices is a disclaimer/line to say that the item descriptors are as they have been added by QPS in the Forensic Register. This should prevent the need for any editing of descriptions that we have for items. This is added under the 'Examination' paragraph. We are working with QPS to improve their descriptions as well.

The request in VSTS is to allow the user to select the appropriate Appendix to be used.

This VSTS job (User Story 23) continues to evolve but I think these adjustments will help with TAT of statements and take another step towards the auto-statement goal. I think this change will take some time to be added to the FR, but I will continue to prioritise it in order to help the statement writing/reviewing TAT.

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 | 39 Kessels Road, Coopers Plains, QLD 4108
w | Queensland Health **e** | [redacted]

HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

Justin Howes

From: Justin Howes
Sent: Monday, 21 May 2018 4:25 PM
To: Jacqui Wilson; Kylie Rika; Sharon Johnstone
Cc: Rhys Parry; Alicia Quartermain
Subject: RE: Minimum standard wording for statements

Thankyou team.

After a couple of other action items (summary of changes), we can move to comms/sharing/feedback phase.

Thanks
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 | 39 Kessels Road, Coopers Plains, QLD 4108
w | Queensland Health e | [redacted]

HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

From: Jacqui Wilson
Sent: Monday, 21 May 2018 3:42 PM
To: Kylie Rika; Sharon Johnstone
Cc: Justin Howes; Rhys Parry; Alicia Quartermain
Subject: Minimum standard wording for statements

Hi all

As discussed in our meeting today, please find attached documents relating to the minimum standard wording proposed for FR statements.

The document relating to 'PP21 wording' describes the proposed auto wording that will populate the statement for in-tube sample results (I've tidied it up following our meeting).

The document relating to the 'standard wording for sub samples' describes the proposed wording for whole item/SAIK/sub sample etc examinations (these do not currently auto populate) and it is intended to standardise the way in which we describe the items and subsequent examinations conducted within Forensic DNA Analysis.

The last document, relating to 'proposed standardised wording for describing sub samples' is one which Allan has come up with for standardising how his team designate areas & sections during their examinations and the aim is to have consistency throughout cases. This is something that I believe he has already implemented.

Allan is currently working on a standard approach to sub sample descriptions, in line with his above document.

Please let us know if there is anything else you would like us to work on in terms of wording within our statements. We will have a think about the Unknown Male/Female designations, as discussed today.

Cheers
Jacqui

Jacqui Wilson B App Sc M Sc
Scientist – Forensic Reporting & Intelligence

Forensic DNA Analysis, Police Services Stream
Forensic & Scientific Services
Health Support Queensland, **Department of Health**

p | [redacted]
a | 39 Kessels Road, COOPERS PLAINS, QLD 4108
w | Queensland Health e | [redacted]

HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

NOTE 1:
When wording your statements 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:

- *A mixed DNA profile was obtained that indicated the presence of three contributors. In order to interpret this DNA profile, I have assumed the presence of three contributors…*

  Or

- *A mixed DNA profile was obtained. Based on the information within this DNA profile, I have assumed the presence of three contributors…*

This could be written for single source in the following ways:

- *A DNA profile was obtained that indicated a single contributor. Assuming one contributor, this DNA profile matched the reference DNA profile of XY.*

  Or

- *A DNA profile was obtained. Based on the information within this DNA profile, I have assumed the presence of one contributor and this DNA profile matches the reference DNA profile of XXX.*

Receipt [redacted]

Unknowns

[redacted] **Swab (A), near rear door**
Swab (D), floor in foyer near charge counter

The DNA profiles obtained from these samples matched each other and did 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
Graph 27; swab; piece of lino

A DNA profile was obtained that indicated a single contributor. Assuming one contributor, this DNA profile matched 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 XY, rather than if the DNA originated from another person, unrelated to XY.

OR

It is estimated that the DNA profile observed is at least 100 billion (or approximately X number) times more likely if the proposition that Person A has contributed to the DNA profile were true rather than the proposition that they have not contributed, and the DNA originated from an unknown, unrelated person.

Non-conditioned Mixture

[redacted] Swab (B), floor near cells

First example least preferred at this point in time (06/06/13):

A mixed DNA profile was obtained from this sample. In order to interpret this DNA profile I have assumed the presence of three contributors.

The reference DNA profiles of [redacted] and [redacted] have been compared with this mixed DNA profile, 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:

[redacted] - It is estimated that the mixed DNA profile obtained is approximately 4.2 times more likely to have occurred if he did contribute DNA rather than not.

In favour of non-contribution:

[redacted] – It is estimated that the mixed DNA profile obtained is approximately 100000 times more likely to have occurred if she did not contribute DNA rather than did contribute.

Inconclusive:

[redacted] – It is estimated that the mixed DNA profile obtained is equally likely if JB has contributed DNA rather than if he had not.

OR

A mixed DNA profile was obtained from this sample that indicated the presence of three contributors. In order to interpret this DNA profile I have assumed the presence of three contributors.

OPTIONAL: The reference DNA profiles of [redacted] and [redacted] have been compared with this mixed DNA profile, 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:

[redacted] - It is estimated that the mixed DNA profile is greater than 100 billion times more likely to have occurred if the DNA originated from [redacted] and two other people, unrelated to [redacted], rather than if the DNA originated from three people, unrelated to [redacted]

In favour of non-contribution:

[redacted] - It is estimated that the mixed DNA profile is xx times more likely to have occurred if the DNA originated from three people, unrelated to [redacted] rather than if the DNA originated from [redacted] and two other people, unrelated to [redacted]

Inconclusive:

[redacted] – It is estimated that the mixed DNA profile obtained is equally likely to have occurred if the DNA originated from either [redacted] and two other people, unrelated to [redacted] or from three people, unrelated to [redacted]

Exclusion:

Based on the assumption of 3 contributors, XXXXX is excluded as a potential contributor of DNA.

OR

In favour of contribution:

The DNA profile observed is at least 100 billion (or approximately X number) times more likely if the proposition that Person A has contributed to the DNA profile were true rather than the proposition that they have not contributed.

In favour of non-contribution:

It is estimated that the DNA profile observed is at least 100 billion (or approximately X number) times more likely if the proposition that Person A has not contributed to the DNA profile were true rather than the proposition that they have.

Inconclusive:

It is estimated that the DNA profile observed is equally likely if the proposition that Person A has contributed to the DNA profile were true as the proposition that they have not contributed.

Conditioned Mixture

Conditioned Mixture

A mixed DNA profile was obtained from this sample that indicated the presence of X contributors. Since this sample is said to have been collected from YYYY, it would not be unexpected to find DNA which could have come from him/her. In order to interpret this mixed DNA profile I have assumed the presence of DNA from X contributors, one of whom is YYYY.

The reference DNA profile of AAAA was compared to this mixed DNA profile, to determine whether or not he/she may have contributed DNA along with YYYY.

Based on statistical analysis it is estimated that:

In favour of contribution:

AAAA - It is estimated that the mixed DNA profile obtained is approximately xx times more likely to have occurred if the DNA originated from YYYY and AAAA, rather than if the DNA originated from YYYY and an unknown person unrelated to AAAA.

In favour of non-contribution:

AAAA - It is estimated that the mixed DNA profile obtained is approximately xx times more likely to have occurred if the DNA originated from YYYY and an

unknown person unrelated to AAAA, rather than if the DNA originated from YYYY and AAAA.

Inconclusive:

AAAA - It is estimated that the mixed DNA profile obtained is equally likely to have occurred if the DNA originated from either YYYY and AAAA, or from YYYY and an unknown person, unrelated to AAAA.

Excluded:

Based on the assumption of X contributors and the presence of DNA from YYYY, the following reference samples are excluded as potential contributors to the mixed DNA profile obtained: AAAA et al

OR

A DNA profile was obtained from this sample. In order to interpret this DNA profile I have assumed (X number) of contributors. I have also assumed that person Z has contributed to this DNA profile.

Based on statistical analysis it is estimated that:

In favour of contribution:

The DNA profile observed is at least 100 billion (or approximately X number) times more likely if the proposition that Person A has also contributed to the DNA profile were true rather than the proposition that they have not contributed.

Conditioned Mix multiple samples

Items attributed to XX:

[redacted]

Item 1b
Item 1c
Item 1d
Item 2a
Item 2b
Item 2d

Mixed DNA profiles were obtained from each of these samples. Since these samples are said to have been collected from clothing attributed to XX, it would not be unexpected to find DNA which could have come from her.

In order to interpret these mixed DNA profiles I have assumed the presence of DNA from three contributors, one of whom is XX.

The reference DNA profile of YY was compared to each of these mixed DNA profiles, to determine whether or not he may also have contributed DNA along with XX. Based on statistical analyses, the results are as follows:

In favour of contribution

It is estimated that the following mixed DNA profiles are more likely to have occurred if the DNA originated from XX, YY and an unknown person unrelated to YY, rather than if the DNA originated from XX and two unknown people unrelated to YY. Approximately:

1300 times more likely for [redacted]
730 times more likely for [redacted]
6400 times more likely for [redacted];

In favour of non-contribution

It is estimated, that the following mixed DNA profiles are more likely to have occurred if the DNA originated from XX and two unknown people unrelated to YY, rather than if the DNA originated from XX, YY and an unknown person unrelated to YY. Approximately:

5 times more likely for [redacted].
42 times more likely for [redacted]
7 times more likely for [redacted]

Not unexpected findings

Rectal swab
Anterior lower gum swab

The DNA profiles obtained from these samples matched each other and also matched the reference DNA profile of XX at all corresponding areas. As these samples are said to have been taken from XX, 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 as such were not statistically analysed.

Same profile, multiple samples ie CM proposal 1
(to consider)

The (mixed) DNA profiles obtained from these samples were the same and matched the result obtained for item XXXX. In this regard, a statistical interpretation has not been undertaken for these samples at this time.

CM Proposal 2: wording for incorporation of low support/non-contribution results

*Will statistical analysis be required on Conditioned/2 pers mix where reference sample(s) can be visually excluded? If not, slight change to initial wording needed.

NOTE 1:
When wording your statements 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.*

Example wording

Unknowns

[redacted] **Swab (A), near rear door**
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 and unrelated to 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 [redacted] and [redacted] 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:

[redacted]- 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:

[redacted]– 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:

[redacted]– 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 [redacted]. Since this sample is said to have been collected from [redacted], 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 [redacted] has been made.

The reference DNA profile of [redacted] has been compared to this mixed DNA profile, to assess whether or not he may have contributed DNA along with [redacted]

Based on statistical analysis it is estimated that:

In favour of contribution:

[redacted]- 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* [redacted] rather than if he has not.

In favour of non-contribution:

[redacted]- 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:

[redacted]- 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 [redacted], the following reference samples are excluded as potential contributors to the mixed DNA profile obtained: [redacted] 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 [redacted] As these samples are said to have been taken from [redacted] 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.

EXH line	Expanded Comment
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.
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.
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.
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.

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.
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.
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.

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.
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.
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.

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.
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.
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 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.
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.

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 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.
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.
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.

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.
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.
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.
Two person mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors.
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.

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.
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.
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.
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.

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.
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.
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.
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.

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.
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.
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.
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.

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.
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.
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.

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.
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.
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.
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.

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.
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.
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.

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.
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.
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.

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.
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.
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.
Three person mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors.

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.
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.
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.
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.

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.
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.
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.
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 evaluated against the mixture without a contribution being assumed and the result reported as a likelihood ratio.

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.
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 exhibit report, comparison to other reference samples may provide a different statistical interpretation.
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 associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.
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.
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.

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.
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.
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.
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.

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.
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.
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.

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.
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.
All items now tested	All items for this exhibit have now been examined
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.
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.
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.

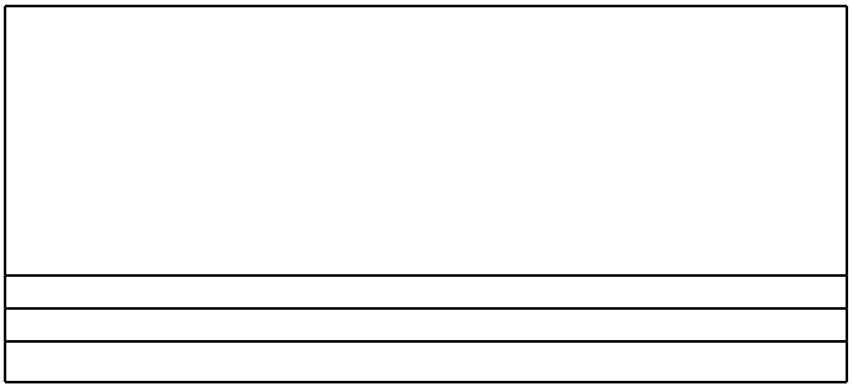
Consistent with being child of	The DNA profile obtained from this exhibit was consistent with being the biological child of the barcode sent with this exhibit report
Consistent with being biological mother	The DNA profile obtained from this exhibit is consistent with being a biological child of the barcode sent with this exhibit report.
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.
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.
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.

ENVM additional quality search conducted see Intel report	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.
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.
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.

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
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 is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained.

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.
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
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.

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
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.
Entire sample consumed	The entire item/sample was consumed during examination
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.
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.
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.



Justin Howes

From: Justin Howes
Sent: Wednesday, 18 April 2018 2:46 PM
To: Alicia Quartermain; Rhys Parry; Jacqui Wilson
Subject: exp comment DIFP

Hi

This is the expanded comment that DNA MGt use for DIFP:

'March 2018: This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling. Please contact the DNA Management Section if this sample is requested to be assessed for further processing.

The wording I sent around in early Feb was:

To report in a statement, the following wording could be used:

Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling.

This is slightly different to the wording written in 2012/13 for these samples (P3) but after some consultation, appears a good starting point.

Something to work with in your doc.

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 | 39 Kessels Road, Coopers Plains, QLD 4108
w | Queensland Health e | [redacted]

HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

Justin Howes

From: Justin Howes
Sent: Friday, 2 March 2018 8:47 AM
To: Sharon Johnstone; Kylie Rika; Matthew Hunt; Paula Brisotto; Allan McNevin; Luke Ryan
Subject: FW: Changes to expanded wording comments

Hi
The expanded comments for DIFP and NISP have changed slightly.

DIFP has changed to be in line with the suggested statement wording and to inform investigators to contact DNA Mgt if requested to be assessed for further processing. DNA Mgt will then pass to FSS if no other intelligence etc and will then be for us to process.

NISP has had an additional line to the expanded comment to alert QPS Investigators that these profiles are suitable for suspect checks/LR comparisons.

The expanded comments for our SOPS will not have the italicised words below. I will add comments to these SOPs.

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 | 39 Kessels Road, Coopers Plains, QLD 4108
w | Queensland Health e | [redacted]

HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

From: McIntyre.OliviaM[redacted] [mailto[redacted]
Sent: Friday, 2 March 2018 7:32 AM
To: Justin Howes
Cc: [redacted]; [redacted]; [redacted]; Taylor.EwenN[redacted]
Subject: Changes to expanded wording comments

Good morning Justin,

Just letting you know that QPS has changed the expanded wording for the following results;

DNA INSUFFICIENT FOR FURTHER PROCESSING

This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling. Please contact the DNA Management Section if this sample is requested to be assessed for further processing *via QPRIME task to Unit Code 3209.*

NO STATISTICAL INTERPRETATION PERFORMED

In the absence of a reference sample/s for comparison, a statistical interpretation has not been performed. To nominate a person of interest for comparison to the mixed DNA Profile obtained from this exhibit, please contact the DNA Management Section *via QPRIME task to Unit Code 3209.*

If you have any questions regarding this, please let me know.

Kind regards

Olivia McIntyre | DNA Management Officer | Profile Management Team | DNA Management Section
Forensic Services Group| Operations Support Command | Queensland Police Service
GPO Box 1440 | Brisbane QLD 4001 | Australia
Level 4, Police Headquarters | 200 Roma Street | Brisbane QLD 4000 | Australia
ph: [redacted]

****
CONFIDENTIALITY: The information contained in this electronic mail message and any electronic files attached to it may be confidential information, and may also be the subject of legal professional privilege and/or public interest immunity. If you are not the intended recipient you are required to delete it. Any use, disclosure or copying of this message and any attachments is unauthorised. If you have received this electronic message in error, please inform the sender or contact securityscanner@police.qld.gov.au. This footnote also confirms that this email message has been checked for the presence of computer viruses.
****

EXH line	Expanded Comment
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.
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.
Single source DNA profile	The DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.
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.
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.

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.
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.
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.
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.
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.

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.
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.
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 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.
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.
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 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.

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.
Single source DNA profile < NCIDD matching stringency	The incomplete DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. The DNA profile was below the QHSS stringency for reporting a match on NCIDD, and has therefore not been loaded to NCIDD. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.
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.
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.

Single source DNA profile- unsuitable for NCIDD searching	The incomplete DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. The DNA profile contained insufficient information for searching on NCIDD, and is therefore unable to be loaded to NCIDD. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.
Two person mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors.
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.
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.
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.
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.

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.
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.
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.
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.
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.
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.

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.
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 is consistent with this partially deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this partially deconvoluted DNA profile has been assigned a sub-sample barcode number. The partially 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.
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.
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.

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 fully deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this fully deconvoluted DNA profile has been assigned a sub-sample barcode number. The fully 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.
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.
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.

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.
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.
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.
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.
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.

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.
2 pers mix remaining consistent with unknown	The mixed DNA profile result for this sample indicated the presence of DNA from two contributors and 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. This remaining contribution is consistent with the unknown designation (previously identified within this case and loaded to NCIDD) sent with this exhibit report. This unknown is therefore a possible donor of DNA to the 'remaining' contribution. It is important to note that this information is provided for intelligence purposes only and a statistical evaluation has not been performed at this time. 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 likelihood ratio will vary. In this instance the likelihood ratio could favour non-contribution.
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.
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.

Mix Rem DNA contrib < NCIDD matching stringency	The mixed DNA profile result for this sample indicates two contributors and 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 is of unknown origin and therefore does not match any DNA profiles obtained from reference samples associated to this case. This remaining contribution is below the QHFSS stringency for reporting a match on NCIDD and has therefore not been 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.
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.
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.
Mix Remaining DNA contribution indicates male origin	The remaining contribution separated after conditioning the mixed DNA profile indicates male origin

Mix Rem DNA contrib unsuitable for NCIDD searching	The mixed DNA profile result for this sample indicates two contributors and 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 is of unknown origin. This remaining contribution is 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.
Three person mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors.
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.
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.
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.
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.

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.
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.
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.
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 evaluated against the mixture without a contribution being assumed and the result reported as a likelihood ratio.
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.
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 exhibit report, comparison to other reference samples may provide a different statistical interpretation.

3 pers mixed profile, mix remaining intel NCIDD	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, a remaining contribution has been separated. This remaining contribution is a mixed DNA profile which 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 is consistent with this partially deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this partially deconvoluted DNA profile has been assigned a sub-sample barcode number. The partially 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.
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 associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.
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.
3 person mixed DNA profile not deconvoluted	This item/sample gave a mixed DNA profile which indicated the presence of DNA from three contributors. This mixed DNA profile has been assessed and it is considered that, if the DNA profile were to be deconvoluted, it may provide sufficient information for upload to NCIDD. Deconvolution of this DNA profile has not been performed at this time. Please contact the laboratory if further interpetation is required.
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.

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.
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.
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.
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.
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.

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.
3 per mix, intel cond, 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.
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.
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.

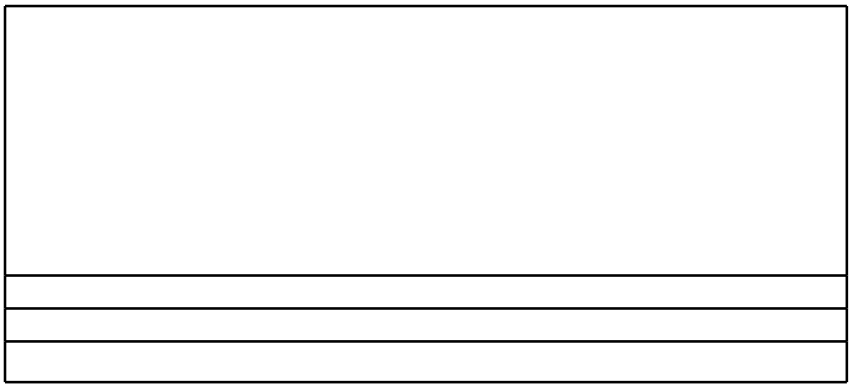
3 person mixed profile, mixture remaining NCIDD	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, a remaining contribution has been separated. This remaining contribution is a mixed DNA profile which has been 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 fully deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this fully deconvoluted DNA profile has been assigned a sub-sample barcode number. The fully 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.
All items now tested	All items for this exhibit have now been examined
Cond mix rem - low supp for contrib or supp non contrib	This item/sample provided a DNA profile that indicated the presence of two or three contributors. One or more of the contributors to this DNA profile has limited information associated with it. All of the reference DNA profiles associated with this case have been compared with this DNA profile separately. When conditioning on the assumed known contributor, then the DNA profile provides limited information as to whether or not some or all of donors of the reference DNA profiles associated with this case are possible donors of DNA to this mixed DNA profile. Please contact the laboratory if more information is required.
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.
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.

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.
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
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.
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.
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.
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.
Excluded from mixed DNA profile	This item/sample provided a mixed DNA profile that indicated the presence of DNA from two or three contributors. All of the reference DNA profiles associated with this case have been compared with this DNA profile separately.The statistical interpretation shows that some or all of the donors of the reference DNA profiles associated with this case are excluded as having contributed to this mixed DNA profile.

ENVM additional quality search conducted see Intel report	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.
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.
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.
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

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 is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained.
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.
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
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.

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
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.
Entire sample consumed	The entire item/sample was consumed during examination
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.
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.
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.



HealthSupport Queensland

Explanations of Exhibit Results for Forensic Register

Not Current

1 Purpose

To provide explanations for the Exhibit Results available for the Forensic Register (FR).

2 Scope

The Forensic Register (FR) is the laboratory information management system (LIMS) used within Forensic DNA Analysis. The FR utilises Exhibit Result lines to report information relating to exhibits to the Queensland Police Service (QPS). These Exhibit Result lines expand to full paragraphs that explain the meaning of the line provided. These result lines were previously reported thorough the EXH page in the laboratory's previous LIMS, AUSLAB, and as such the result line explanations contained within this document also apply to this system.

This document provides the explanations for the Exhibit Result lines which are available for Forensic DNA Analysis staff within the FR.

Some of the Exhibit Result lines are generated automatically by the completion of specific fields within the FR. This information can be found in the relevant Evidence Recovery SOPs.

Each Exhibit Result line is accompanied by a mnemonic for ease of selection from a drop-down list.

3 Evidence Recovery Exhibit Results

3.1 Blood Examination

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
Generation = automatic

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
Generation = automatic

Presumptive blood test neg.
This item/sample tested negative to a presumptive test for blood (TMB).
Mnemonic = PBTN
Generation = automatic

Presumptive blood test positive
This item/sample tested positive to a presumptive test for blood (TMB).
Mnemonic = PREBT
Generation = automatic

Not Current

3.2 Seminal Fluid Examination

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
Generation = automatic

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
Generation = automatic

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
Generation = automatic

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
Generation = automatic

Micro neg for sperm
Spermatozoa were not detected on this item/sample by microscopy.
Mnemonic = MNS
Generation = automatic

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
Generation = automatic

3.3 Saliva Examination

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

Not Current

Generation = automatic

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
Generation = automatic

Presump saliva test negative
This item/sample tested negative to a presumptive test for saliva (Phadebas).
Mnemonic = PSTN
Generation = automatic

Presump saliva test positive
This item/sample tested positive to a presumptive test for saliva (Phadebas).
Mnemonic = PSTP
Generation = automatic

3.4 Hair Examination

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
Generation = manual

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
Generation = manual

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
Generation = manual

Application of above line:
This 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.

Not Current

3.5 General Examination

Submitted-results pending
This item/sample was submitted for DNA testing. Results are pending.
Mnemonic = SRP
Generation = automatic

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
Generation = manual

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
Generation = manual

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
Generation = manual

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
Generation = manual

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
Generation = manual

Application of above line:
This 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.

Entire sample consumed
The entire item/sample was consumed during examination.
Mnemonic= ESCD
Generation = manual

Not Current

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
Generation = manual

Application of above line:
This 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.

All items now tested
All items for this exhibit have now been examined.
Mnemonic = AINT
Generation = manual

Application of above line:
This comment must follow "Multiple items – not all tested"

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
Generation = manual

Application of above line:
This 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.

3.6 Exception reporting to QPS for Evidence Recovery

Sample required manual intervention prior to DNA 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
Generation = automatic

Application of above line:
This comment can be used when manipulation of an item examined by QPS was undertaken by Forensic DNA Analysis staff prior to submitting for DNA extraction, manual or automated. This result line should be used for general manipulation only. More specific result lines are listed below.

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

Not Current

DNA extraction process. The ideal stick length should be no more than 24mm total length (swab stick plus swab head).
Mnemonic = MISSTL
Generation = automatic

Application of above line:
This comment can be used when manipulation of a swab submitted by QPS was undertaken by Forensic DNA Analysis staff prior to submitting for DNA extraction, manual or automated, due to the swab stick being too long.

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
Generation = automatic

Application of above line:
This comment can be used when manipulation of an item examined by QPS was undertaken by Forensic DNA Analysis staff prior to submitting for DNA extraction, manual or automated, due to excess substrate.

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
Generation = automatic

Application of above line:
This comment can be used when manipulation of a tapelift examined by QPS was undertaken by Forensic DNA Analysis staff prior to submitting for DNA extraction, manual or automated, due to the tapelift being rolled incorrectly.

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
Generation = manual

Application of above line:
This 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

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
Generation = automatic

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
Generation = manual

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 cannot 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 Forensic DNA Analysis Laboratory
Mnemonic = LDIS
Generation = automatic

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
Generation = automatic

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 submit whole cigarette butts in a Crime Scene Sample envelope or as a sub-sample of the filter paper.
Mnemonic = ISCB
Generation = manual

Extra information on reverse of crime scene sample envelope
This exhibit had extra information on the back of the crime scene sample envelope. Where writing or barcodes are present on the back of a CSSE, an extra photograph is taken which must be reviewed during examination and prior to final results being released. These extra reviews increase the processing time for samples and slow down the release of final results. Please ensure all information is limited to one side of the envelope.

Not Current

Mnemonic = EXREV
Generation = automatic

4 Exhibit Result lines for DNA profile interpretation

Unless otherwise stated, all Exhibit Result lines relating to DNA profile interpretation can either be generated manually or through clicking the 'Add Results' icon once Profile Data Analysis has been complete.

The following Exhibit Result lines cover samples processed using the Profiler Plus (P+) and Powerplex 21 (PP21) amplification kits. Some Exhibit Result lines are to be used for one kit only. Other Exhibit Result lines are generic and can be used for either kit. At the end of each comment, the kit or kits that the Exhibit Result line can be used with will be denoted in brackets.

The first Exhibit Result line will refer to the number of contributors to the DNA profile e.g. Single source DNA profile or 2/3/4 person mixed DNA profile (with a subsequent result line referring to an LR if a reference evidence sample is compared). (See Figure 1, Figure 2, Figure 3, Figure 4)

For single source profiles ONLY, the unknown designation or the reference sample barcode will only be entered into the Linked No. field for the DNA profile result. No designations will be added to the NCIDD upload lines for single source profiles.

Date / Time	Technique	Testing	Linked No	Employee	Reviewer
07/04/2017 10:46	Result	1SS - Single source DNA profile	UKM1	440121	
07/04/2017 10:46	Result	1SSNCD - NCIDD upload single source DNA profile		440121	

Figure 1 - Single source DNA profile

Date / Time	Technique	Testing	Linked No	Employee	Reviewer
07/04/2017 10:52	Result	1SS20L - Single source 20 loci DNA profile LR > 100 billion	564285936	440121	
07/04/2017 10:53	Result	1SSNCD - NCIDD upload single source DNA profile		440121	

Figure 2 - Single source DNA profile with reference sample

For two or three person mixed DNA profiles, the first line will describe the number of contributors regardless of whether a LR for a reference evidence sample comparison has been calculated. The following line will refer to the LR or non-contribution line (if calculated). The next line whether a sample is deconvoluted or a profile is available for upload to NCIDD. (See Figure 3, Figure 4)

Date / Time	Technique	Testing	Linked No	Employee	Reviewer
07/04/2017 10:57	Result	2MX - Two person mixed DNA profile		440121	
07/04/2017 10:57	Result	2MXNCD - NCIDD upload - mixed DNA profile	UKM1	440121	

Figure 3 - Deconvoluted mixed profile with no reference sample

Not Current

Date / Time	Technique	Testing	Linked No	Employee	Reviewer
07/04/2017 11:00	Result	2MX - Two person mixed DNA profile		440121	
07/04/2017 11:00	Result	2MX7 - 2 person mix profile - support for contrib > 100 billion	[redacted]	440121	
07/04/2017 11:01	Result	2MXIND - NCIDD upload - Intel mixed DNA profile		440121	

Figure 4 - Deconvoluted mixed profile with reference sample

For all final results containing a match to a reference barcode, the QPS DRMU update the expanded comments as per the following example:

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.

4.1 PowerPlex 21 and STRmix Exhibit Result lines

The following Exhibit Result lines are for use with results processed using PowerPlex 21 and interpreted with STRmix.

4.1.1 Single Source DNA profiles

Single Source DNA profile
The DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.
Mnemonic = 1SS
(PP21)

Single Source- low support for contribution LR 2 - 100
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

Not Current

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)

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)

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)

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)

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.
Mnemonic = 1SS9L4
(PP21)

Not Current

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)

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)

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)

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)

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

Not Current

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 = 1SS9L9
(PP21)

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)

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)

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)

Not Current

The following comments will be applied when a single source DNA profile is selected for loading to the National Criminal Investigation DNA Database (NCIDD). These are not stand alone comments and should be preceded by an Exhibit Result line for the profile e.g. Single Source DNA Profile.

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)

The following two comments are to be used when a sample has been selected for loading to NCIDD for Intelligence purposes only, and should only be used after consultation with a Senior Scientist.

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 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)

Application of above line:
This comment is to be used when a single source profile is obtained which is less than the stringency for reporting a match on NCIDD (<12 alleles).

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)

Application of above line:
This comment is to be used when a single source profile is obtained which is undergoing rework, however a profile has been selected for loading to NCIDD for intelligence purposes.

The following comments will be applied when a single source DNA profile is unable to be loaded to NCIDD (these Exhibit Result lines are required if the only sample in a case).

Single source DNA profile < NCIDD matching stringency
The incomplete DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. The DNA profile was below the QHSS stringency for reporting a match on NCIDD, and has therefore not been loaded to

Not Current

NCIDD. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.
Mnemonic = 1SSLND
(PP21)

Application of above line:
This comment is to be used when the DNA profile consists of 6-11 alleles for both unknowns and reference sample comparisons.

Single source DNA profile- unsuitable for NCIDD searching
The incomplete DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. The DNA profile contained insufficient information for searching on NCIDD, and is therefore unable to be loaded to NCIDD. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.
Mnemonic = 1SSUND
(PP21)

Application of above line:
This comment is to be used when the DNA profile consists of 1-5 alleles for both unknowns and reference sample comparisons.

4.1.2 Mixed DNA profiles

Similar result to previous DNA profile
This item/sample provided a mixed DNA profile that indicated the presence of DNA from two or three contributors. This DNA profile has been assessed and is considered to provide similar information to the DNA profile obtained from the sample barcode sent with this exhibit report and therefore has not been statistically evaluated at this time. Please contact the laboratory if you require a more detailed interpretation of this DNA profile.
Mnemonic = SRPP
(PP21)

Application of above line:
This comment is to be used when a mixed DNA profile is likely to produce a similar result to one already reported from the same scene and is a stand-alone Exhibit Result line. This DNA profile will not be deconvoluted in STRmix.

3 person mixed DNA profile not deconvoluted
This item/sample gave a mixed DNA profile which indicated the presence of DNA from three contributors. This mixed DNA profile has been assessed and it is considered that, if the DNA profile were to be deconvoluted, it may provide sufficient information for upload to NCIDD. Deconvolution of this DNA profile has not been performed at this time. Please contact the laboratory if further interpetation is required.
Mnemonic = 3MXND
(PP21)

Not Current

Application of above line:
This comment is to be used for three person mixed DNA profiles with a priority of 3 only and is a stand-alone Exhibit Result line.

The following lines will be used as the first line for all two or three person mixtures. These lines describe the number of contributors to the DNA profile. Subsequent lines will refer to, including, but not limited to: reference sample comparisons and NCIDD upload lines.

Two person mixed DNA profile
This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Mnemonic = 2MX
(PP21)

Three person mixed DNA profile
This item/sample provided a DNA profile that indicated the presence of DNA from three contributors.
Mnemonic = 3MX
(PP21)

The following line will be used for unknown contributors only where there is no reference sample for comparison and no DNA profile for upload to NCIDD. This line will follow the Exhibit Result line “Two person mixed DNA profile” or “Three person mixed DNA profile”.

No statistical interpretation performed
In the absence of a reference sample/s for comparison, a statistical interpretation has not been performed.
Mnemonic = NSIP
(PP21)

4.1.3 Mixed DNA profiles with reference sample comparisons

Non-conditioned Exhibt Result lines

The following comments will be used when a reference evidence sample/s is/are provided for comparison. These lines will follow the Exhibit Result line “Two person mixed DNA profile” or “Three person mixed DNA profile”.

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)

Not Current

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)

2 person mix - low support for contribution 2 to 100
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 Forensic DNA Analysis if further information is required.
Mnemonic = 2MXLOW
(PP21)

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)

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)

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)

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

Not Current

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)

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)

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)

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)

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)

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 exhibit report, comparison to other reference samples may provide a different statistical interpretation.

Not Current

Mnemonic = 3MXINC
(PP21)

3 person mix - low support for contribution 2 to 100
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 associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.
Mnemonic = 3MXLOW
(PP21)

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)

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)

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)

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

Not Current

(PP21)

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)

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)

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)

The following comments can be used when there is numerous reference samples in the case to describe the LRs produced for a group of reference samples. There will be no information in the linked number field. If reference samples are excluded then EMDP can be used.

Mixture - low support for contrib or supports non contrib
This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or three contributors. One or more of the contributors to this DNA profile has limited information associated with it. All of the reference DNA profiles associated with this case have been compared with this DNA profile separately.The DNA profile provides limited information as to whether or not some or all of donors of the reference DNA profiles associated with this case are possible donors of DNA to this mixed DNA profile. Please contact the laboratory if more information is required.
Mnemonic = MLSONC
(PP21)

Not Current

Excluded from mixed DNA profile
This item/sample provided a mixed DNA profile that indicated the presence of DNA from two or three contributors. All of the reference DNA profiles associated with this case have been compared with this DNA profile separately. The statistical interpretation shows that some or all of the donors of the reference DNA profiles associated with this case are excluded as having contributed to this mixed DNA profile.
Mnemonic = EMDP
(PP21)

The following comment can be used for all mixture types where a single reference sample is compared and the outcome is that this reference sample is excluded as a potential contributor. This Exhibit Result line may be used for a case with only one or two reference samples or when a reference sample is received after the comparison of the other reference samples in the case (and EMDP has been used). The linked no. field will be filled in with the reference sample barcode. Also applies to conditioned/remaining profiles. E.g. conditioned on Person A, excluded Person B

Single evidence sample excluded
This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or three contributors. The statistical interpretation shows that the associated barcode sent with this exhibit report has been compared, and can be excluded as having contributed to this mixed DNA profile.
Mnemonic = EVDEXC
(PP21)

Conditioned/Remaining Exhibit Result lines

Remember to not use NSIP for any conditioned mixtures

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. These lines will follow the Exhibit Result line “Two person mixed DNA profile” or “Three person mixed DNA profile”.

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)

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

Not Current

(PP21)

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)

2 person mix remaining - low support for contrib. 2 to 100
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)

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)

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)

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

Not Current

(PP21)

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)

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)

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)

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)

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

Not Current

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)

3 person mix remaining - low support for contrib. 2 to 100
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)

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)

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)

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)

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

Not Current

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)

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)

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)

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)

Cond mix rem - low supp for contrib or supp non contrib
This item/sample provided a DNA profile that indicated the presence of two or three contributors. One or more of the contributors to this DNA profile has limited information associated with it. All of the reference DNA profiles associated with this case have been compared with this DNA profile separately. When conditioning on the assumed known contributor, then the DNA profile provides limited information as to whether or not some or all of donors of the reference DNA profiles associated with this case are possible donors of DNA to this mixed DNA profile. Please contact the laboratory if more information is required.

Not Current

Mnemonic = CMLSNC
(PP21)

Application of above line:
This comment is to be used when there are numerous reference samples in the case to describe the LRs produced for a group of reference samples. There will be no information in the linked number field. If reference samples are excluded then EMDP can be used.

Remaining contribution – inconclusive
This item/sample provided a DNA profile that indicated the presence of two or three contributors. When conditioning on the assumed know contributor, the statistical interpretation in relation to the associated barcode is inconclusive.
Mnemonic = MXREMI

Application of above line:
This comment will be applied when the Likelihood ratio calculated by STRmix, using the conditioning function, equals 1 and can be used for 2 or 3 person mixtures.

2 pers mix remaining consistent with unknown
The mixed DNA profile result for this sample indicated the presence of DNA from two contributors and 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. This remaining contribution is consistent with the unknown designation (previously identified within this case and loaded to NCIDD) sent with this exhibit report. This unknown is therefore a possible donor of DNA to the 'remaining' contribution. It is important to note that this information is provided for intelligence purposes only and a statistical evaulation has not been performed at this time. 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 likelihood ratio will vary. In this instance the likelihood ratio could favour non-contribution.
Mnemonic = 2MXRCU
(PP21)

Application of above line”
This comment is to be used where a remaining contribution from a 2 person conditioned profile matches a previously identified unknown DNA profile. There are no reference samples to compare and the remaining is single source.

Remaining contribution indicates male origin
The remaining contribution separated after conditioning the mixed DNA profile indicates male origin.
Mnemonic = 2MXUNM
(PP21)

Application of above line:
This comment is to be used when a remaining DNA profile is unable to be loaded to NCIDD (only required if the only sample in a case). An unknown designation will not accompany

Not Current

these Exhibit Result lines. There are no reference samples to compare and the remaining is single source.

The following comments are to be applied when a remaining DNA profile is unable to be loaded to NCIDD (if a result is required if the only sample in a case). An unknown designation will not accompany these result lines. There are no reference samples to compare and the remaining is single source.

Mix Rem DNA contrib < NCIDD matching stringency (6-11 alleles)
The mixed DNA profile result for this sample indicates two contributors and 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 is of unknown origin and therefore does not match any DNA profiles obtained from reference samples associated to this case. This remaining contribution is below the QHFSS stringency for reporting a match on NCIDD and has therefore not been 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 = 2MXRLM

Mix Rem DNA contrib unsuitable for NCIDD searching (1-5 alleles)
The mixed DNA profile result for this sample indicates two contributors and 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 is of unknown origin and has therefore been designated as unknown. This remaining contribution is 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 = 2MXUNS

4.1.4 NCIDD Exhibit Result lines for mixed DNA profiles

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.

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 fully deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this fully deconvoluted DNA profile has been assigned a sub-sample barcode number. The fully 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

Not Current

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)

Application of above line:
This comment should be used when a two or three person mixed DNA profile has been obtained, from which a DNA contribution has been fully deconvoluted and selected for loading to NCIDD.

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)

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)

Application of above line:
This comment should be used when a two person mixed DNA profile has been conditioned on a reference sample, and the remaining contributor has been selected for loading to NCIDD.

3 person mixed profile, mixture remaining NCIDD
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, a remaining contribution has been separated. This remaining contribution is a mixed DNA profile which 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

Not Current

barcode/unknown designation sent with this exhibit report is consistent with this fully deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this fully deconvoluted DNA profile has been assigned a sub-sample barcode number. The fully 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 = 3MXRND
(PP21)

Application of above line:
This comment should be used when a three person mixed DNA profile has been conditioned on a reference sample, and the remaining contribution consists of more than one contributor, from which a DNA profile has been fully deconvoluted for loading to NCIDD.

Intel lines

There are two types of Intel Exhibit Report lines that can be used to describe the following two scenarios:

A. A mixture that is not fully deconvoluted, so a partial profile is loaded to NCIDD and/or compared against a reference sample
B. A profile that has been generated for comparison from a mixture using non-standard interpretation guidelines

Intel type A

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 is consistent with this partially deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this partially deconvoluted DNA profile has been assigned a sub-sample barcode number. The partially 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)

3 pers mixed profile, mix remaining intel NCIDD
This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, a remaining contribution has been

Not Current

separated. This remaining contribution is a mixed DNA profile which 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 is consistent with this partially deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this partially deconvoluted DNA profile has been assigned a sub-sample barcode number. The partially 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 = 3MXIND
(PP21)

Intel type B

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)

Application of above line:
This comment should be used for a two person mixture when the mixed DNA profile has been conditioned on an unknown or reference sample for intelligence purposes only. For example, conditioned on an unknown female profile from a SAIK (sexual assault investigation kit), or an intelligence reference sample for a victim in the absence of an evidence reference sample.

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 evaluated against the mixture without a contribution being assumed and the result reported as a likelihood ratio.
Mnemonic = 3MXCI
(PP21)

Application of above line:
This comment should be used for a three person mixture when the mixed DNA profile has been conditioned on an unknown or reference sample for intelligence purposes only. For example, conditioned on an unknown female profile from a SAIK (sexual assault investigation kit), or an intelligence reference sample for a victim in the absence of an evidence reference sample.

Not Current

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)

Application of above line:
This comment should be used for a two person mixture when the mixed DNA profile has been conditioned on an unknown or reference sample for intelligence purposes only (e.g. UKF1 from a SAIK, or an Intel reference sample), and the remaining profile is to be loaded to NCIDD. This Exhibit Result should follow the line 2MXCI.

3 pers mix, intel cond, 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)

Application of above line
This comment should be used for a three person mixture when the mixed DNA profile has been conditioned on an unknown (e.g. UKF1 from a SAIK, or an Intel reference sample), and the remaining profile is to be loaded to NCIDD. The remaining profile may be either fully or partially deconvoluted, either way it is an intelligence upload. This Exhibit Result line should follow the line 3MXCI.

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

Not Current

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)

Application of above line:
The 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. This Exhibit Result line will generally be used when no other line is suitable, or when the interpretation cannot be appropriately explained by Exhibit Result lines.

3 person Mix Rem DNA contrib. unsuitable for NCIDD
The mixed DNA profile result for this sample indicates three contributors and has been deconvoluted in an attempt to resolve and 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 = 3MXRUN
(PP21)

Application of above line:
This comment is to be used when there are no reference samples to compare and the remaining is a 2p mixture and the remaining DNA profile is unsuitable for NCIDD searching, or when an additional DNA profile has been deconvoluted and it matches a previously reported unknown profile.

4.2 Suspect Check Results (PP21 and P+)

These lines will follow an Exhibit Result line that describes the DNA profile result: e.g. "Two person mixed DNA profile" or "Three person mixed DNA profile".

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+)

This 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.

Suspect check – match
The DNA profile obtained from the nominated reference barcode sent with this exhibit report matches, where information was obtained, the DNA components of this full or partial DNA profile. This comparison was done for intelligence purposes only. A reference

Not Current

evidence sample should be provided if this information and subsequent statistical calculations are required in a statement for court.
Mnemonic = SCM
(P+)

Suspect check – major profile match
The DNA profile obtained from the nominated reference barcode sent with this exhibit report matches, where information was obtained, the full or partial major DNA profile separated from this mixed DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information and subsequent statistical calculations are required in a statement for court.
Mnemonic = SCMAJM
(P+)

Suspect check – minor profile match
The DNA profile obtained from the nominated reference barcode sent with this exhibit report matches, where information was obtained the full or partial minor DNA profile separated from this mixed DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information and subsequent statistical calculations are required in a statement for court.
Mnemonic = SCMINM
(P+)

Suspect check – cannot exclude
The DNA profile obtained from the nominated reference barcode sent with this exhibit report cannot be excluded as a possible contributor of DNA to this mixed DNA profile. A reference evidence sample should be provided if this information is required in a statement for court. A statistical analysis may not be possible for this interpretation.
Mnemonic = SCCE
(P+)

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+)

Application of above line:
This 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.

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). These lines will follow the result lines “Two person mixed DNA profile” or “Three person mixed DNA profile”.
Suspect check inconclusive – mixed DNA profile

Not Current

The statistical interpretation in relation to the nominated suspect is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other nominated suspects may provide a different statistical interpretation. A reference evidence sample should be provided if this information is required in a statement for Court.
Mnemonic = SCINMX
(PP21)

Suspect check – supports non contribution
The statistical interpretation provides support for the proposition that the nominated suspect has not contributed 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 = SCSNC
(PP21)

Suspect check – low support or non contrib.
One or more of the contributors to this DNA profile has limited information associated with it. All of the profiles from nominated reference barcodes have been compared with this DNA profile separately. The DNA profile provides limited information as to whether or not some or all of the donors are possible donors of DNA to this mixed DNA profile. Please contact the laboratory if more information is required.
Mnemonic = SCLNSC
(PP21)

Suspect check - low support for contribution 2 to 100
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)

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)

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

Not Current

(PP21)

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)

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)

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)

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)

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)

Not Current

4.3 NSD or no further processing Exhibit Result lines (PP21 and P+)

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+)

Application of above line:
This comment will be used when there are no peaks observed in the DNA profile obtained.

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
(P+ and PP21)

Application of above line:
This 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.

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.
Mnemonic = NDNAD
(PP21 or P+)

Application of above line:
For Powerplex 21: This comment is used 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: This comment is used for Volume Crime Priority 3 samples only when the quantitation value is undetermined, and there is no indication of inhibition.

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 Forensic DNA Analysis if further information is required.
Mnemonic = DIFP
(PP21)

Not Current

Application of above line:
This comment is entered for samples only 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.

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
(P+)

Application of above line:
This 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.

4.4 General Final Results (PP21 and P+)

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 and P+)

Application of above line:
This 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.

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+)

Application of above line:
This comment will be used when QPS have advised they do not require testing on an item.

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

Not Current

(PP21 or P+)

Application of above line:
This 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.

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+)

Application of above line:
This comment will be used when information has been obtained from the Queensland Police Service that testing is now required for an item.

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+)

Application of above line:
This 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.

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+)

Application of above line:
This 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). This line should be validated at the same time as the new/updated result.

Sample undergone further work – conditioned
This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or three contributors. Based on information provided to the laboratory, this mixed DNA profile has now been conditioned.
Mnemonic = SUFWC
(PP21)

Not Current

Application of above line:
This comment is to be used upon receipt of a reference sample from a person who has had intimate contact with the item in question or when information is obtained about the item in question that indicates its ownership.

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+)

Application of above line:
This 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).

4.5 Profiler® Plus Exhibit Result Lines

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 result lines below that can be used for both PP21 and P+, as indicated by the kit in brackets after the comment.

4.5.1 Full Profile Results (P+)

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+)

Application of above line:
This comment should be used when a full DNA profile was obtained from the sample and this profile is to be uploaded to NCIDD.

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+)

Application of above line:
This comment should be used when a full DNA profile was obtained from the sample. This sample will not be uploaded to NCIDD.

Not Current

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+)

Application of above line:
This 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.

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+)

Application of above line:
This 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.

4.5.2 Partial Profile Final Results

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+)

Application of above line:
This 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

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+)

Application of above line:
This 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).

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+)

Application of above line:
This 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.

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+)

Application of above line:
This 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.

Note for the following 3 Exhibit Result lines:
Please ensure that the sub threshold peaks do not interfere with the rest of the profile

Not Current

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+)

Application of above line:
This 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 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.

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+)

Application of above line:
This 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.

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).
Mnemonic = PPINPT
(P+)

Not Current

Application of above line:
Consideration should be given as to whether an Intelligence upload may be appropriate and the relevant comment(s) applied, after consultation with a Senior Scientist. See p13

This 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.

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+)

Application of above line:
This 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 Exhibit Result 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.

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+)

Application of above line:
This 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 Exhibit Result 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.

Not Current

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+)

Application of above line:
This 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 Exhibit Result 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.

4.5.3 Mixed DNA Profile Results

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+)

Application of above line:
This 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.

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+)

Application of above line:
This 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.

Not Current

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+)

Application of above line:
This 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.

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+)

Application of above line:
This 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.

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+)

Application of above line:
This 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.

Not Current

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+)

Application of above line:
This 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.

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+)

Application of above line:
This 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.

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+)

Application of above line:
This 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.

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

Not Current

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+)

Application of above line:
This 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.

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+)

Application of above line:
This 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. This sample should not be uploaded to NCIDD.

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+)

Application of above line:
This 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.

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

Not Current

report cannot be excluded as being a possible contributor of DNA to the minor component of this mixed DNA profile.
Mnemonic = MDNA1
(P+)

Application of above line:
This 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. UKM1) 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.

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 reference sample has been received for direct comparison; or alternatively, comparison with additional reference samples may be possible if forthcoming.
Mnemonic = MPRO
(P+)

Application of above line:
This 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.

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+)

Application of above line:
This 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.

Not Current

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+)

Application of above line:
This 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 Exhibit Result line will provide this information.

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
(P+)

Application of above line:
This 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 Exhibit Result 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.

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+)

Not Current

Application of above line:
This 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 Exhibit Result 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.

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+)

Application of above line:
This 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 Exhibit Result 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.

4.5.4 No major/minor DNA profiles / Even Mixed DNA profiles (2 contributors)

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+)

Application of above line:
This 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.

Not Current

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+)

Application of above line:
This 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.

4.5.5 Conditioned Mixed DNA profiles

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+)

Application of above line:
This 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.

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 profile remaining after the conditioning matches the DNA profile obtained from the barcode sent with this exhibit report.
Mnemonic = MPRP
(P+)

Application of above line:
This 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.

Not Current

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+)

Application of above line:
This 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.

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+)

Application of above line:
This 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.

Mixed profile. Remain profile after cond – insuff 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 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).

Not Current

Mnemonic = MPRPAC
(P+)

Application of above line:
This 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. This sample should not be uploaded to NCIDD. This comment must always follow MPCO, or MIPDNA.

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+)

Application of above line:
This 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 Exhibit Result 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.

4.6 Complex Mixed DNA profiles (more than 2 contributors) (P+ or PP21)

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+)

Not Current

Application of above line:
This 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.

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+)

Application of above line:
This 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 as there are no reference samples/unknown profiles to compare to within the case.

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+)

Application of above line:
This comment should be used when a mixed DNA profile was obtained from multiple contributors. This may be due to indications of four contributors, where the number of contributors is unknown or a partial mixed DNA profile is obtained and therefore no meaningful interpretation or comparison could be performed. There will be no name associated with this sample in the *Linked No.* field.

4.7 Intelligence Results (PP21 or P+)

These Exhibit Result lines indicate a profile is to be loaded to NCIDD for intelligence purposes only, and further interpretations need to be made in a statement. This may include results where a clear major and minor profile cannot be resolved at one or more loci, and when subthreshold information interferes with the overall interpretation. 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.

Not Current

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 Exhibit Result lines.

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+)

Application of above line:
Consider whether the specific Intelligence EXH's listed in this section may be more relevant. This comment may be useful when the other EXH/EXR lines are unable to explain the result.

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+)

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+)

Not Current

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+)

Mixed profile-no major/minor. INTEL Major loaded to NCIDD
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors and could not be clearly separated into major and minor DNA profiles. An attempt was made to separate the contributors to this mixed DNA profile in order to load intelligence information to the National Criminal Investigation DNA Database (NCIDD) for intelligence purposes only. The Intel Major DNA profile loaded to NCIDD for matching purposes 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 is important to note that this process has been performed for intelligence purposes only, and any reference samples subsequently received which match these DNA components will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile.
Mnemonic = IMAJUN
(P+)

Application of above line:
This line is to be used when the mixed DNA profile approximates the 3:1 major/minor ratio, and there is DNA that could be loaded to NCIDD for intelligence purposes only. If there is no reference DNA profile, this is the only line to be used in the Exhibit Result line eg. 'Complex unable to load' is not necessary. If a reference sample is profiled *before* the interp stage, the result line MPNMM or 'Complex cannot exclude' will need to be used as well as using this result line with the reference barcode in the Linked No. field. This will demonstrate to QPS that the profile is 'cannot exclude' as the official interp, but there is an INTEL profile loaded to NCIDD from this sample. If a reference sample is profiled ***after*** the sample, and this result line has been used, the line will need to be replicated with the reference barcode in the Linked No field to demonstrate the loaded profile is the same as the reference profile. The MPNMM/Complex cannot exclude line will also need to be used to detail the final interp. If there is a locus that is difficult to determine alleles for loading in this situation, omit the locus. Aim to load 12 alleles as the primary objective.

Mixed profile-no major/minor. INTEL Minor loaded to NCIDD
This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors and could not be clearly separated into major and minor DNA profiles. An attempt was made to separate the contributors to this mixed DNA profile in order to load intelligence information to the National Criminal Investigation DNA Database (NCIDD) for intelligence purposes only. The Intel minor DNA profile loaded to NCIDD for matching purposes 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 is important to note that this process has been performed for intelligence purposes only, and any reference samples subsequently

Not Current

received which match these DNA components will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile.
Mnemonic = IMINUN
(P+)

Application of above line:
This line is to be used when the mixed DNA profile approximates the 3:1 major/minor ratio, and there is DNA that could be loaded to NCIDD for intelligence purposes only. If there is no reference DNA profile, this is the only Exhibit Result line to be used eg. 'Complex unable to load' is not necessary. If a reference sample is profiled *before* the interp stage, the result line MPNMM or 'Complex cannot exclude' will need to be used as well as using this result line with the reference barcode in the Linked No. field. This will demonstrate to QPS that the profile is 'cannot exclude' as the official interp, but there is an INTEL profile loaded to NCIDD from this sample. If a reference sample is profiled *after* the sample, and this result line has been used, the line will need to be replicated with the reference barcode in the Linked No. field to demonstrate the loaded profile is the same as the reference profile. The MPNMM/Complex cannot exclude line will also need to be used to detail the final interp. If there is a locus that is difficult to determine alleles for loading in this situation, omit that locus. Aim to load 12 alleles as the primary objective.

INTEL-mix DNA profile conditioned on unknown DNA profile
This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors and could not be separated into major and minor DNA profiles. For intelligence purposes only, 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 reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile and may include a statistical analysis. This result should always be used in conjunction with “INTEL-mix profile remaining after cond on unknown-NCIDD”
Mnemonic = IMCOU
(P+)

Application of above line:
This line is only to be used when a designated DNA profile has been obtained by a sample in the same case, and this unknown profile when conditioned on in an even mixed DNA profile will leave a remaining profile that is suitable for uploading for intelligence purposes. This line must be used in conjunction with IMROU that will designate a new unknown person for the remaining profile.

INTEL – mix profile remaining after cond on unknown-NCIDD
This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors and could not be separated into major and minor DNA profiles. When conditioning on the assumed known contributor for intelligence purposes only, a remaining DNA profile was obtained. This Intel remaining 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. If the assumption for conditioning no longer holds, then any reference sample will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile and may include a statistical analysis. This result should always be used in conjunction with “INTEL-mix DNA profile conditioned on unknown DNA profile”.

Not Current

Mnemonic = IMROU
(P+)

Application of above line:
If a reference sample is profiled *before* the interp stage, the Exhibit Result line MPNMM will need to be used as well as using this Exhibit Result line with the reference barcode in the Linked No. field. This will demonstrate to QPS that the profile is 'cannot exclude' as the official interp, but there is an INTEL profile loaded to NCIDD from this sample. If a reference sample is profiled *after* the sample, and this line has been used, the line will need to be replicated with the reference barcode in the Linked No. field to demonstrate the loaded profile is the same as the reference profile. The MPNMM line will also need to be used to detail the final interp.

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+)

This comment should be used when the DNA profile obtained cannot sufficiently be explained by an Exhibit Result line and an Intelligence report is required to be sent to QPS DRMU in order to explain the interpretations made.

4.8 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.

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+)

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+)

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

Not Current

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+)

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 repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.
Mnemonic = INTER4
(PP21 or P+)

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+)

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+)

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

Not Current

major DNA profile matched the DNA profile for the barcode sent with this exhibit report. Final results are pending.
Mnemonic = INTER7
(P+)

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.
Mnemonic = IRMMC
(P+)

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+)

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+)

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)

Not Current

4.9 Paternity Results (PP21 or P+)

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+)

Application of above line:
This comment is to be used in instances where the questioned father contains all of the obligate paternal alleles. This Exhibit Result line is to be placed on the child reference sample or product of conception page with and the questioned father barcode in the linked no field.

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+)

Application of above line:
This 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 Exhibit Result line is to be placed on the child reference sample or product of conception page with and the questioned father barcode in the linked no field.

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+)

Application of above line:
This comment is to be used in instances where the questioned mother contains alleles that are present in the child's DNA profile. This Exhibit Result line is to be placed on the child reference sample or product of conception page with and the questioned father barcode in the linked no field.

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+)

Application of above line:
This 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 Exhibit Result line is to be placed on the child reference sample or product of conception page with and the questioned mother barcode in the linked no field.

Not Current

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+)

Application of above line:
This 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.

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+)

Application of above line:
This 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.

4.10 Quality control failure Results (PP21 or P+)

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+)

Application of above line:
This 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.

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+)

Application of above line:
This 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.

Not Current

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+)

Application of above line:
This 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.

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+)

Application of above line:
This 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.

4.11 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 Exhibit Results 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 Exhibit Result 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 lines:

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 Forensic DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained
Mnemonic = ENFDP
(PP21 or P+)

Not Current

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 Forensic DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained
Mnemonic = ENPDP
(PP21 or P+)

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+)

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+)

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 is restricted to the Forensic DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained.
Mnemonic = ENMDP
(PP21 or P+)

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

Not Current

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+)

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 Forensic DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained
Mnemonic = ENMIDP
(PP21 or P+)

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+)

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). If a barcode has been associated to this exhibit report, then the DNA profile obtained from that barcode cannot be excluded as being a possible contributor of DNA to this mixed DNA profile. If no barcode has been associated to this exhibit report, then no further interpretation can be conducted at 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

ENVM additional quality search conducted see Intel report
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

Not Current

is restricted within Forensic 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+)

5 Associated Documents

QIS: 34308 – Procedure for Intelligence Reports and Interstate/Interpol Requests in the Forensic Register
QIS: 17117 – Procedure for Case Management
QIS: 34245 – Reference Sample Result Management
QIS: 34006 – Forensic Register procedure for the release of results
QIS: 17140 – Procedure for the Identification and Examination of Hairs
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: 33798 – Examination of Sexual Cases (Forensic Register)
QIS: 33800 – Examination of Items (Forensic Register)
QIS: 33771 – Examination of In-tube samples (Forensic Register)
QIS: 33998 – Phadebas Test for Saliva (Forensic Register)

6 Amendment History

Version	Date	Author/s	Amendments
1	May 2017	E Caunt	First Issue
2	9 Oct 2018	H Pattison	Added SPFRU, SPP, 2MXRLM and 2MXUNS explanations to document. Updated associated documents and hyperlink. Removed references to 'EXH'. Expanded scope to cover AUSLAB as well as FR. Minor formatting and wording changes.

7 Appendices

Appendix 1 – Case management/reporting of single source DNA profiles

Not Current

Appendix

Profile Data Analysis of single source profiles

The following table outlines the appropriate Exhibit Result lines to add for single source profiles when matching Unknown and Reference DNA profiles.

Single-source DNA Profiles			
Profile Matching:	**Alleles**	**First sample**	**Subsequent sample/s**
Unknown	12 to 40	1SS (and 1SSNCD)	1SS
	6 to 11	1SSLND	1SSLND
	1 to 5	1SSUND	1SSUND
Reference Sample	40	1SS20L (and 1SSNCD)	1SS20L^
	32 to 39	1S9L10 (and 1SSNCD)	1S9L10^
	1 to 31	Various 1SSx lines^^ (and relevant NCIDD indicator)	Various 1SSx lines^^

Notes

^ Does not require an LR.

^^ run in STRmix to determine appropriate LR EXH line

Not Current

PP21 statements

FR to pull in barcode and item description then add wording as below depending on the interpretation (from PDA page).

For single source profiles (1 contributor)

If only 1 reference sample in the case and doesn't match the reference sample:

The DNA profile obtained from this sample does not match the DNA profile of *<name of reference sample>*. This DNA profile indicated *<male if X,Y or female if X,X>* gender.

If >1 reference samples in the case and doesn't match any of the reference samples:

The DNA profile obtained from this sample does not match any of the reference DNA profiles associated with this matter. This DNA profile indicated *<male if X,Y or female if X,X>* gender.

If profile matches reference sample and 'AC' box checked for this reference sample:

The DNA profile obtained from this sample matches the DNA profile of *<name of reference sample>*. As this sample is said to have been taken from *<name of reference sample>*, the finding of DNA which could have come from *< 'him' if reference is X,Y; 'her' if reference is X,X>* is not unexpected, and therefore no statistical analysis has been performed.

If profile matches reference sample:

The DNA profile obtained from this sample matches the DNA profile of *<name of reference sample>*.

Based on statistical analysis, it is estimated that the DNA profile obtained is *<'approximately LR' if LR is less than 100 billion; 'greater than 100 billion' if LR is greater than 100 billion>* times more likely to have occurred if *<name of reference sample>* had contributed DNA rather than if *< 'he' if reference is X,Y; 'she' if reference is X,X>* had not.

For 2 or 3 contributors and NO conditioning ('AC' box not checked) and only 1 reference sample in the case

The mixed DNA profile obtained from this sample indicates the presence of DNA from *<'two' or 'three'>* contributors. As such, an assumption of *<'two' or 'three'>* contributors has been made for statistical analysis.

The DNA profile of *<name of reference sample>* has been compared with this mixed DNA profile, in order to assess whether or not *< 'he' if reference is X,Y; 'she' if reference is X,X>* may have contributed DNA.

The next paragraph depends on the LR

If H1 box checked:

Based on statistical analysis, it is estimated that the mixed DNA profile obtained is *<'approximately LR' if LR is less than 100 billion; 'greater than 100 billion' if LR is greater than 100 billion>* times more likely to have occurred if *<name of reference sample>* had contributed DNA rather than if *< 'he' if reference is X,Y; 'she' if reference is X,X>* had not.

If H2 box checked:

Based on statistical analysis, it is estimated that the mixed DNA profile obtained is *<'approximately LR' if LR is less than 100 billion; 'greater than 100 billion' if LR is greater than 100 billion>* times more likely to have occurred if *<name of reference sample>* had not contributed DNA rather than if *< 'he' if reference is X,Y; 'she' if reference is X,X>* had.

If LR = 1:

Based on statistical analysis, it is estimated that the mixed DNA profile obtained is equally likely to have occurred if *<name of reference sample>* had or had not contributed DNA.

If LR = 0:

<name of reference sample> can be excluded as having contributed DNA to this mixed DNA profile.

For 2 or 3 contributors and NO conditioning ('AC' box not checked) and 2 or more reference samples in the case

The mixed DNA profile obtained from this sample indicates the presence of DNA from *<'two' or 'three'>* contributors. As such, an assumption of *<'two' or 'three'>* contributors has been made for statistical analysis.

Each of the reference DNA profiles associated to this case has been compared with this mixed DNA profile, in order to assess whether or not either of them may have contributed DNA.

Based on statistical analysis, the results are as follows:

Commented [EC1]: This is currently displaying as digits can we have it in words please

Commented [EC2]: words

Commented [EC3]: words

Commented [EC4]: words

Commented [EC5]: This should say "any"

The next paragraphs depend on the LR. There should be one paragraph per reference sample and they should be ordered by significance, i.e. large LR favouring contribution (H1) first, then low LR favouring H1, then LR=1, then low LR favouring H2, then large LR favouring H2 then LR=0

If H1 box checked:

It is estimated that the mixed DNA profile obtained is *<'approximately LR' if LR is less than 100 billion; 'greater than 100 billion' if LR is greater than 100 billion>* times more likely to have occurred if *<name of reference sample>* had contributed DNA rather than if *< 'he' if reference is X,Y; 'she' if reference is X,X>* had not.

If H2 box checked:

It is estimated that the mixed DNA profile obtained is *<'approximately LR' if LR is less than 100 billion; 'greater than 100 billion' if LR is greater than 100 billion>* times more likely to have occurred if *<name of reference sample>* had not contributed DNA rather than if *< 'he' if reference is X,Y; 'she' if reference is X,X>* had.

If LR = 1:

It is estimated that the mixed DNA profile obtained is equally likely to have occurred if *<name of reference sample>* had or had not contributed DNA.

If LR = 0:

<name of reference sample> can be excluded as having contributed DNA to this mixed DNA profile.

For 2 or 3 contributors and profile is conditioned ('AC' box checked) and only 2 reference samples in the case

The mixed DNA profile obtained from this sample indicates the presence of DNA from *<'two' or 'three'>* contributors. Since this sample is said to have been collected from *<name of reference sample with 'AC' box checked>*, it would not be unexpected to find DNA which could have come from *< 'him' if reference is X,Y; 'her' if reference is X,X>*. In order to interpret this mixed DNA profile an assumption of DNA from *<'two' or 'three'>* contributors, one of whom is *<name of reference sample with 'AC' box checked>*, has been made.

The DNA profile of *<name of reference sample with LR>* has been compared to this mixed DNA profile, to assess whether or not *< 'he' if reference is X,Y; 'she' if reference is X,X>* may have contributed DNA along with *<name of reference sample with 'AC' box checked>*.

Commented [EC6]: words

Commented [EC7]: words

The next paragraph depends on the LR

If H1 box checked:

Based on statistical analysis, it is estimated that the mixed DNA profile obtained is *<'approximately LR' if LR is less than 100 billion; 'greater than 100 billion' if LR is greater than 100 billion>* times more likely to have occurred if *<name of reference sample>* had contributed DNA rather than if *< 'he' if reference is X,Y; 'she' if reference is X,X>* had not.

If H2 box checked:

Based on statistical analysis, it is estimated that the mixed DNA profile obtained is *<'approximately LR' if LR is less than 100 billion; 'greater than 100 billion' if LR is greater than 100 billion>* times more likely to have occurred if *<name of reference sample>* had not contributed DNA rather than if *< 'he' if reference is X,Y; 'she' if reference is X,X>* had.

If LR = 1:

Based on statistical analysis, it is estimated that the mixed DNA profile obtained is equally likely to have occurred if *<name of reference sample>* had or had not contributed DNA.

If LR = 0:

<name of reference sample> can be excluded as having contributed DNA to this mixed DNA profile.

For 2 or 3 contributors and profile is conditioned ('AC' box checked) and 3 or more reference samples in the case

The mixed DNA profile obtained from this sample indicates the presence of DNA from *<'two' or 'three'>* contributors. Since this sample is said to have been collected from *<name of reference sample with 'AC' box checked>*, it would not be unexpected to find DNA which could have come from *< 'him' if reference is X,Y; 'her' if reference is X,X>*. In order to interpret this mixed DNA profile an assumption of DNA from *<'two' or 'three'>* contributors, one of whom is *<name of reference sample with 'AC' box checked>*, has been made.

Each of the remaining reference DNA profiles associated to this case has been compared to this mixed DNA profile separately, to assess whether or not either of them may have contributed DNA along with *<name of reference sample with 'AC' box checked>*.

Based on statistical analysis, the results are as follows:

Commented [EC8]: words

Commented [EC9]: words

Commented [EC10]: This should say "any"

The next paragraphs depend on the LR. There should be one paragraph per reference sample and they should be ordered by significance, i.e. large LR favouring contribution (H1) first, then low LR favouring H1, then LR=1, then low LR favouring H2, then large LR favouring H2 then LR=0

If H1 box checked:

It is estimated that the mixed DNA profile obtained is *<'approximately LR' if LR is less than 100 billion; 'greater than 100 billion' if LR is greater than 100 billion>* times more likely to have occurred if *<name of reference sample>* had contributed DNA rather than if *< 'he' if reference is X,Y; 'she' if reference is X,X>* had not.

If H2 box checked:

It is estimated that the mixed DNA profile obtained is *<'approximately LR' if LR is less than 100 billion; 'greater than 100 billion' if LR is greater than 100 billion>* times more likely to have occurred if *<name of reference sample>* had not contributed DNA rather than if *< 'he' if reference is X,Y; 'she' if reference is X,X>* had.

If LR = 1:

It is estimated that the mixed DNA profile obtained is equally likely to have occurred if *<name of reference sample>* had or had not contributed DNA.

If LR = 0:

<name of reference sample> can be excluded as having contributed DNA to this mixed DNA profile.

For profiles with the 'CX' box checked

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.

For 'no DNA detected' samples

DNA was not detected in this sample and therefore it was not tested further.

For 'insufficient DNA' samples

This sample contained insufficient DNA to be suitable for analysis and was not tested further.

Queensland Government

Forensic and Scientific Services

STATEMENT OF WITNESS

Peer Reviewed..... Yes/ No

Case Analyst..... E Caunt

Peer Analyst..... JS

Date Issued..15 February 2022

Client Reference : [redacted]
Report Number : 7212794

QUEENSLAND)
TO WIT)

I, Emma-Jayne CAUNT, of Brisbane in the State of Queensland, do solemnly and sincerely declare that:-

1. I am employed by Queensland Health Forensic and Scientific Services (QHFSS) at Coopers Plains, Brisbane.

2. I hold the position of scientist in the Forensic DNA Analysis laboratory of QHFSS.

3. I was awarded a Bachelor of Science with Honours from the University of Manchester Institute of Science and Technology (UMIST), UK.

4. This is my statement in relation to the alleged offence that Occurrence Number [redacted] refers. The defendant in this matter is [redacted]. The complainant in this matter is [redacted]

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone
Fax
Email [redacted]

5. Laboratory records show that on 23 September 2021, [redacted] delivered the following 3 items:

   [redacted]

6. Laboratory records show that on 30 September 2021, [redacted] delivered the following reference sample:

   [redacted] 07/05/1963

7. The results of the scientific examinations conducted in the laboratory are as follows:

   [redacted] **Reference sample from** [redacted]

   The DNA profile of [redacted] has been determined from the reference sample.

   [redacted] **- EXHIBIT A, NO STAIN, METAL, TRACE DNA SWAB [SWAB] Trigger of shotgun located during search warrant**

   The mixed DNA profile 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 DNA profile of [redacted] has been compared with this mixed DNA profile, in order to assess whether or not he may have contributed DNA.

   Based on statistical analysis, it is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had contributed DNA rather than if he had not.

   [redacted] **- EXHIBIT B, NO STAIN, WOOD, TRACE DNA SWAB [SWAB] Front section of shotgun located during search warrant**

   This sample contained insufficient DNA for further processing and was not tested further.

   [redacted] **- EXHIBIT C, NO STAIN, PLASTIC, TRACE DNA SWAB [SWAB] Shotgun shell removed from firearm chamber**

   DNA was not detected in this sample and was not processed further.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone
Fax
Email [redacted]

APPENDIX

Procedural and technical overview of DNA profiling at Forensic DNA Analysis, Forensic and 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.

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), 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.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone [redacted]
Fax
Email

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 Queensland Health 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.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone [redacted]
Fax
Email

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.

DNA profiles are initially assessed to determine the number of contributors. This value will be the minimum number of people that are required to reasonably explain the observed profile, however, it is noted that there is always the possibility that the profile is a result of a different number of contributors.

As such, 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 are 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.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone
Fax
Email [redacted]

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

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA

PO Box 594 Archerfield QLD 4108 AUSTRALIA

Phone [redacted]
Fax
Email

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.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone Fax Email [redacted]

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.

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 February 2022 and contained in the pages numbered 1 to 8 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.

[redacted]

Emma-Jayne CAUNT

Signed at BRISBANE on 15 February 2022

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA

PO Box 594 Archerfield QLD 4108 AUSTRALIA

Phone Fax Email [redacted]

Queensland Government

Forensic and Scientific Services
HealthSupport Queensland

STATEMENT OF WITNESS

Peer Reviewed.....Yes/ No

Case Analyst..... [redacted] .....

Peer Analyst. CLJ as per FR record.

Date Issued. 12.05.2022

Client Reference : [redacted]
Report Number : 7300837

QUEENSLAND)
TO WIT)

I, Allan Russell MCNEVIN, of Brisbane in the State of Queensland, do solemnly and sincerely declare that:-

1. I am employed by Queensland Health Forensic and Scientific Services (QHFSS) at Coopers Plains, Brisbane.
2. I hold the position of scientist in the Forensic DNA Analysis laboratory of QHFSS.
3. I was awarded a Bachelor of Applied Science from Queensland University of Technology.
4. I am a member of the Australian and New Zealand Forensic Science Society.
5. This is my statement in relation to the alleged offence that Occurrence Number [redacted] refers. The defendant in this matter is [redacted] The complainant in this matter is [redacted]

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone
Fax
Email [redacted]

6. Laboratory records show that on 3 December 2021 [redacted] delivered the following 6 items:

   [redacted]

7. Laboratory records show that on 4 January 2022, [redacted] delivered the following reference sample:

   [redacted] 25/03/2005

8. The results of the scientific examinations conducted in the laboratory are as follows:

   [redacted] **25/03/2005**
   The DNA profile of [redacted] has been determined from the reference sample.

   [redacted] **- EXHIBIT B - PLASTIC [TRACE] inside driver's door handle**
   This sample contained insufficient DNA to be suitable for DNA analysis, therefore it was not tested further.

   [redacted] **- EXHIBIT C - PLASTIC [TRACE] inside front passenger's door handle**
   The mixed DNA profile 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 DNA profile of [redacted] has been compared with this mixed DNA profile, in order to assess whether or not he may have contributed DNA.

   Based on statistical analysis, it is estimated that the mixed DNA profile obtained is approximately 39 billion times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

   [redacted] **- EXHIBIT F1 - SYNTHETIC FABRIC [TRACE] disposable surgical mask from front passenger foot well**
   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.

   [redacted] **- EXHIBIT G1 - SYNTHETIC FABRIC [TRACE] disposable surgical mask from under front passenger seat**
   The mixed DNA profile 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 DNA profile of [redacted] has been compared with this mixed DNA profile, in order to assess whether or not he may have contributed DNA.

   Based on statistical analysis, it is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

   [redacted] **- EXHIBIT H1 - GAUZE FABRIC [TRACE] inside / white side of disposable mask**
   The mixed DNA profile 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 DNA profile of [redacted] has been compared with this mixed DNA profile, in order to assess whether or not he may have contributed DNA.

   Based on statistical analysis, it is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had contributed DNA rather than if he had not.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing
39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA
PO Box 594 Archerfield QLD 4108 AUSTRALIA
Phone Fax Email [redacted]

STATEMENT OF WITNESS

Client Reference : [redacted]

[redacted]- EXHIBIT I1- ACRYLIC FABRIC [TRACE] inside neckline of hooded jumper

The mixed DNA profile obtained from this sample indicates the presence of DNA from two contributors. As such, an assumption of two contributors has been made for statistical analysis. The DNA profile of [redacted] has been compared with this mixed DNA profile, in order to assess whether or not he may have contributed DNA.

Based on statistical analysis, it is estimated that the mixed DNA profile obtained is approximately 8.5 million times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

NATA Accredited Laboratory 41
Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone
Fax
Email [redacted]

APPENDIX

Procedural and technical overview of DNA profiling at Forensic DNA Analysis, Forensic and 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.

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), 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.

NATA Accredited
Laboratory 41
Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone
Fax
Email [redacted]

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 Queensland Health 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.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone
Fax
Email [redacted]

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.

DNA profiles are initially assessed to determine the number of contributors. This value will be the minimum number of people that are required to reasonably explain the observed profile, however, it is noted that there is always the possibility that the profile is a result of a different number of contributors.

As such, 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 are 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.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA

PO Box 594 Archerfield QLD 4108 AUSTRALIA

Phone [redacted]
Fax
Email

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:

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road Coopers Plains QLD 4108 AUSTRALIA

PO Box 594 Archerfield QLD 4108 AUSTRALIA

Phone [redacted]
Fax
Email

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.

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone
Fax
Email [redacted]

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.

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 12 May 2022 and contained in the pages numbered 1 to 9 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.

.....[redacted].....

Allan Russell MCNEVIN

Signed at BRISBANE on 12 May 2022

NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

Phone
Fax
Email [redacted]

Assessment of results obtained from 'automatic-microcon' samples

Josie Entwistle, Allison Lloyd, Kylie Rika, Thomas Nurthen, Cathie Allen

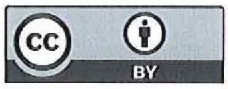
August 2015

Great state. Great opportunity.

Queensland Government

Assessment of results obtained from 'automatic-microcon' samples

Published by the State of Queensland (Queensland Health), July 2015



This document is licensed under a Creative Commons Attribution 3.0 Australia licence.
To view a copy of this licence, visit creativecommons.org/licenses/by/3.0/au

© State of Queensland (Queensland Health) 2015

You are free to copy, communicate and adapt the work, as long as you attribute the State of Queensland (Queensland Health).

For more information contact:
Forensic DNA Analysis, Department of Health, GPO Box 48, Brisbane QLD 4001

Disclaimer:
The content presented in this publication is distributed by the Queensland Government as an information source only. The State of Queensland makes no statements, representations or warranties about the accuracy, completeness or reliability of any information contained in this publication. The State of Queensland disclaims all responsibility and all liability (including without limitation for liability in negligence) for all expenses, losses, damages and costs you might incur as a result of the information being inaccurate or incomplete in any way, and for any reason reliance was placed on such information.

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: Josie Entwistle
Title: Scientist – Forensic Intelligence & Reporting
Phone:
Email: [redacted]

Version history

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

This document has been **approved** by:

Name	Position	Signature	Date
Cathie Allen	Managing Scientist	[redacted]	22/12/15

This document has been **endorsed** by:

Name	Position	Signature	Date
Justin Howes	Team Leader FRIT	[redacted]	17.12.15
Luke Ryan	A/Team Leader ER & Q	[redacted]	18.12.2015
Sharon Johnstone	Senior Scientist Intel Team	[redacted]	22/12/2015
Kirsten Scott	Senior Scientist Q & P	[redacted]	17/12/2015
Allan McNevin	Senior Scientist ER	[redacted]	17/12/2015.
Megan Matheison	A/Senior Scientist Analytical	[redacted]	21/12/15
Amanda Reeves	Senior Scientist Reporting 1	[redacted]	18 12 2015
Kylie Rika	Senior Scientist Reporting 2	[redacted]	17/12/2015.

Contents

Figures

Tables

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.

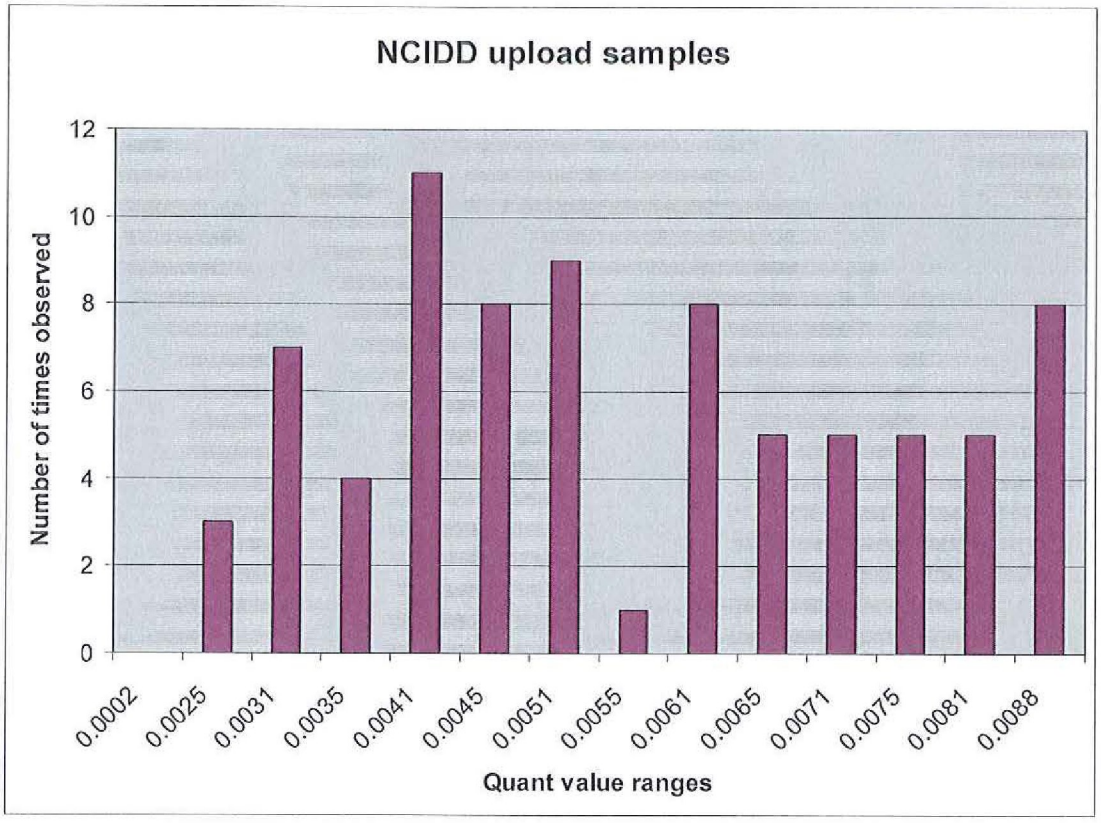


Figure 1 NCIDD upload samples

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.

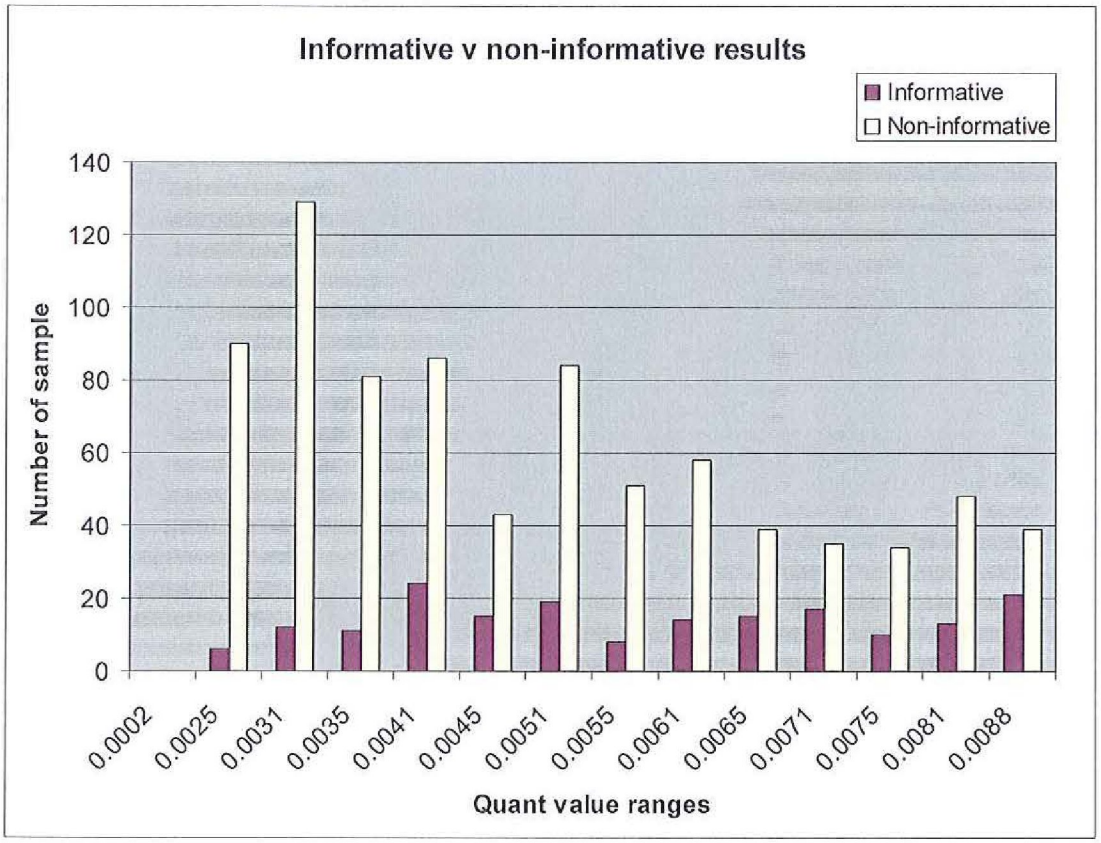


Figure 2 Informative v non-informative results

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.

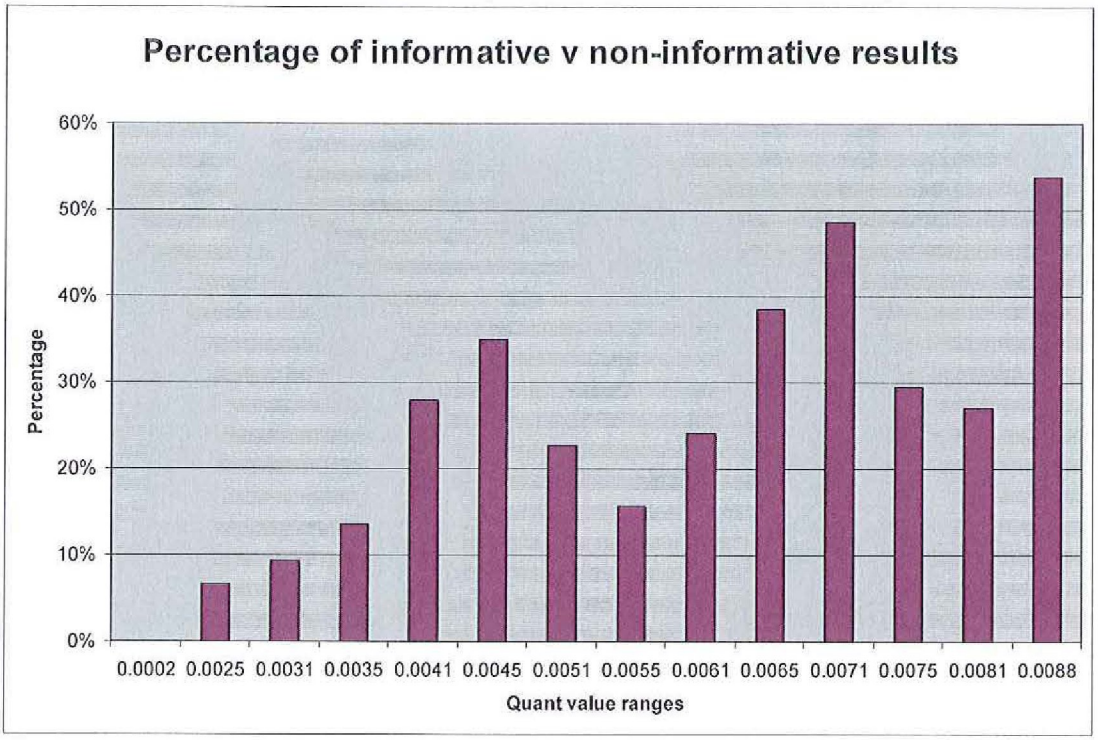


Figure 3 Percentage of informative v non-informative results

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.

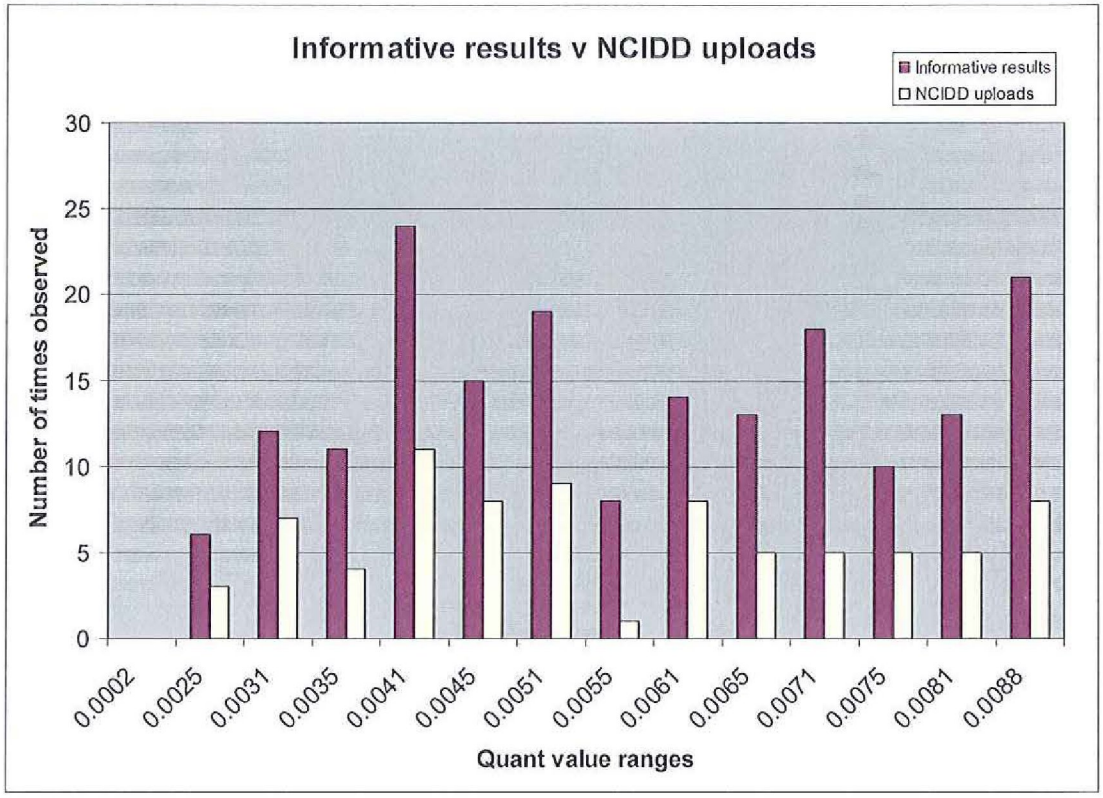


Figure 4 Informative results v NCIDD uploads

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.

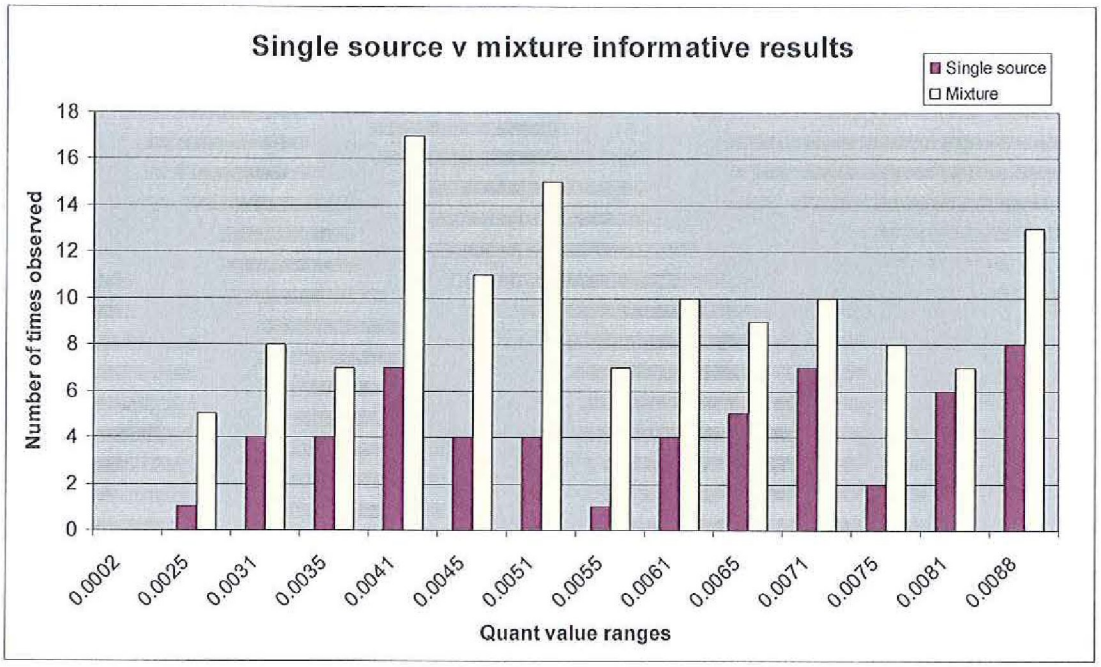


Figure 5 Single source v mixture informative results

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.

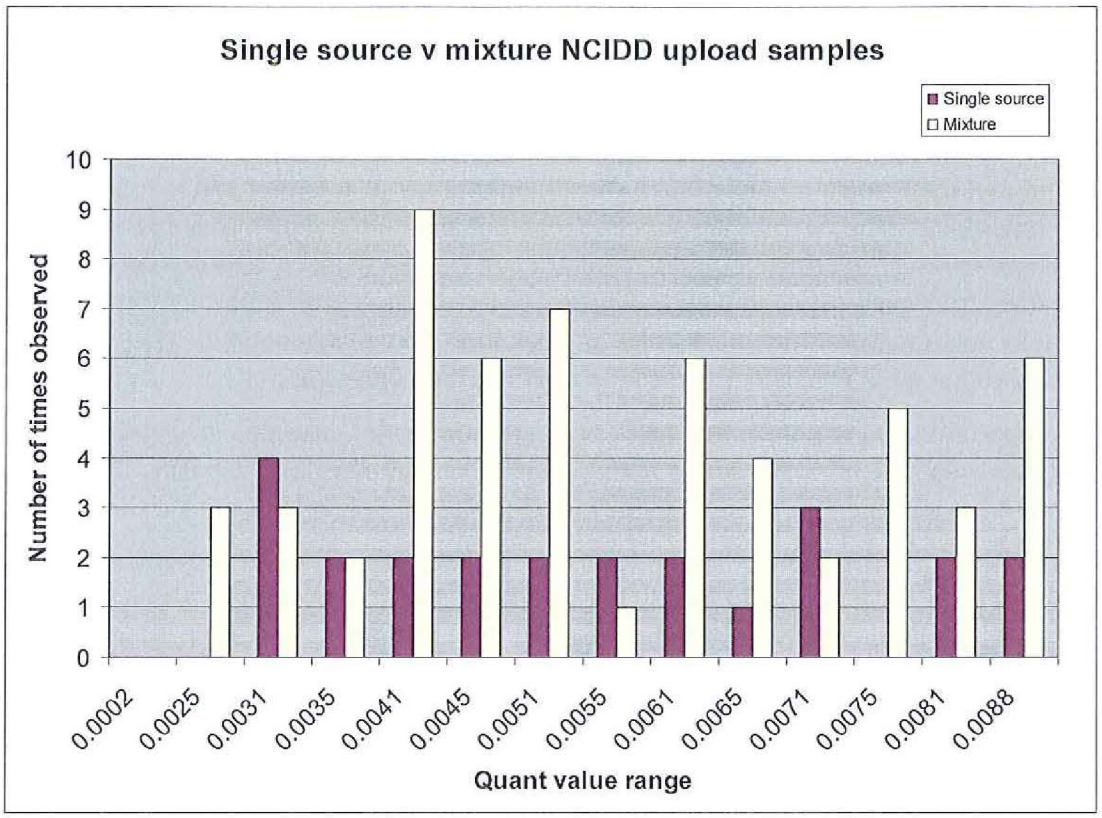


Figure 6 Single source v mixture NCIDD upload samples

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

EXH line	Expanded Comment
No DNA	
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.
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.
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.
Unsuitable for Interp	
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.
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.

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.
Single Source	
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.
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.

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.
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.
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.

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.
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.
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.

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.
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 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.
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.

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.
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.
Non contributions lines LR <1	
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.
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.
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.

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.
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.
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 exhibit report, comparison to other reference samples may provide a different statistical interpretation.
Mixed DNA Profiles	
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.
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.

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.
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.
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.
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.

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.
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.
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 associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.
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.

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.
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.
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.
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.

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.
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.
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.
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.
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.

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.
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.
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.

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.
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.
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.

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.
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.
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.
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.

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.
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.
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.

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.
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.
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.

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.
Unknown Contributors	
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.
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.
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.
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.

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.
Interim Results	
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.
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 repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.
Interim result- no profile obtained- undergoing rework	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 repeated or additional testing to improve the DNA profile is being undertaken. The interim result is no DNA profile. Final results are pending.
Interim Result. Sample undergoing rework	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 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.
NCIDD Upload	

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.
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.

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.

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.
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 assosicated 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.
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.
Intel	

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 as a likelihood ratio.
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 evaluated against the mixture without a contribution being assumed and the result reported as as a likelihood ratio.
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.

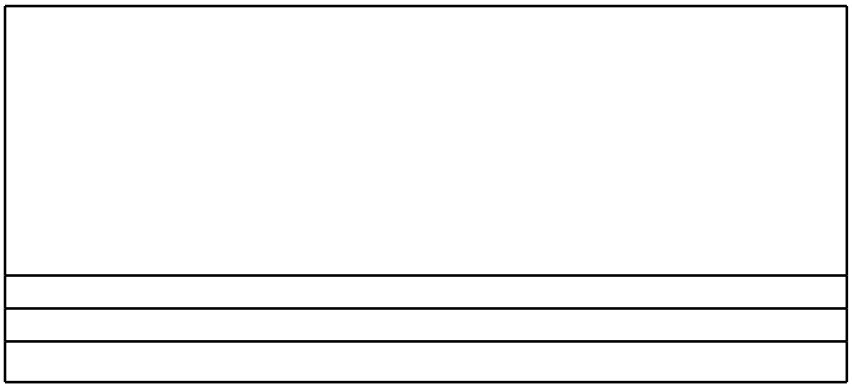
3 person mixed profile - remaining Intel - NCIDD	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor for intelligence purposes only, some or all of the components of the DNA profile from the designated unknown sent 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.
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 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.

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.
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.
Intel report required for further information	The results for this item/sample require further explanation which will follow in an intelligence report.
Suspect check actioned - no match	The nominated suspect can be excluded as a potential contributor to the DNA profile obtained from this item/sample.
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.

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.
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.
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.
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.
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.

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.
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.
For suspect check - exclusion for mixtures, use non contribution lines.	LR <1
Paternity	
Current line. No change	
ENVM samples	
Current line. No change	
Quality failures	
Current line. No change	
General EXHs	
No further work required as per advice from QPS	Current line, no change.
QPS advised no further work required - results available	Current line, no change.
Testing restarted on advice from QPS	Current line, no change.

This sample have undergone further processing	Current line, no change.
No further work able to be conducted on this sample	Current line, no change.



Document Management: 23008 - V13.0 - Explanations of EXR/EXH Results

Version Status: Superseded

View Document | Print Comments | History

General | Reviews and Approvals | Notifications | **Comments** | Controlled Copies | Version History | Associations | Records | Workflow

Comments By	Comment Date	Response By	Response Date	Comment Noted
☑ Sharon JOHNSTONE	10/12/2012	Paula BRISOTTO	12/12/2012	Noted
☐ Paula BRISOTTO	03/01/2013			Not Required
☐ Justin HOWES	19/12/2012	Paula BRISOTTO	21/01/2013	Noted

Comments

10/12/2012 12:33:29 PM Sharon JOHNSTONE:

4.7 1 Could do with explanation to say it could be full or partial profiles
9 Why use "less" when all other EXH's have "<"
10-12 I would use "9 loci or more" I find it eaiser to understand than "9 loci or above"
16 Shaould there be a note to say this only happens rarely and after consulataion with a senior scientist?
4.8 3 could have on the end "or NCIDD"
24 & 32 to be consistent 10 000 needs the space
26 & 34 to be consistent 100 000 nedds the space
43 & 44 Should there be an explanation as to when this should be attempted?
45 & 46 How are these possible? We condition on a ref sample or condition on an Unknown designation that should be better defined prior and therefore that would be a better sample to put into NCIDD, or is this to show another person is present? Could use an explanation on how to use these.
52 & 53 Explanation requires to be used when LR = 1
4.9 5 This isn't clear how this is different from 1
4.11 11Could do with explanation to expalian these it is used in conjunction with other lines
ENVM major and minor EXH's. How can we use these for PP21?

Response

12/12/2012 3:26:32 PM Paula BRISOTTO:

4.7 1 Could do with explanation to say it could be full or partial profiles
Response: There is no full or partial profiles for any of the new EXHs anymore, but noted. Will include in next revision if required.
9 Why use "less" when all other EXH's have "<"
Response: avoid symbols where we can as can cause transfer issues, however due to space limitations, need < or >
10-12 I would use "9 loci or more" I find it eaiser to understand than "9 loci or above"
Response - wording in consultation with QPS. Coded comment - cannot be changed.
16 Shaould there be a note to say this only happens rarely and after consulataion with a senior scientist?
Response - Not essential for this revision. Can be put into next revision if required.
4.8 3 could have on the end "or NCIDD"
Response - coded comment - cannot be changed. Not needed, as expanded comment is what contains the pertinent information.
24 & 32 to be consistent 10 000 needs the space
Response: no, due to space limitations
26 & 34 to be consistent 100 000 nedds the space
Response: no, due to space limitations
43 & 44 Should there be an explanation as to when this should be attempted?
Response: Noted - next revision. Not essential for this revision.
45 & 46 How are these possible? We condition on a ref sample or condition on an Unknown designation that should be better defined prior and therefore that would be a better sample to put into NCIDD, or is this to show another person is present? Could use an explanation on how to use these.
Response: Same as for 43 and 44.
52 & 53 Explanation requires to be used when LR = 1
Response: Explanation there - use when LR = 1
4.9 5 This isn't clear how this is different from 1
Response: EXH already existed. Comment is above EXH line in SOP.
4.11 11Could do with explanation to expalian these it is used in conjunction with other lines
ENVM major and minor EXH's. How can we use these for PP21?
Response - decision by management that interp of ENVM samples remain the same, as they are for intel purposes. EXHs therefore remain unchanged.

Last Modified at 12/12/2012 3:26 PM by Paula BRISOTTO, Created on 10/12/2012 12:33 PM by Sharon JOHNSTONE

Quality Information System (v2.10.7482 26/06/2020 Release Notes) Copyright © 2020, Health Support Queensland, Queensland Health - All Rights Reserved -

APPENDIX

Procedural overview for DNA Analysis, Forensic and Scientific Services (FSS), Health Services Support Agency

Examinations

Unless otherwise stated, the examinations of items for biological material were conducted by officers within the Queensland Police Service (QPS). Sub-samples from these items were forwarded to Forensic and Scientific Services (FSS), Health Services Support Agency, for the purposes of conducting DNA analysis.

DNA Analysis operates under the premise that 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 FSS DNA Analysis. 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.

Some items may be submitted to this laboratory for the purposes of both examination and DNA profiling. This occurs at the discretion of the QPS. These examinations are performed in accordance with the SOPs of this laboratory. For these items, notes are made at the time of the examination by the examining scientist and form part of the casefile.

Chain of Custody

All DNA Analysis 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 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 exhibit packaging prior to processing. The packaging and labelling of any exhibit is checked and recorded before the sample undergoes DNA analysis.

Entry into DNA Analysis is restricted to authorised persons only, via electronically encoded proximity access cards. DNA Analysis forms part of a Health Services Support Agency campus site which has access controlled and monitored by a security team. Records of Visitors to DNA Analysis are retained.

Accreditation

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 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. For details of the current ISO/IEC 17025 Field Application Document, Forensic Science, Supplementary requirements for accreditation, please refer to the NATA website:

http://www.nata.com.au

Technical information relating to DNA profiling at DNA Analysis, Forensic and Scientific Services (FSS), Health Services Support Agency

DNA Profiling

DNA is a complex chemical found in almost all cells in the human body. It carries genetic information which determines the physical and chemical characteristics of a person. The testing system used at DNA Analysis looks at 21 regions of DNA, 20 of which contain highly variable Short Tandem Repeats (STRs). The 21st region gives an indication as to the gender of the donor (for details see Table 1). This technique involves the use of a method known as Polymerase Chain Reaction (PCR), used to amplify these specific regions of the DNA to produce numerous copies. In this way, minimal amounts of DNA isolated from small or degraded samples can be increased to a level where they are able to be detected, profiled and compared with other samples.

The individual components (alleles) of a DNA profile are represented by a series of peaks which are measured and given a designation using standard sizing ladders. A person will have two peaks for each STR, one inherited from their mother and one inherited from their father, unless the same STR is inherited from both parents, in which case only one peak will be seen.

A DNA profile obtained from biological material such as blood, semen, saliva, hair or cells (eg. touch DNA) can be compared with the DNA profile obtained from a reference sample from any person. If there is no indication of a contribution by more than one person, then a DNA profile is described as being “single source”. Conversely, if there are indications of two or more contributors, then a DNA profile is described as a “mixed” DNA profile.

Statistical Analysis of DNA profiles

In order to statistically evaluate DNA profiles, it is necessary to make a reasonable assessment of the possible number of people who may have contributed DNA to that DNA profile, based on the information observed.

DNA profiles assumed to originate from one person (single source)

A person can be excluded as a possible source of the biological material if corresponding regions of the crime-scene DNA profile are different from that person's reference DNA profile. If the corresponding regions of the DNA profiles contain the same information, then that person, together 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 DNA originated from the person of interest;
Proposition 2: the 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 DNA components that make up the DNA profile. Upon request, an internationally accepted verbal scale to describe the support for one proposition over another can be used to offer some non-numerical explanation for the likelihood ratio (see Table 2).

If less than the 21 regions of DNA are seen in a DNA profile (termed an 'incomplete or partial DNA profile') this will be reflected by a smaller likelihood ratio than the likelihood ratio that would be obtained from a full DNA profile. In other words, the more incomplete the DNA profile, the greater the likelihood of obtaining the DNA profile if it came 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 could or could not have contributed to a mixed DNA profile, a set of competing propositions (similar to a single source DNA profile) are considered. For example, for a two person mixture:

Proposition 1: the DNA originated from the person of interest and an unknown person unrelated to the person of interest;
Proposition 2: the DNA originated from two unknown people unrelated to the person of interest.

The likelihood ratio provides a statistical assessment of a particular contribution of DNA being contained within the mixed DNA profile.

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 intimate area, then it may be possible to make the reasonable assumption that the donor of the sample 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 known donor, such that the presence of the DNA components corresponding with the donor'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, for example:

Proposition 1: the DNA has originated from the complainant and the person of interest;
Proposition 2: the DNA has originated from the complainant and an unknown individual unrelated to the person of interest.

When it appears that a large number of people could have contributed to a mixed DNA profile, it can be difficult to exclude individuals as potential contributors. It can be equally difficult to determine whether a person could in fact be a contributor to the DNA profile. If it is not possible to determine the number of contributors to a mixed DNA profile, or if there is very limited information available, then a mixed DNA profile may be described as unsuitable for interpretation.

If information is received such that the assumptions made in an interpretation are not accepted, then 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, irrespective of whether the DNA profile is single source or mixed. A correction factor θ (theta) is applied to all statistical calculations in order to correct for the possibility of common ancestry (sharing of DNA components inherited from a common ancestor) between people in the general population. The nationally agreed figures for theta are θ=0.02 for the Australian Caucasian dataset, θ=0.03 for South East Asian dataset, and θ=0.05 for the Australian Aboriginal dataset. Unless otherwise specified, the default dataset used in DNA Analysis is the Australian Caucasian dataset. The other datasets are available upon request.

In addition to theta, the calculation of the likelihood ratio also includes an allowance for the sampling variability of the dataset. In other words, if a new dataset were generated it allows for any difference the new dataset could make to the likelihood ratio.

Often the calculated likelihood ratio produces numbers of hundreds (100s) or even thousands (1000s) of billions. To avoid the use of potentially confusing terminology, a 'ceiling figure' for the likelihood ratio of 100 billion has been determined (this is called truncation). For example, a calculated likelihood ratio of "150 000 billion times more likely", would be reported as "more than, or at least 100 billion times more likely". The actual calculated figure can be provided upon request.

The above listed values for the 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 random fashion in which DNA from parents combines, the probability that two siblings would share the same 20 STR regions 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 is thought that a close blood relative may have been involved, a more meaningful approach would be to submit the reference sample from the relative in question for analysis and direct comparison to the crime stain DNA profile.

Standard DNA (STR) profiling system at DNA Analysis, Forensic and Scientific Services (FSS), Health Services Support Agency

Table 1: PowerPlex® 21 multiplex 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

Table 2: Verbal scale to describe Likelihood Ratios
(adapted from Evett IW and Weir BS 1998 *Interpreting DNA Evidence*. Sinauer, Sunderland, MA)

RANGE OF VALUE	LEVEL OF SUPPORT
>1 million	Extremely Strong
100 000 – 1 million	Very Strong
10 000 – 100 000	Strong
1000 – 10 000	Moderately Strong
100 – 1000	Moderate
10 – 100	Low Level
1 – 10	Slight
1	Inconclusive

Procedure for the Release of Results

1 PURPOSE

1 To describe the correct format for statements or reports issued from the DNA Analysis Unit.

2 To document the procedures for issuing reports within the DNA Analysis Unit.

3 To document workflows leading to the releasing of information via Exhibit Reports to the Queensland Police Service.

2 SCOPE

1 This standard operating procedure relates to all statements or reports issued by case analysts to clients.

3 REFERENCES

1 ISO/IEC 17025 Field Application Document Forensic Science: Supplementary Requirements for Accreditation in the Field of Forensic Science.
2 Evidence Act 1977

4 ASSOCIATED DOCUMENTS

10623 FSS – Laboratory Report Format, Content and Handling
16004 AUSLAB Users Manual – Forensic Biology
17088 Procedure for recording handwriting specimens in DNA Analysis
17117 Procedure for Case Management
17047 Court Testimony Monitoring Evaluation Form
17142 Examination of Items
18034 FSS Court Testimony and Attendance Requirements
22619 Creating and Reviewing Links
23008 Explanations of EXR/EXH Results
23602 Environmental Monitoring
23890 Uploading and Actioning Samples on NCIDD
23955 Disaster Victim Identification Preliminary DNA Reports
23968 DNA Analysis Unit Communications Procedure
24015 Procedure for Intelligence Reports and Interstate/Interpol Requests
26874 Procedure for Paperless Case Management and Review
29024 Use of offline Forensic Reporting templates
29008 Statement of Witness template – address – no NATA endorsement
29009 Statement of Witness template – blank – no NATA endorsement
29010 Statement of Witness template – stamp
29011 Intelligence report template
30799 DNA Evidentiary Certificate Checklist
31523 Interpretation and Statistical Analysis of DNA profiles using the STRmix Expert System

5 DEFINITIONS

EXR/EXH – Exhibit Report.

No Current

QIS2 – Quality Information System version 2
QPS – Queensland Police Service
SMU – Sample Management Unit (QPS)
SSLU – Scientific Services Liaison Unit (FSS)

6 PRESUMPTIVE EXHIBIT REPORTS

1 The formats of the accepted EXR/EXH comments are located in QIS2 23008 Explanations of EXR/EXH results.
2 A Presumptive EXR/EXH should include the following information:

a. **Overall Status**: This should reflect the result. This only applies to EXRs, and does not apply to EXHs.

i. Negative (Forensic Value) – Used for items that are examined but not submitted for testing.
ii. Negative (Not examined) – Used for items that are received but not examined.
iii. Not Received at FSS – Used for items that are not received at FSS
iv. Positive (Forensic Value) – Any sample submitted for DNA testing will have this status result.

b. **Lab No**: The results are reported under the individual sub-sample. Refer to Appendix 11 for specific guidelines.

c. **Result Status** – All result options are available using the F1 lookup function. The results status should reflect any presumptive & confirmatory tests that were conducted and include whether the sample was submitted for DNA testing.

Example 1: If a TMB test was performed that was negative and the swab was submitted as cells but also had a hair attached which was observed under microscopy as not suitable for DNA testing the following lines would be entered:

234967280 Presumptive blood test neg. Submitted as cells.
234967280 Hair located. Not suitable for analysis

Example 2: If different testing was performed on 2 sub-samples with a positive TMB test recorded for the first which was submitted and both an AP pos and the presence of spermatozoa detected by microscopic examination on the second the following lines would be entered:

234967280 Presumptive blood test pos, submitted – results pending
234967281 Presump sem fluid test pos, submitted – results pending.
234967281 Micro positive for sperm. Submitted – results pending.

d. Linked No and Warm Link name are not required for presumptive EXR/EXHs

7 FINAL EXHIBIT REPORTS

1 **Format**: The formats of the accepted EXR/EXH comments are located in QIS2 23008 Explanations of EXR/EXH results.

2 **Quality Checking**: Final EXR/EXHs can only be interpreted and released after the GMID-x batch has been read and Quality Flag checked (and Extraction Batch checked

Not Current

where appropriate) – refer Appendices 15-16. Quality Flag checking is usually performed by a Senior Scientist, EB checking is usually performed by a case manager.

3 **Information**: A Final EXR/EXH should include the following information (refer to Appendix 6):

a. **Overall Status**: This does not need to be changed from the Overall Status of the Presumptive Exhibit Report. Note, this does not apply to EXHs.

b. **Lab No**: The sub-sample no. of the results being reported. This should include the results with most evidential value however any previously reported sub-samples (reported by a presumptive EXR/EXH) should also have a result entered. If there are no sub-samples, the EXR/EXH of the Item should be entered.

c. **Result/Status**: A description of the result (eg 9 loci, partial, no DNA profile). All result options are available using the F1 lookup function. There may be more than one EXR/EXH line which is suitable however the EXR/EXH must fully describe the result. For example if there is a major and minor profile an EXR/EXH line must be entered for both the major and minor profiles.

Example 1:

234967280	Mixed DNA Profile. Major component uploaded to NCIDD	UKM1
234967280	Mixed profile, minor component insuff for NCIDD matching	UKM2

d. **Linked No**:

i. <u>If the Crime Scene profile matches an Evidence Sample</u>: The barcode no. of the evidence sample is added to the Linked No. field.

ii. <u>No Evidence Sample</u>: If there are no evidence samples, then the profile will be unknown. A unique barcode should be registered for each different profile that does not match a reference sample in that case (refer QIS 17117). The designations of 'UK' should be used for unknowns with 'F' (female) or 'M' (male) used to provide further information and 'UKP' should be used if the sex of the DNA profile is unable to be determined. These should be recorded in the Warm Link Name field (below). 1 should be used to denote the first male, female or person profile obtained.

Example 1: Three different male profiles would each be reported on a different line with UKM1, UKM2 & UKM3 used to distinguish between the contributors.

Example 2: A single (1) unknown male would be reported as UKM1.

NB: If an unknown profile is reported to QPS and an evidence sample is subsequently received that matches the unknown profile, any further unknown profiles continue sequentially eg. If UKM1 matches John SMITH, then the next unknown male in the case is designated UKM2 (it does not replace the UKM1).

e. **Warm Link Name**:

i The name of the evidence sample the profile matches to.

ii If there is no evidence sample, and the profile is unknown, then this field is used to record the designation (eg. UKM1).

Not Current

4 **Suspect Checks**: These are only reported in a final EXR/EXH if they do not match. Suspect checks are useful when a profile is insufficient for NCIDD upload and a permanent barcode/profile exists for a suspect. For profiles sufficient for NCIDD, the matches are reported via LKRs (QIS2 23890 Uploading and Actioning Samples on NCIDD and QIS2 22619 Creating and Reviewing Links). For Intelligence Report templates, see QIS2 24015 Procedure for Intelligence Reports and Interstate/Interpol Requests.

a. Suspect checks are nominated by the SSLU or SMU. This information may be found in the UR notes (this must always contain the barcode) and the CS screen (Sus Chk).

b. If the profile does not match, the result must be recorded in an EXR/EXH
   i. Result/Status: "Suspect Check Actioned – No Match"
   ii. Linked No.: Barcode of the nominated suspect.
   iii. No names are entered.

c. If there is a suspect check match and the DNA profile is less than the stringency for searching on NCIDD, an Intelligence Report should be issued to QPS DNA Results Management Unit.

d. For Profiler® Plus interpretations, if the DNA profile is 'complex' or 'no major/minor' and the suspect check is performed resulting in a 'cannot exclude' interpretation, an Intelligence Report should be issued to QPS.

Intelligence samples may be received by DNA Analysis associated to particular cases. These samples need to be compared to the case. If the crime scene profile is on NCIDD and the Intel sample is 'Unlimited Purpose', a match will be reported to QPS DRMU as a cold link. If the Intel sample is 'Limited Purpose', the match needs to be reported in an Intelligence Report. If the Intel sample does not match a crime scene profile, the non-match does not need to be reported in an EXR/EXH.

5 **Interstate/International Requests** – Refer to QIS2 24015

6 **Urgent (Priority 1) result communication on Fridays only.**

Regarding Priority 1 urgent samples as requested by QPS, if results are likely to be available on Fridays, email DRMU in the morning with the relevant barcodes and expected time of release. Aim to release prior to the 3pm GSI transfer and call DRMU if the results are likely to be released later than 3pm.
When results are reviewed, email DRMU that results have been released and if in the 3pm transfer, 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.

8 STATEMENTS AND CERTIFICATES

1 AUSLAB TEMPLATE

Not Current

a. For the layout of a Statement of Witness, refer to Appendix 1: Example of 1st page
b. There is a footer on each page that includes the NATA endorsement, the page number and total number of pages, the case reference number, date, name and signature of Reporting Scientist authorising the statement.
c. Allows the inclusion of a version of the statement Appendix that lists test methodologies (refer to Appendix 2).
d. Includes a Justice's Declaration Act (refer to Appendix 3) at the end of the Appendix.
e. The AUSLAB template is the same as the offline templates available in QIS2 (refer to QIS2 29010).
f. Template pulls in the case details, including the reference and crime scene sample receipt details, Reporting Scientist details, Defendant and Complainant, Appendix and Justice's Act.
g. The person who presses F6 on the statement page in AUSLAB will have their details pulled into the statement.

2 STATEMENT REQUIREMENTS (AUSLAB Test Code: FBSOW):

NB. FBSTAT was the testcode used for statements until the FBSOW was activated in February, 2012.

a. Declaration & Details of the Reporting Scientist (eg. Name, State)
b. Place of Employment and position (eg. Scientist within the DNA Analysis Unit)
c. Qualifications held by the Reporting Scientist (eg. B.Sc.)
d. ANZFSS Code of Ethics (if applicable)
e. Offence details including Defendant and Complainant details. If there is a deceased involved, the complainant is Regina.
f. Details relating to the receipt of items & reference samples including the date of receipt, and the delivery officer (including Australia Post). A list of the barcoded items received.
g. Summaries/ Preambles are added by the Reporting Scientist and may include some, all or slight variations of the following depending on case and profile types (see Appendices 10-12):
    - The Role of a Forensic Biologist
    - Examinations (if performed by another analyst)
    - DNA Profiling
    - Mixed DNA Profiles
    - Blood Stains
    - Seminal Stains
    - Saliva
    - Semen Staining on Items
    - Persistence of Semen in the Vagina
    - Statistics
h. A summary of test results of the Reference Samples, and the type of sample (eg. Blood, Mouth/Buccal, Hair)
i. Description and results of each of the Items:
    - If Items were examined by QPS, or by QPS and QHFSS, it should be made clear which category the Items fit into.
    - Description of the Item including barcode information e.g. 123456789. Receipt sub-numbering e.g. 987654321-002 is optional.
    - Condition of the Item (if examined by QHFSS)
    - Area of staining (if examined by QHFSS)
    - Areas submitted for testing (if examined by QHFSS)
    - Results obtained (eg. Did it match the reference sample and a Kinship Match Probability obtained?). Where relevant, opinions, explanations for opinions and interpretations or summary. A statement of uncertainty where relevant. Reference to other information which may be relevant to

Not Current

the validity or application of the results, e.g. in support of an opinion, explanation or statement of uncertainty.

Note: If a summary of results is required, it should be included at the beginning of the result section of the statement.

Note: It is recommended that the Items are grouped per Receipt. Within each receipt, the similar results are recommended to be grouped together.

j. All items received but not tested are listed (listed under each receipt).

k. Appendix including information about:
   - Accreditation
   - Chain of Custody
   - DNA Profiling
   - Interpreting DNA Profiles
   - Use of statistics

l. Justices Act 1886 – Signature of Reporting Scientist required. The Justices Act must not be on a page by itself. The number of pages to be written within the Justice's Act should be the same as the number of pages for the whole statement.

3 SUBSEQUENT / ALTERNATIVE STATEMENTS:

a. **Further versions (AUSLAB Test Code: FBSOW)** – AUSLAB has the ability for further versions of statements to be produced under the same testcode (see point 5c below). This is useful for replacing statements.

b. **Addendum Statement (AUSLAB Test Code: FBADDE)** - If a subsequent statement is issued (this may be due to additional exhibits being delivered or an additional request for further interpretation), it must be clearly marked as an addendum to the original statement. This test code is also used for pre-AUSLAB cases and other cases that feature manual receipts. APPVER testcode should be ordered at the same time as FBADDE to enable the Appendix field to be edited and the FBADDE to be used as a standalone statement (on its own barcode). If on a standalone barcode, an FBSOW needs to be ordered as well to enable the original completed date to populate. The date in this FBSOW needs to be in the same format as the way the date is typed into the FBADDE eg. DDMMYY or DD/MM/YYYY.

c. **Amended Statement (AUSLAB Test Code: FBAMEN)** - If, after the issue of a statement, an error is detected, the original statement shall be withdrawn and, where necessary replaced by one which is clearly indicated as being a replacement statement. This testcode is rarely used since AUSLAB is able to create new versions (see 'a.' above).

d. **Intelligence Reports (AUSLAB Test Code: FBINTL)** (refer to QIS2 24015). If there is information that cannot 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. The report is written within AUSLAB where the addressee and reviewer's details can be entered.

   i. Intelligence Reports written regarding Quality issues, should be directed to the Inspector DNA Management Section (QPS). Other Intelligence Reports should be directed to the Senior Sergeant DNA Results Management Section (or delegate).

Not Current

ii. Matches on NCIDD that are below our standard match reporting stringency can be reported to DRMU via intelligence reports.
iii. The signed report can be included in the case file, except where it relates to linking information from NCIDD. In these situations, the signed report should be scanned into AUSLAB and the original stored in a folder held in the Intelligence Team area.
iv. A scanned pdf of the signed intelligence report should be sent via QPS email to DRMU. An unsigned pdf (created after validation and saved from AUSLAB when viewed (Shift Insert)) should be sent with the signed copy to DRMU.
v. The template for offline Intelligence Reports is available in QIS2 29011.
vi. The FBAR to record the review of the Intelligence Report can be ordered on the same barcode as the FBINTL, as can the FBIOLR testcode to record the release details.

e. **DNA Evidentiary Certificates (AUSLAB Test Code: FBEVC)** – (Refer to Section 95A Evidence Act 1977)

This is a certificate (in an approved form) that must be signed by a DNA Analyst.

Current staff who hold appointments (in accordance with Section 133A of the Evidence Act 1977) as DNA Analysts are held with the Managing Scientist.

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.

If an Evidentiary Certificate is requested, a workflow has been devised to assist the checking involved in order to sign the certificate (see Appendix 17).

A checklist should be used to record the information examined by the DNA Analyst (refer to QIS2 30799). There are instructions to complete this checklist recorded in a worksheet tab within the actual checklist file.

If the information gathered to be checked prior to issuing the Evidentiary Certificate is to be considered part of the casefile, then an FBAR page needs to be requested in AUSLAB and the pages should be numbered and have the case identifier added.

f. **Other Reports – Crime and Misconduct Commission (CMC) or Ethical Standards unit of the QPS**.

Due to the confidential nature of these cases, results cannot be entered into AUSLAB in either EXR/EXH or STATEMENT format (as this information is accessible by QPS and other FSS staff). Barcodes will need to be registered to facilitate analytical processing.
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 Team. Clarification from the requesting

Non-Current

party will need to be sought if any results are ok to send via the GSI to QPS, or if by standard means (above). 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, 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 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:

1. Receipt details of reference samples and exhibits
2. Blurbs (Role of a Forensic Scientist, DNA Profiling and appropriate blood or semen blurbs)
3. List of Reference Samples (and results)
4. Results of testing for exhibits submitted
5. 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. This report shall **NOT** be scanned into AUSLAB. **All results are to be included in the case file only.**

h. **Statements including coronial samples.**
To ensure samples delivered by the Coronial Support Unit (CSU) are pulled through correctly into Statements, the receipted items require an FTAR testcode to be requested (and the delivery officer etc to be recorded), and the Specimen type to be changed to FTAE. If it has correct CRISP association in the registration in AUSLAB, the receipt details should then pull into the Statement of Witness.

4 EXTERNAL TESTING (Example Low Copy No. or Mitochondrial DNA) IN STATEMENTS

a. 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.
   i. 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.

5 RECORDS

a. All statements issued must bear a stamp on the front page that lists the date of issue, the case analyst's signature and the signature of the analyst who performed the technical review of the statement. The stamp is automatically added to statements by AUSLAB.

Not Current

b. A copy of the statement issued for any test/examination must be retained in the case file. After the statement has been reviewed, F6 to validate will change the statement to PDF format. The person pressing F6 to validate will have their details auto-populated by AUSLAB. This means the Reporting Scientist needs to perform this function. A time and date stamp will appear in the footer.

c. Further versions can be created of statements and can be viewed in AUSLAB prior to printing - Press Shift –Insert on the validated statement page (to view PDF Report Table) and F8 to view HTML Report. The original (validated) statement can also be viewed by pressing F5 on this page, or scrolling to the version you wish to view.

6 OFFLINE STATEMENTS

a. If a Statement of Witness needs to be written outside of AUSLAB (eg. when AUSLAB is down, or the testcode is corrupted), the templates are available in QIS2. Templates exist for Statements of Witness and Intelligence Reports - see the following documents:
   i. 29010 – Statement of Witness template – stamp
   ii. 29008 – Statement of Witness template – address – no NATA endorsement
   iii. 29009 – Statement of Witness template – blank – no NATA endorsement
   iv. 29024 – Use of offline Forensic Reporting templates
   v. 29011 – Intelligence report template

b. This type of statement may be written in cases where someone other than the Case 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 Case Scientist.

c. These statements should be scanned into AUSLAB upon completion.

9 STATEMENT/REPORT AUTHORISATION

1. Qualified DNA Analysis Unit Reporting Scientists are authorised to sign statements and reports given that all policy and procedure requirements have been satisfactorily fulfilled.
2. All Staff are authorised to sign and initial worksheets, reports etc according to their level of competence.
3. A staff list with signatures and initials of all staff (QIS2 17088) is kept for reference. This is located in the Quality area of the Administration compactus.
4. DNA Analysts can sign Evidentiary Certificates.
5. Another scientist with the same or greater level of competence can sign as Peer Reviewer.

10 FURTHER DOCUMENTATION REQUESTS (EG. AUDIT TRAILS)

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 LALU (Legal Unit) who will ask the

Not Current

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: 'FSS_[redacted] (formerly SSED email account) 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, an FBAR page should be requested in AUSLAB and 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 QIS2 17117. Having said this, it is recommended that this occurs as it is helpful if/when it is referred to in court proceedings. 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.

Not Current

11 RELEASE OF REPORTS

1 STATEMENT OF WITNESS and DNA EVIDENTIARY CERTIFICATES

The signed document is copied and stamped as 'copy'. The copied document is included in the casefile and page numbered. The original is scanned and emailed to SMU by SSLU for uploading directly to QPRIME, and is sent by SSLU to the Investigating Officer (or delegate, which could include the DPP). Urgent documents could be faxed where appropriate.

2 INTELLIGENCE REPORTS

The Intelligence Report is sent via QPS email to DRMU as a signed pdf file, and an unsigned pdf that is created by AUSLAB post-validation.

3 CORONIAL and DISASTER VICTIM IDENTIFICATION (DVI) REPORTS

These 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.

12 COURT MONITORING

Every Reporting Scientist should have their testimony evaluated every 12 months. The evaluation can be performed by another Reporting Scientist, a court official (DPP or Defence) or QPS Officer.

The first page of the Court Testimony Monitoring Evaluation Form (QIS2 17047) 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 QIS2 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.

A report of every 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 '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.

Refer to FSS Court Testimony and Attendance Requirements (QIS2 18034) for more information.

Not Current

13 AMENDMENT HISTORY

Version	Date	Author/s	Amendments
	24 Feb 1999	V Ientile	
QIS Edition			
1	8 Oct 2001	V Ientile	
2	23 Jan 2004	L Freney	Changes to references, update appendices
3	11 Mar 2004	V Ientile	No interim unchecked results to be issued
4	10 Aug 2006	M Gardam	Combined with 17158, amended the title and updated statement requirements, included intelligence reports, statement blurbs & Evidential Reports. Added Reference to Communication SOP, Added EXR reporting guidelines.
5	31 May 2007	M Gardam	Sub-numbering is optional when giving a description of the item.
6	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
7	August 2009	J Howes	Updated Forensic Biology to DNA Analysis, added EXH, added complete preambles, added Evidentiary Certificate workflow,

			Quality flag checking workflow, updated Statement of Witness and Appendices examples, DNA Analyst list removed, relative frequency paragraph removed from Intel letter example and updated with match probability, EXH table improvements and current lines added to examples.
8	June 2010	J Howes	Added EB checking workflow, added to Quality Flag workflow, moved Quality paragraphs to own Appendix, deleted Pathology and Scientific services logo
9	August 2010	J Howes	Changed FIRMU to DRMU, added some more information to paternity preamble
10	April 2011	J Howes	Changed Appendix 3 to include latest version of Justice's Act, changed HP4/HP5 to 'senior' in Evidentiary Certificate workflow, added some suspect check information.
11	05 April 2012	J Howes	Changed DNA Unit to Sample Mgt Unit, changed 'Evidential Reports' to 'Other Reports', added info to Statement and Intel Report field, changed the number/bullet/paragraph systems to be consistent, added new Appendix version (5), added new preambles, added new Statement of Witness template, add ability to create statement versions, added Offline statement section, removed Appendices 4 and 5 (covered by 24005), added F6 validation to RECORDS, added Release of Reports section, removed Example 6 (multiple items) from Appendix 9, added Coronial/DVI report release section, add Environmental samples to QFLAG workflow, updated QFLAG and EB checking process, added template for Evidentiary Certificates, updated FBSOW for FBSTAT and workflow, added link to Evidentiary Certificate checklist, added Ethical Standards/CMC information, added Court Monitoring information, added information to Intel report section, added Urgent P1 result communication on Fridays, added FTAs associated to the case (under Suspect Check section).
12	29 Nov 2012	J Howes	Added new HSSA Header, removal of FBSHRT reference that was part of Section 3 and the workflow from Appendix, Linked No. field updated to include use of barcodes for unique profiles, FBEVC added, information on who receives Intel reports added, Intelligence Report section re-organised, added information to negotiate timeframe with requesting party re audit trails, Appendix 6 for statements added to Appendix 2 in this document,

Not Current

			added APPVER to workflow for FBADDE and to Section 3, added Appendix 17, added Reference Sample section to Appendices 9-11 to be used where appropriate, Tho1 changed to TH01, Appendix 14 workflow changed to not include AUSLAB matches, added Profiler Plus for 'cannot exclude' interpretation for suspect check,

Not Current

14 DOCUMENTATION

1 **Appendix 1** An example of the layout of the front page of a Statement of Witness

2 **Appendix 2** Procedural overview and test methodology (Appendices 5 and 6).

3 **Appendix 3** Example of the Justice's Declaration Act.

4 **Appendix 4** Completing Exhibit Reports in AUSLAB

5 **Appendix 5** Review of Exhibit Reports in AUSLAB

6 **Appendix 6** Creating an Addendum Statement in AUSLAB

7 **Appendix 7** Creating a Statement with Receipt Details in AUSLAB

8 **Appendix 8** EXR/EXH Reporting (Sub-Sample No. Rules)

9 **Appendix 9** Complete Casework Preamble – Examinations by QHFSS

10 **Appendix 10** Complete Casework Preamble – Examinations by QPS and QHFSS

11 **Appendix 11** Complete Paternity Preamble

12 **Appendix 12** Quality Paragraphs (relating to statements including results of DNAIQ Extractions in period October 2007 – July 2008)

13 **Appendix 13** DNA Evidentiary Certificate Workflow

14 **Appendix 14** Quality Flag Checking Workflow

15 **Appendix 15** Extraction Batch Checking Workflow

16 **Appendix 16** DNA Evidentiary Certificate template (and Appendix v5)

17 **Appendix 17** DNA Evidentiary Certificate Workflow in AUSLAB

Not Current

APPENDIX 1

Queensland Government

CaSS | Forensic and Scientific Services
A CLINICAL AND STATEWIDE SERVICE

STATEMENT OF WITNESS

Peer Reviewed .....Yes/No Client Reference : [redacted]

Case Analyst .....

Peer Analyst .....

Date Issued .....

QUEENSLAND)
TO WIT)

I, Justin Anthony HOWES, of Brisbane in the State of Queensland, do solemnly and sincerely declare that:-

1. I am employed by Queensland Health Forensic and Scientific Services (QHFSS) at Coopers Plains, Brisbane.
2. I hold the position of Senior Scientist in the DNA Analysis Unit of QHFSS.
3. I was awarded a Bachelor of Science from University of Queensland.

   I was awarded a Bachelor of Arts from University of Queensland.

   I was awarded a Master of Science (Forensic Science) from Griffith University.
4. I am a member of the Australian and New Zealand Forensic Science Society.
5. This is my statement in relation to the alleged offence that Occurrence Number: [redacted] refers. The defendant in this matter is defendant. The complainant in this matter is complainant.

Procedural Overview and Test Methodology (Appendices 5 and 6)

APPENDIX (version 5)

Procedural overview for the DNA Analysis Unit, Queensland Health Forensic and Scientific Services (QHFSS)

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.
For details of the current ISO/IEC 17025 Field Application Document, Forensic Science, Supplementary requirements for accreditation, please refer to the NATA website:
http://www.nata.asn.au/publications

Not Current

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 DNA Analysis Unit of Queensland Health Forensic and Scientific Services (QHFSS)

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,

Not Current

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.

Not Current

DNA (STR) profiling systems available at the DNA Analysis Unit, Queensland Health Forensic and Scientific Services (QHFSS)

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

Not Current

APPENDIX (version 6)

Procedural overview for DNA Analysis,
Forensic and Scientific Services (FSS), Health Services Support Agency

Examinations

Unless otherwise stated, the examinations of items for biological material were conducted by officers within the Queensland Police Service (QPS). Sub-samples from these items were forwarded to Forensic and Scientific Services (FSS), Health Services Support Agency, for the purposes of conducting DNA analysis.

DNA Analysis operates under the premise that 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 FSS DNA Analysis. 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.

Some items may be submitted to this laboratory for the purposes of both examination and DNA profiling. This occurs at the discretion of the QPS. These examinations are performed in accordance with the SOPs of this laboratory. For these items, notes are made at the time of the examination by the examining scientist and form part of the casefile.

Chain of Custody

All DNA Analysis 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 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 exhibit packaging prior to processing. The packaging and labelling of any exhibit is checked and recorded before the sample undergoes DNA analysis.

Entry into DNA Analysis is restricted to authorised persons only, via electronically encoded proximity access cards. DNA Analysis forms part of a Health Services Support Agency campus site which has access controlled and monitored by a security team. Records of Visitors to DNA Analysis are retained.

Accreditation

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 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

Not Current

- 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.
For details of the current ISO/IEC 17025 Field Application Document, Forensic Science, Supplementary requirements for accreditation, please refer to the NATA website:

http://www.nata.asn.au/publications

Technical information relating to DNA profiling at DNA Analysis, Forensic and Scientific Services (FSS), Health Services Support Agency

DNA Profiling

DNA is a complex chemical found in almost all cells in the human body. It carries genetic information which determines the physical and chemical characteristics of a person. The testing system used at DNA Analysis looks at 21 regions of DNA, 20 of which contain highly variable Short Tandem Repeats (STRs). The 21st region gives an indication as to the gender of the donor (for details see Table 1). This technique involves the use of a method known as Polymerase Chain Reaction (PCR), used to amplify these specific regions of the DNA to produce numerous copies. In this way, minimal amounts of DNA isolated from small or degraded samples can be increased to a level where they are able to be detected, profiled and compared with other samples.

The individual components (alleles) of a DNA profile are represented by a series of peaks which are measured and given a designation using standard sizing ladders. A person will have two peaks for each STR, one inherited from their mother and one inherited from their father, unless the same STR is inherited from both parents, in which case only one peak will be seen.

A DNA profile obtained from biological material such as blood, semen, saliva, hair or cells (eg. touch DNA) can be compared with the DNA profile obtained from a reference sample from any person. If there is no indication of a contribution by more than one person, then a DNA profile is described as being “single source”. Conversely, if there are indications of two or more contributors, then a DNA profile is described as a “mixed” DNA profile.

Statistical Analysis of DNA profiles

In order to statistically evaluate DNA profiles, it is necessary to make a reasonable assessment of the possible number of people who may have contributed DNA to that DNA profile, based on the information observed.

DNA profiles assumed to originate from one person (single source)

A person can be excluded as a possible source of the biological material if corresponding regions of the crime-scene DNA profile are different from that person’s reference DNA profile. If the corresponding regions of the DNA profiles contain the same information, then that person, together with any other person who has the same reference DNA profile, can be considered as a potential contributor of the DNA.

Not Current

The evidential significance of such a match is assessed by considering two competing propositions:

Proposition 1: the DNA originated from the person of interest;
Proposition 2: the 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 DNA components that make up the DNA profile. Upon request, an internationally accepted verbal scale to describe the support for one proposition over another can be used to offer some non-numerical explanation for the likelihood ratio (see Table 2).

If less than the 21 regions of DNA are seen in a DNA profile (termed an 'incomplete or partial DNA profile') this will be reflected by a smaller likelihood ratio than the likelihood ratio that would be obtained from a full DNA profile. In other words, the more incomplete the DNA profile, the greater the likelihood of obtaining the DNA profile if it came from someone other than, and unrelated to the person of interest.

Not Current

DNA profiles assumed to originate from more than one person (mixed DNA profiles)

In order to assess whether a person could or could not have contributed to a mixed DNA profile, a set of competing propositions (similar to a single source DNA profile) are considered. For example, for a two person mixture:

Proposition 1: the DNA originated from the person of interest and an unknown person unrelated to the person of interest;
Proposition 2: the DNA originated from two unknown people unrelated to the person of interest.

The likelihood ratio provides a statistical assessment of a particular contribution of DNA being contained within the mixed DNA profile.

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 intimate area, then it may be possible to make the reasonable assumption that the donor of the sample 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 known donor, such that the presence of the DNA components corresponding with the donor'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, for example:

Proposition 1: the DNA has originated from the complainant and the person of interest;
Proposition 2: the DNA has originated from the complainant and an unknown individual unrelated to the person of interest.

When it appears that a large number of people could have contributed to a mixed DNA profile, it can be difficult to exclude individuals as potential contributors. It can be equally difficult to determine whether a person could in fact be a contributor to the DNA profile. If it is not possible to determine the number of contributors to a mixed DNA profile, or if there is very limited information available, then a mixed DNA profile may be described as unsuitable for interpretation.

If information is received such that the assumptions made in an interpretation are not accepted, then 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, irrespective of whether the DNA profile is single source or mixed. A correction factor θ (theta) is applied to all statistical calculations in order to correct for the possibility of common ancestry (sharing of DNA components inherited from a common ancestor) between people in the general population. The nationally agreed figures for theta are θ=0.02 for the Australian Caucasian dataset, θ=0.03 for South East Asian dataset, and θ=0.05 for the Australian Aboriginal dataset. Unless otherwise specified, the default dataset used in DNA Analysis is the Australian Caucasian dataset. The other datasets are available upon request.

In addition to theta, the calculation of the likelihood ratio also includes an allowance for the sampling variability of the dataset. In other words, if a new dataset were generated it allows for any difference the new dataset could make to the likelihood ratio.

Often the calculated likelihood ratio produces numbers of hundreds (100s) or even thousands (1000s) of billions. To avoid the use of potentially confusing terminology, a 'ceiling figure' for the likelihood ratio of 100 billion has been determined (this is called truncation). For example, a calculated likelihood ratio of "150 000 billion times more likely", would be reported as "more than, or at least 100 billion times more likely". The actual calculated figure can be provided upon request.

The above listed values for the 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 random fashion in which DNA from parents combines, the probability that two siblings would share the same 20 STR regions 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 is thought that a close blood relative may have been involved, a more meaningful approach would be to submit the reference sample from the relative in question for analysis and direct comparison to the crime stain DNA profile.

Not Current

Standard DNA (STR) profiling system at DNA Analysis, Forensic and Scientific Services (FSS), Health Services Support Agency

Table 1: PowerPlex® 21 multiplex 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

Table 2: Verbal scale to describe Likelihood Ratios
(adapted from Evett IW and Weir BS 1998 *Interpreting DNA Evidence*. Sinauer, Sunderland, MA)

RANGE OF VALUE	LEVEL OF SUPPORT
>1 million	Extremely Strong
100 000 – 1 million	Very Strong
10 000 – 100 000	Strong
1000 – 10 000	Moderately Strong
100 – 1000	Moderate
10 – 100	Low Level
1 – 10	Slight
1	Inconclusive

Not Current

APPENDIX 3

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 XXXX, and contained in the pages numbered 1 to _____ 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.

_____

Signature

Signed at BRISBANE on XXXX.

Not Current

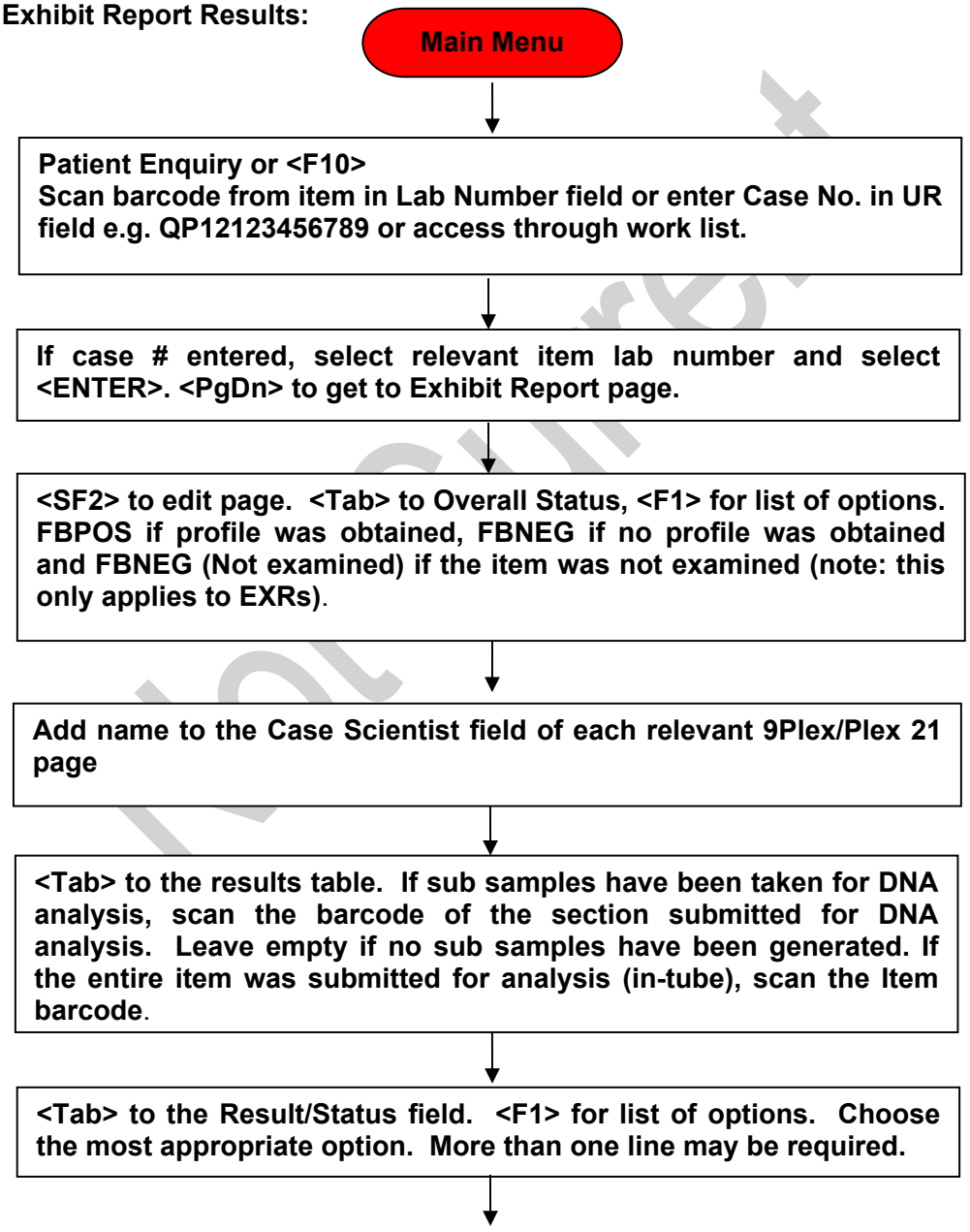
APPENDIX 4

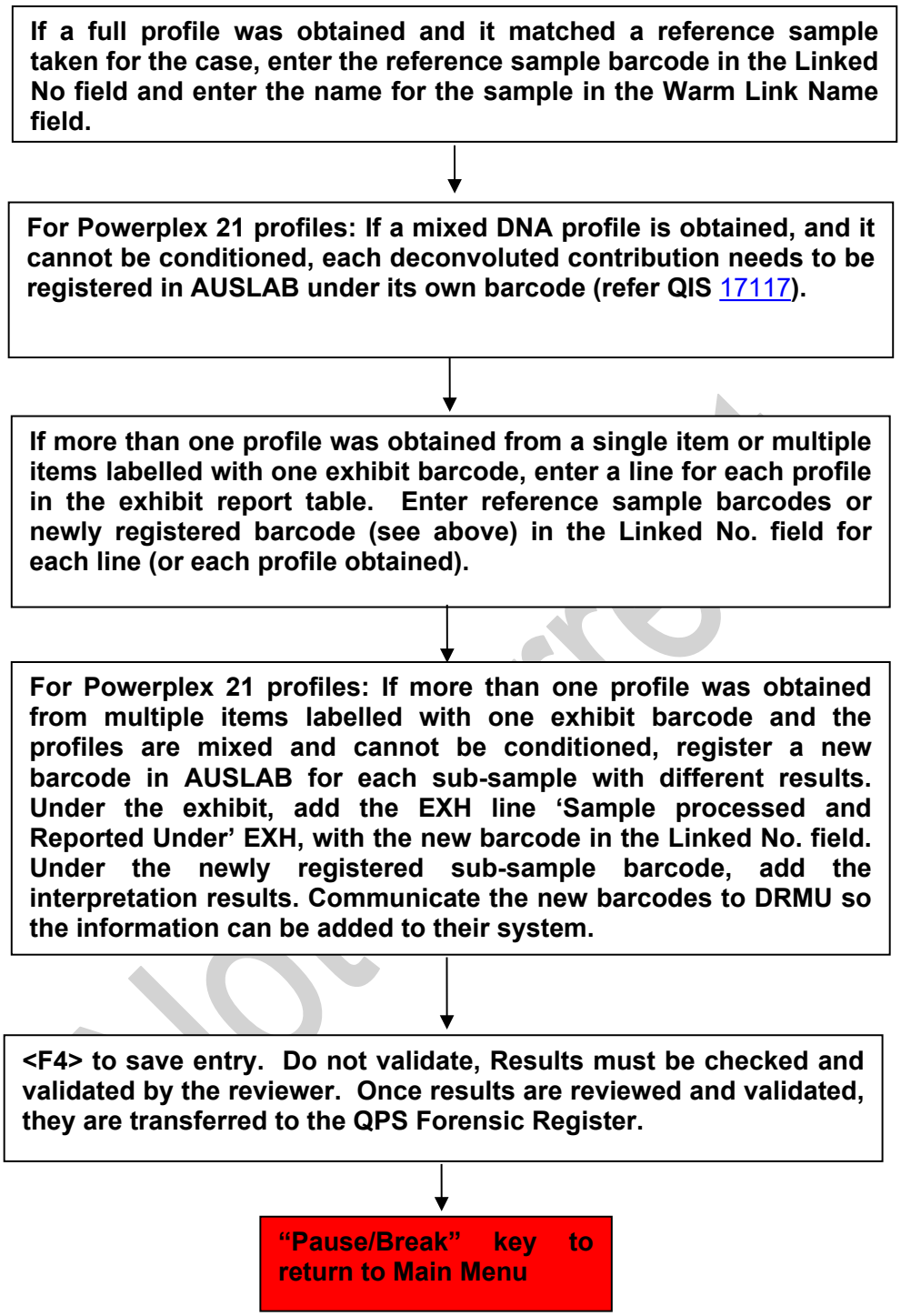
Completing Exhibit Reports

AUSLAB Test Code: EXR/EXH

Purpose: Exhibit Reports are a summary of results for each item received. The information stored in the exhibit reports is transferred to the QPS Forensic Register once the results have been checked and validated. Exhibit Reports can contain information about examinations performed, screening test results and DNA profile results. Interim results can be entered and sent to the QPS Forensic Register once they have been validated.

To enter Exhibit Report Results:





NOTE:

- All mixed DNA profiles that can be separated into major/ minor contributions (for Profiler® Plus), should have the designations filled out under the MIXT testcode for 9Plex/ Profiler® Plus, and on the COMIX page for Powerplex 21.
- All mixed DNA profiles that can be 'conditioned' should have the designations filled out under the MIXC testcode for 9Plex/ Profiler® Plus, and on the COMIX page for Powerplex 21).

- If the interpretation is a conditioned mixture and for intelligence purposes only (eg. conditioned in the absence of a reference sample but using an unknown profile from the same case), this should be made clear in the comments section of the mixture pages.
- If the mixture is major/ minor but the major is mixed and used for POPSTATS purposes, an MIXT testcode should be used and the contributions added to this page. This only applies to 9Plex/ Profiler® Plus profiles.
- If the mixture is major/minor and the major is mixed, and a conditioned interpretation is applied to the major, it may be appropriate to use the MIXC testcode and to record the minor components to the specimen notes (and have these peer reviewed). The comments section can also be used to make it clear what actions have occurred. This should only be relevant for 9Plex/ Profiler® Plus profiles.

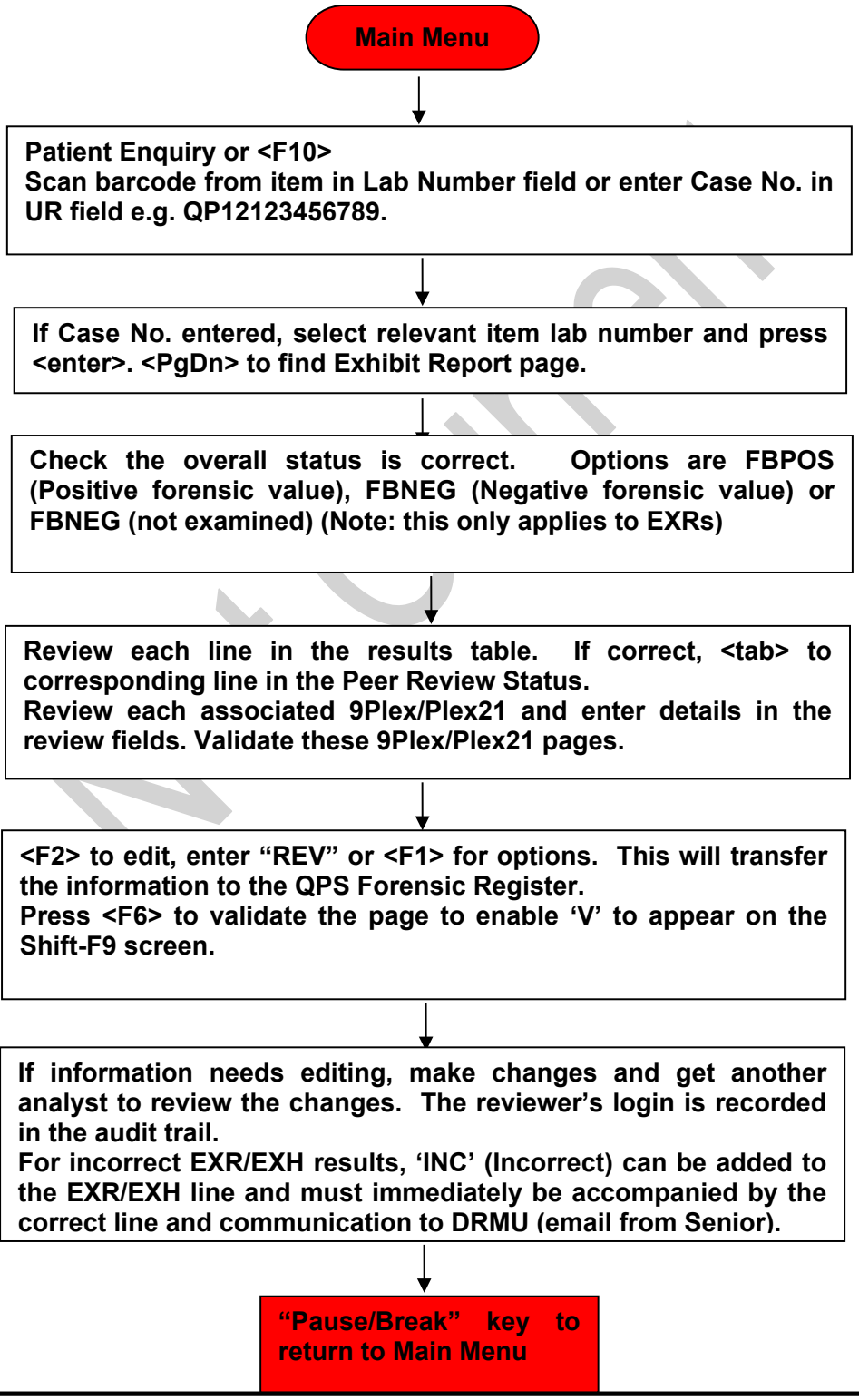
Not Current

APPENDIX 5

Review of Exhibit Reports

Purpose: An Exhibit report is created for each item as a way of transferring results back to the QPS Forensic Register. Each line of an exhibit report must be reviewed before it can be released and sent to the QPS Forensic Register.

To review an exhibit report:

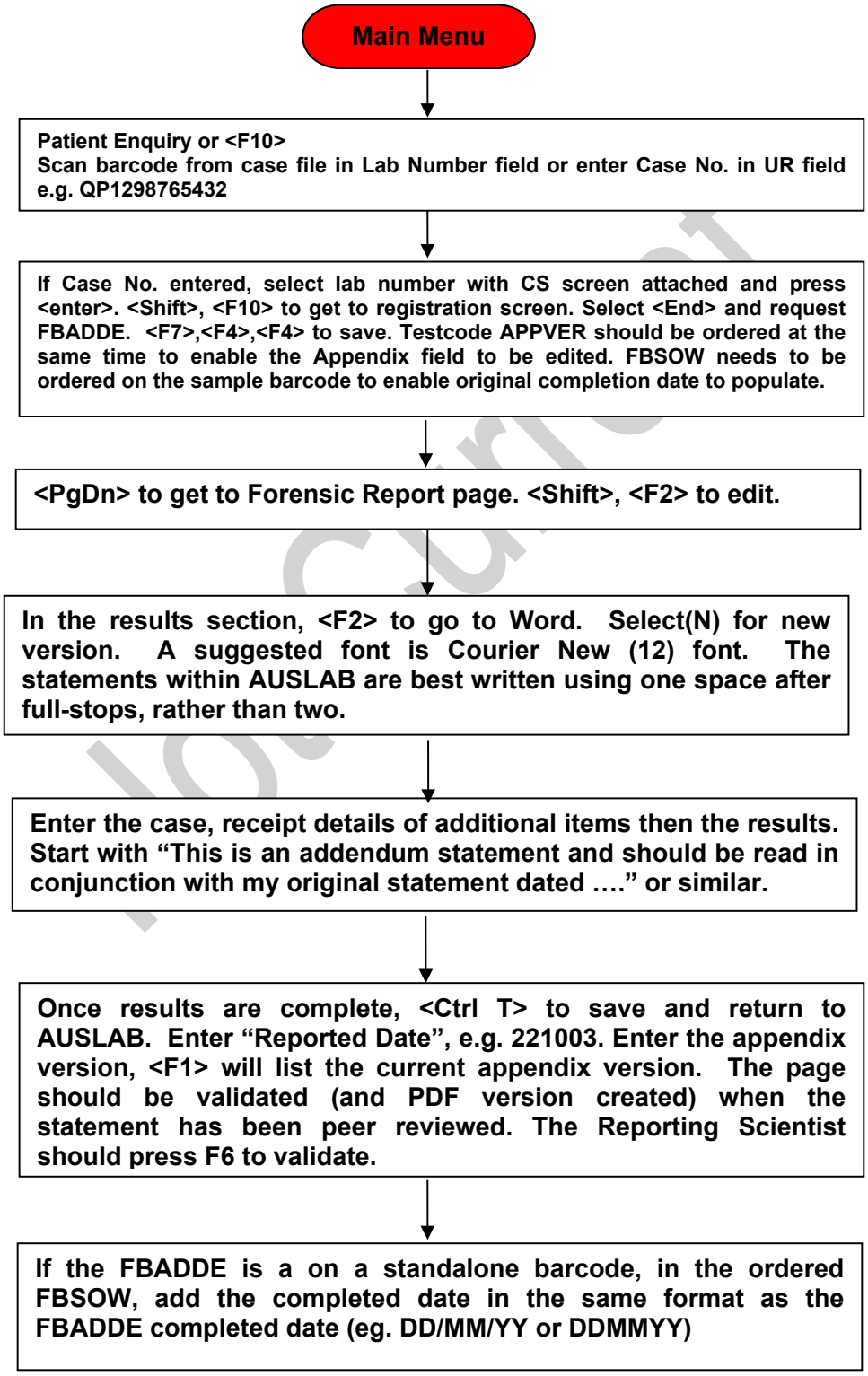


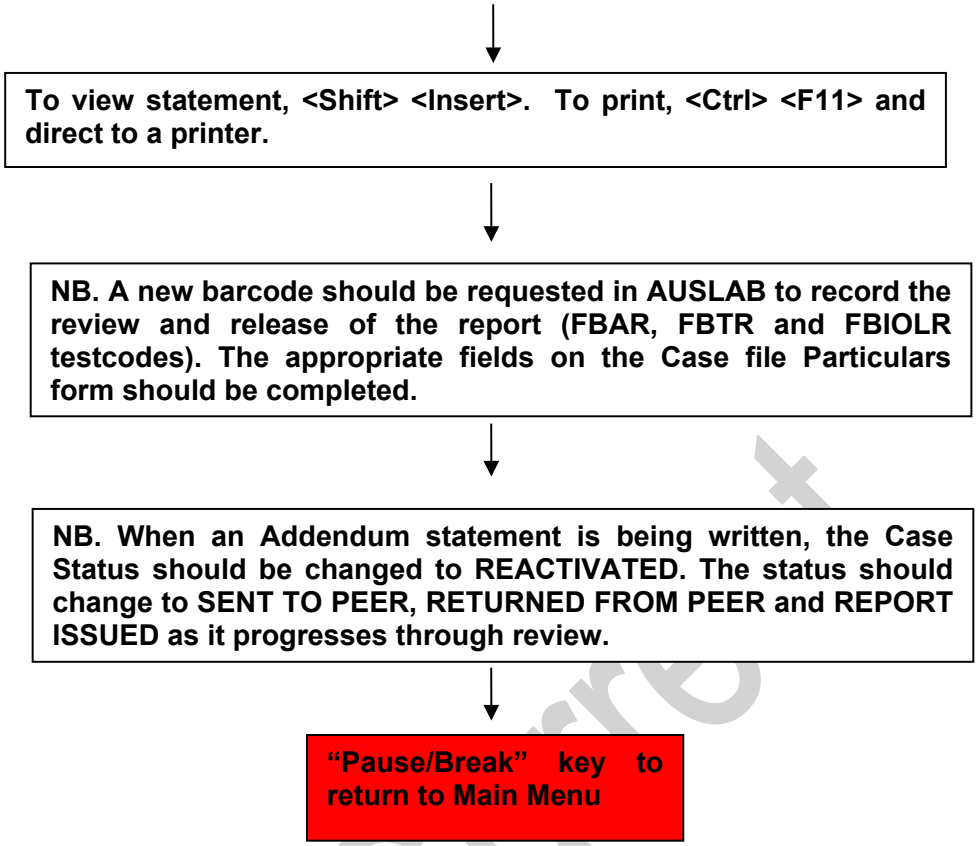
APPENDIX 6

Creating an Addendum Statement

Purpose: The test code FBADDE creates a statement without the receipt details automatically entered. All statement test codes include the scientist's details, and appendix details. This format is used for cases where an additional statement is being written.

To create an addendum statement:




To view statement, <Shift> <Insert>. To print, <Ctrl> <F11> and direct to a printer.
NB. A new barcode should be requested in AUSLAB to record the review and release of the report (FBAR, FBTR and FBIOLR testcodes). The appropriate fields on the Case file Particulars form should be completed.
NB. When an Addendum statement is being written, the Case Status should be changed to REACTIVATED. The status should change to SENT TO PEER, RETURNED FROM PEER and REPORT ISSUED as it progresses through review.
"Pause/Break" key to return to Main Menu

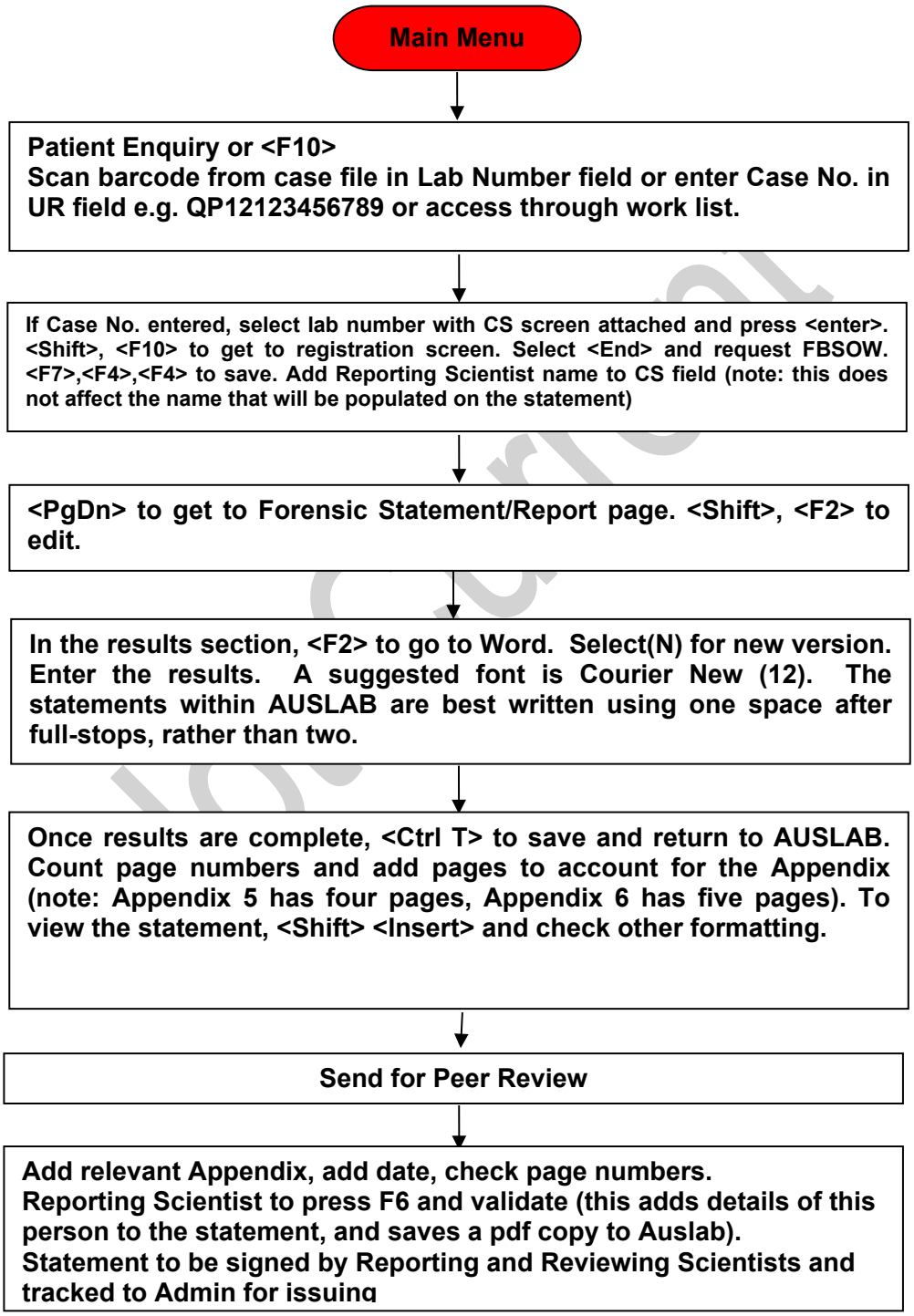
Not Current

APPENDIX 7

Creating a Statement with Receipt Details

Purpose: The test code FBSOW creates a statement with the receipt details automatically entered.

To create a statement with receipt details:



APPENDIX 8

EXR/EXH REPORTING (Sub-Sample No. Rules)

This appendix is for the process of reporting back results via EXR/EXHs, to the Queensland Police DNA Result Management Unit (DRMU) for individual items by staff of DNA Analysis. Note, the examples provided are relevant to Profiler® Plus interpretations and EXH lines. See 23008 Explanations of EXR/EXH Results for the complete list of EXHs relevant for Profiler® Plus and Powerplex 21 in conjunction with the use of STRmix™

- Since 1 July 2008, the bulk of the examinations have been performed by QPS. After their examinations, samples are received by DNA Analysis in-tubes. The barcode on the tubes relate to an EXH barcode and as such, the presumptive and final results are reported back on the single barcode.

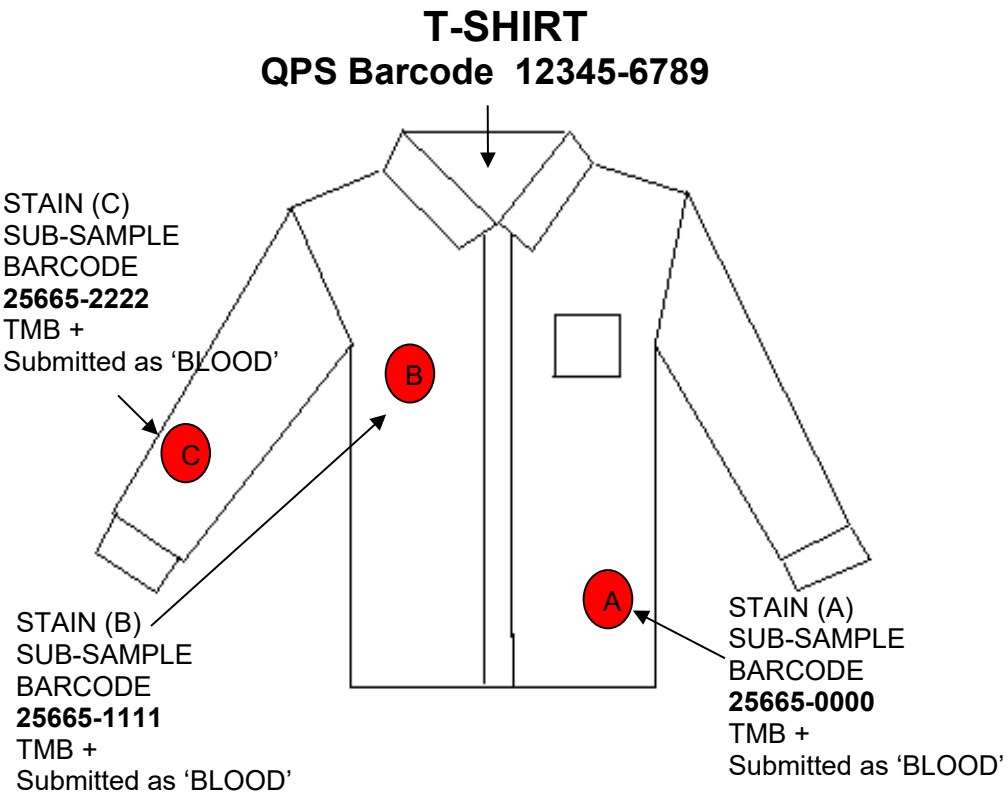
- Different scenarios have been included in examples given in the following pages. These scenarios relate to reporting of non-in tube cases, and the table format is as per EXH pages (excluding the 'Peer Review' column). For more information, refer to QIS2 17142.

- Examples of different scenarios are depicted below. Some of these examples use Profiler® Plus interpretations (eg. '9Loci DNA profile'):

1. **One Item – multiple stains** = same presumptive result and only one type of extraction requested.
2. **One Item – multiple stains** = different presumptive results and two types of extractions requested.
3. **One Item – multiple stains** = different presumptive results (but with same extraction request) as well as three differing types of extractions requested.
4. **Swabs** – where no sub-sample barcode is required
5. **Cigarette Butts** – where no sub-sample barcode is required
6. **Sexual Assault Investigation Kits** (SAIK) & clothing
7. **Sexual Assault investigation Kits** (SAIK) – negative results.

Not Current

EXAMPLE 1.



Not Current

EXR/EXH TEST CODE is **registered under 12345-6789 (T-SHIRT)**

Only sub-samples are used to report back presumptive tests & final results

PRESUMPTIVE RESULTS

LAB NO.	Result/Status	Linked No.	Warm Linked Name
25665-0000	Presumptive blood test pos. Submitted – results pending		

Note as all three stains were TMB positive, only one presumptive test result needs to be entered. (Any one of the three sub-samples for the stains can be entered)

FINAL RESULTS

If all three DNA profiles are the same, then only one result needs to be reported back. If this is the case, then use the same sub-sample as used to originally report back the presumptive test results.

LAB NO.	Result/Status	Linked No.	Warm Linked Name
25665-0000	Presumptive blood test pos. Submitted – results pending		
25665-0000	9 loci DNA profile	[redacted]	

OR

If the sub-sample originally used is not the best profile, you still need to report back on it – but you will also need to add the sub-sample number which does give you the best profile.

LAB NO.	Result/Status	Linked No.	Warm Linked Name
25665-0000	Presumptive blood test pos. Submitted – results pending		
25665-0000	Partial DNA profile	[redacted]	
25665-1111	9 loci DNA profile		

OR

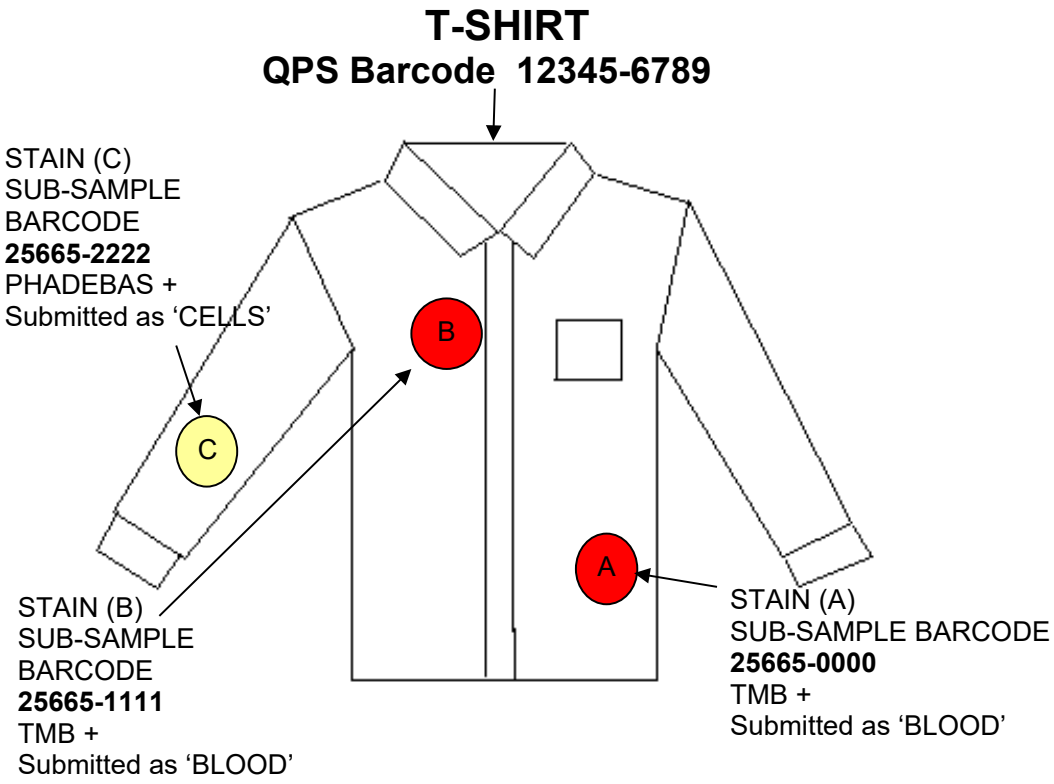
If there are two or three differing DNA profiles resulting from the three stains submitted for analysis, then **report back all differing profiles** using their sub-sample barcodes (as above).

LAB NO.	Result/Status	Linked No.	Warm Linked Name
25665-0000	Presumptive blood test pos. Submitted – results pending		
25665-0000	9 loci DNA profile	[redacted]	
25665-1111	9 loci profile. Uploaded to NCIDD	UKM1	

Not Current

25665-2222	9 loci profile. Uploaded to NCIDD	UKM2	

EXAMPLE 2.



EXR/EXH TEST CODE is registered under 12345-6789 (T-SHIRT)

Only sub-samples are used to report back presumptive tests & final results.

PRESUMPTIVE RESULTS

LAB NO.	Result/Status	Linked No.	Warm Linked Name
25665-0000	Presumptive blood test pos. Submitted – results pending		
25665-2222	Presumptive saliva positive. Submitted – results pending		

Note as two stains were TMB positive, you only need one TMB+ presumptive test result to be sent back to QPS DRMU for this item. Any one of the two sub-samples for the TMB+ stains can be entered (as above). A second presumptive result is sent back for the Phadebas + result as well.

FINAL RESULTS

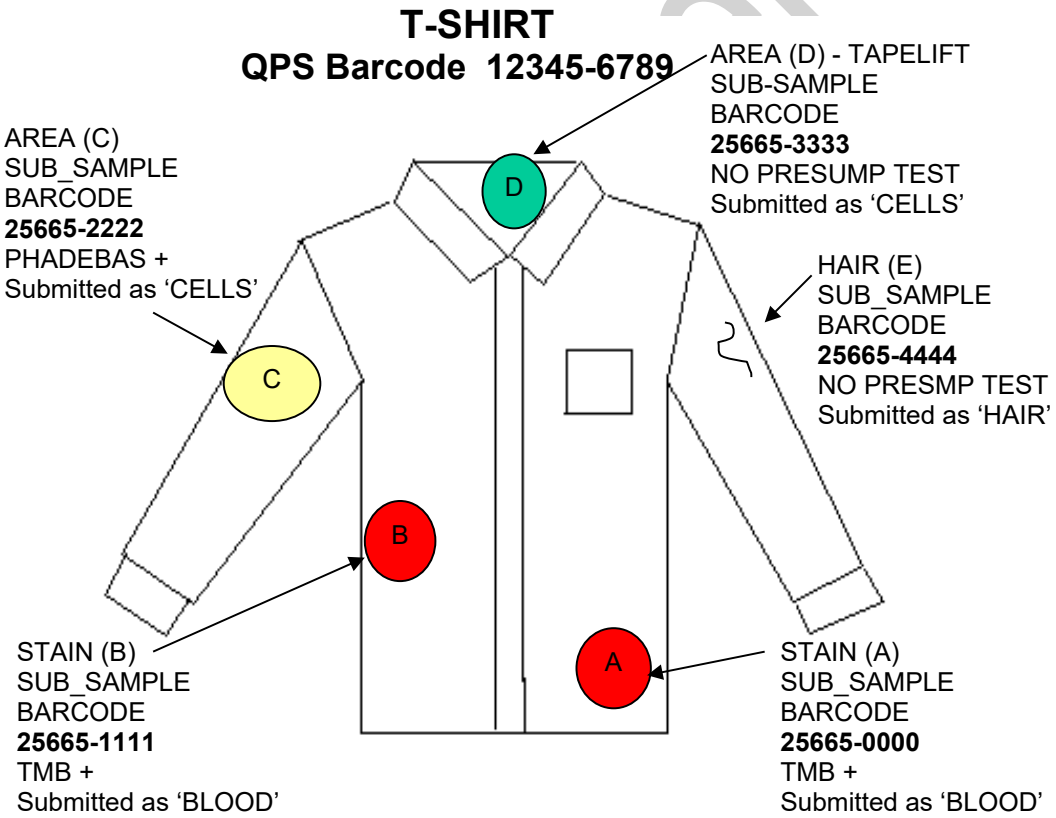
LAB NO.	Result/Status	Linked No.	Warm Linked Name
25665-0000	Presumptive blood test pos. Submitted – results pending		

25665-2222	Presumptive saliva positive. Submitted – results pending		
25665-0000	9 loci profile. Uploaded to NCIDD	[redacted]	
25665-2222	9 loci profile		
26665-1111	9 loci profile. Uploaded to NCIDD		

As two presumptive results were sent to DRMU initially, both the final results from these sub-samples need to be reported back – regardless if these profile end up being from the same source. By doing this DRMU can associate the resulting profiles to a possible cell source.

If the two samples submitted for the blood extraction result in the same DNA profile, then only one result needs to be reported back – use the same sub-sample as reported in the presumptive test results. If the profiles differ then both are reported back via their sub-samples.

EXAMPLE 3



EXR/EXH TEST CODE is **registered under 12345-6789 (T-SHIRT)**

PRESUMPTIVE RESULTS

LAB NO.	Result/Status	Linked No.	Warm Linked Name
25665-0000	Presumptive blood test pos. Submitted – results pending		

25665-2222	Presumptive saliva positive. Submitted – results pending		
25665-4444	Hair located. Submitted – results pending		

FINAL RESULTS

LAB NO.	Result/Status	Linked No.	Warm Linked Name
25665-0000	Presumptive blood test pos. Submitted – results pending		
25665-2222	Presumptive saliva positive. Submitted – results pending		
25665-4444	Hair located. Submitted – results pending	[redacted]	
25665-0000	9 loci DNA profile. Uploaded to NCIDD		
25665-2222	Partial DNA profile		
25665-4444	No DNA Profile		
25665-1111	9 loci DNA profile. Uploaded to NCIDD	UKF1	

As three presumptive results were sent to DRMU initially, all three final results from these sub-samples need to be reported back – regardless if these profile end up being from the same source. By doing this DRMU can associate the resulting profiles to a possible cell source.

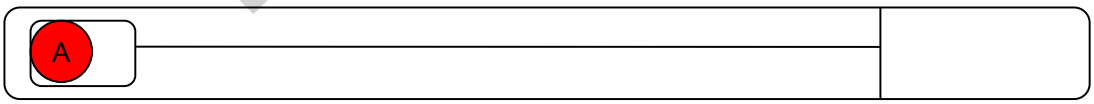
If the two samples submitted for the blood extraction result in the same DNA profile, then only one result needs to be reported back – use the same sub-sample as reported in the presumptive test results.

If the profiles differ then both are reported back via their sub-samples (as shown above).

Not Current

EXAMPLE 4.

SWAB - QPS BARCODE 12345-6789 (-001)



STAIN (A)
NO SUB NUMBER BARCODE GIVEN
TMB +
Submitted as 'BLOOD'

No sub-numbering required for this item as the entire sample is exhausted

PRESUMPTIVE AND FINAL EXR/EXH ON SWAB EXR/EXH BARCODE

LAB NO.	Result/Status	Linked No.	Warm Linked Name

12345-6789	Presumptive blood test pos. Submitted – results pending		
12345-6789	9 loci DNA profile. Uploaded to NCIDD	[redacted]	

EXAMPLE 5.

CIG BUTT - QPS BARCODE 12345-9999 (-001)

AREA (A)
NO SUB NUMBER
BARCODE GIVEN
NO PRESUMPTIVE TEST
Submitted as 'CELLS'

No sub-numbering required for this item

PRESUMPTIVE AND FINAL EXR/EXH ON CIGERETTE BUTT EXR/EXH BARCODE

LAB NO.	Result/Status	Linked No.	Warm Linked Name
12345-9999	Submitted results pending		
12345-9999	9 loci DNA profile. Uploaded to NCIDD	[redacted]	

Not Cu

EXAMPLE 6.

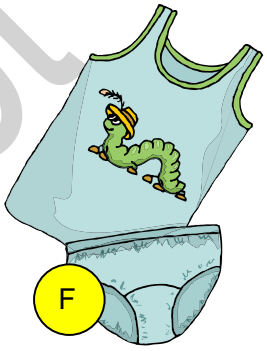
SAIK = QPS BARCODE 12345-6789

SAIK CONTAINS FIVE SWABS and TWO CLOTHING ITEMS (NOT BARCODED BY QPS)

A	SUB-BARCODE – 25665-0000 MICRO POS FOR SPERMATOZOA	HV SWAB
B	SUB-BARCODE – 25665-1111 MICRO POS FOR SPERMATOZOA	LV SWAB
C	SUB-BARCODE – 25665-2222 AP NEG MICRO NEGATIVE FOR SPERM	VULVAL SWAB
D	SUB-BARCODE – 25665-3333 AP NEG MICRO NEGATIVE FOR SPERM	PERIANAL SWAB
E	SUB-BARCODE – 25665-4444 AP NEG MICRO NEGATIVE FOR SPERM	RECTAL SWAB

TWO CLOTHING ITEMS:

SUB-BAROCDE: 25665-6666
ITEM: UNDERPANTS
AP POSITIVE
MICRO POS FOR SPERM



SUB –BARCODE: 25665-5555
ITEM: SINGLET TOP
AP NEGATIVE

Reporting back on SAIK via EXR/EXH registered under barcode 12345-6789.

PRESUMPTIVE RESULTS

	Result/Status	Linked No.	Warm Linked Name
25665-0000	Micro positive for sperm. Submitted results pending		
25665-5555	Semen not detected.		
25665-6666	Micro positive for sperm. Submitted results pending		

Not Current

Note: only the high vaginal swab is reported back to QPS out of the five swabs submitted. In this example: three swabs share the same positive results and two swabs are negative. The EXR/EXH to QPS is reported back on the most probative of all the positive swabs – the high vaginal swab.

There is no need to report back the negative swabs results as these results do not add any information needed by QPS at this stage.

Both items of clothing also have their presumptive results reported back via the same SAIK EXR/EXH to QPS. The SAIK and the clothing have their own FBEXAM registered to record the examination details.

When the profile in the Epithelial fraction matches the donor, and is therefore not an unexpected finding, this result is not usually reported in the EXR/EXH.

FINAL RESULTS

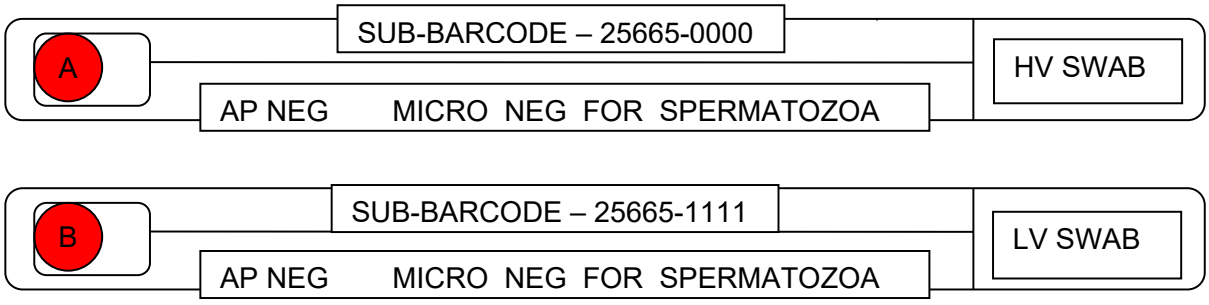
	Result/Status	Linked No.	Warm Linked Name
25665-0000	**Micro positive for sperm. Submitted results pending**		
25665-5555	**Semen not detected.**		
25665-6666	**Micro positive for sperm. Submitted results pending**		
25665-0000	Mixed profile, major component uploaded to NCIDD.	[redacted]	
25665-0000	Mixed profile, partial minor component.		
25665-1111	Mixed DNA profile, conditioned on.		
25665-1111	Mixed DNA profile. Remaining profile after conditioning.		
25665-6666	Mixed part profile. No major/minor. Unable to load to NCIDD.		

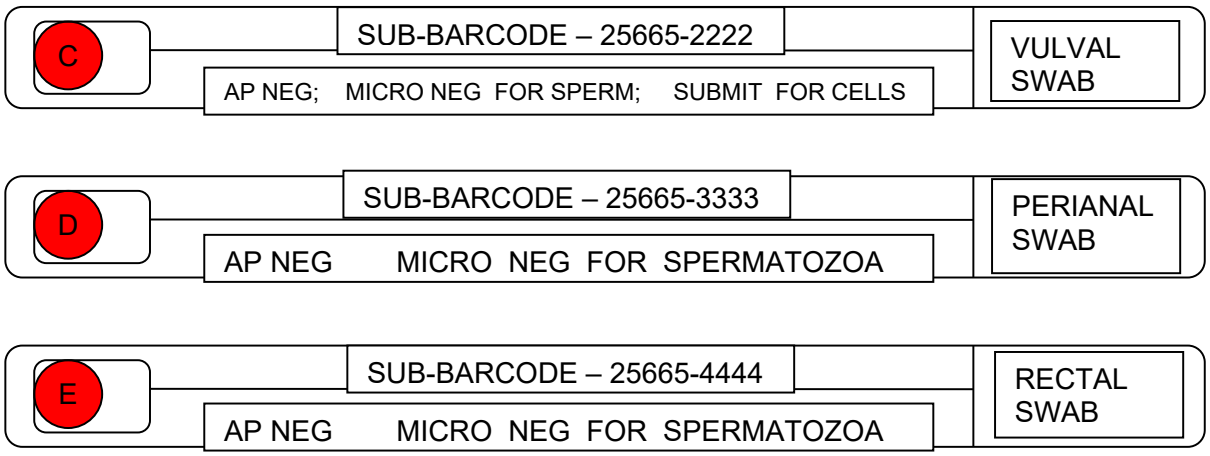
Not Current

EXAMPLE 7.

SAIK = QPS BARCODE 12345-6789

SAIK CONTAINS FIVE SWABS (NOT BARCODED BY QPS)





PRESUMPTIVE RESULTS

	Result/Status	Linked No.	Warm Linked Name
12345-6789	Semen not detected.		
25665-2222	Submitted as cells		

In this example, the five swabs were all negative for AP and microscopy, and the EXR/EXH has the parent barcode as the barcode entered to summarise that the whole item did not have semen detected. The two items of clothing are also reported back as negative to QPS. However, even though the vulval swab was also negative to all presumptive testing, it will still be submitted for a 'cell' extraction. DNA analysis is requested for the vulval swab as a last ditch effort, given both the SAIK and clothing are negative for all testing performed.

If QPS request an item for specific testing (eg blood) and the whole item was negative (eg Presump blood test neg), then the EXR/EXH will use the item/parent barcode to report back the results.

FINAL RESULTS

	Result/Status	Linked No.	Warm Linked Name
12345-6789	Semen not detected.		
25665-2222	Submitted as cells		
25665-2222	No DNA profile		

Not Current

APPENDIX 9

COMPLETE CASEWORK PREAMBLE – EXAMINATIONS BY QHFSS

Forensic Biology

As a forensic biologist, it is my role to report on the examination of items submitted in relation to this 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. Any DNA profiles which are obtained from these samples are then compared with the DNA profiles obtained from an individual's reference sample.

Examinations

The examinations described in this Statement of Witness were carried out by colleagues. The notes, which have been referred to in the preparation of this report, were made at the time of examination. All examinations were performed in accordance with the SOPs of this laboratory.

As a representative of the laboratory, I am only able to comment on the processes performed within the DNA Analysis Unit.

DNA Profiling

Please refer to the Appendix for an overview of DNA profiling.

Reference Samples

One or more reference sample/s provided for this case have been profiled using the PowerPlex21 system, which tests twenty regions (loci) of DNA containing STRs, and an additional region which provides an indication of gender of the DNA source. All other item/s within this case have been profiled using the Profiler® Plus system (nine regions plus gender). Of the twenty regions of DNA that the PowerPlex21 system tests, nine of them are the same as those tested using the Profiler® Plus system. Comparisons made between the reference sample/s and all other item/s within the case, and any statistical analyses undertaken, have been made based on the nine regions of DNA common to both systems.

Unknown DNA Profiles

If DNA profiles are obtained which do not match any of the reference DNA profiles associated to the case, they are considered to be of unknown origin. Where possible, these DNA profiles are assessed for gender, and then assigned sequential numerical designations (eg. Unknown Male 1, Unknown Male 2). If it is not possible to assign gender, the term Unknown Person is applied. Please note that numerical designations may be applied prior to the availability of reference DNA profiles. This means that if a reference DNA profile is found to match a DNA profile designated as Unknown Male 1, then Unknown Male 1 will not be referred to in the statement.

Mixed DNA profiles

Not Current

When more than one person has contributed DNA to a sample, the DNA profile obtained is referred to as a mixed DNA profile. The mixture of DNA can happen in many ways, however the resultant DNA profile can often be explained in terms of the following categories:

Major / minor mixtures – these generally occur when one person contributes more DNA to a sample than another person. It is possible to resolve these mixtures into individual contributions, referred to as major and minor DNA profiles.

Even mixtures – these generally occur when two (or more) people contribute DNA to a sample in approximately equal proportions. It is not possible to determine individual contributions to these mixtures, unless we can assume a contribution of DNA from a particular person (this is referred to as 'conditioning').

Conditioning can be performed on mixed DNA profiles obtained from samples taken from body surfaces, intimate swabs or clothing, where the person / owner is clearly identified through information provided to the laboratory. In these circumstances it is not unexpected to find DNA that could have originated from that person in the sample. Therefore if it is assumed that this person has contributed DNA to the mixed DNA profile, then the components of their DNA profile can be effectively subtracted from the mixture. This may leave a remaining DNA profile which can be used for comparison purposes.

Note: If the relevant information provided to the laboratory changes, for example regarding the ownership of an item of clothing, then the interpretation of the mixture may change in that it may no longer be appropriate to condition the mixture.

Complex mixtures - this is when the DNA profile contains an unknown number of contributors, and / or provides too limited an amount of information for meaningful comparison purposes. In some cases it may be possible to compare the reference DNA profile of a person with the DNA components within these complex mixtures. If it appears that the person's DNA profile is represented within the complex DNA profile, then this person can be described as not being excluded as a potential contributor of DNA. In other cases the mixed DNA profile may be so complex or incomplete that it may not be possible to draw any conclusions as to whether a person may have contributed DNA. In these instances, the complex DNA profile may be deemed unsuitable for comparison purposes.

Note: Additional complexity may arise when interpreting mixed DNA profiles where multiple potential contributors of DNA to the mixture are genetically related. This is due to the increased potential for related individuals to share genetic information.

Not Current

Touch DNA / Transfer of DNA

When a person touches a surface, it is possible for their cellular material to be transferred onto that surface. This transferred cellular material can often be recovered 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.

The generation of a DNA profile will depend on many factors. These include the amount of cellular material transferred, the nature of the surface being touched and the amount of cellular material a person has available to transfer.

The persistence of any transferred cellular material on a surface will depend largely upon the nature of the surface and the conditions under which it has been kept in the time between deposition and recovery of the DNA. For example, cellular material could be lost from the surface by washing or mechanical action such as abrasion.

It therefore follows that the absence of a DNA profile from a touched surface does not necessarily mean that that person has not come into contact with it, as it is possible for a person to come into contact with a surface without a detectable amount of their DNA being transferred or recovered.

Blood stains

Potential blood stains 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

The presence of semen on an item can be indicated by the use of a presumptive chemical test which detects a major constituent of seminal fluid (Acid Phosphatase – AP). This constituent does, however, exist in other body fluids, such as vaginal secretions. Additional presumptive chemical testing (Prostate Specific Antigen – PSA / p30) can be undertaken and a positive reaction to both AP and PSA / p30 makes it highly likely that seminal fluid is present. The presence of semen can be confirmed via the microscopic identification of spermatozoa (sperm heads).

Samples may undergo a differential lysis extraction process which aims to separate spermatozoa and epithelial / cellular 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 the DNA Analysis Unit is for epithelial fractions from intimate female SAIK samples to be stored following a Differential Lysis Extraction process. This is primarily due to the fact that when the vast majority of these fractions are profiled, they are found to match the person from whom the sample was taken. Given the intimate nature of these samples, this finding is not unexpected. These epithelial fractions will be 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. Any semen which 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 likelihood 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.

The greater the delay between deposition and sampling, the less chance there is of finding semen. 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 which can include the following:
- drainage of semen from the vagina;

Not Current

- loss of semen by bathing or washing (especially on external sites);
- degradation of the spermatozoa.

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 fluids and anal secretions, although usually at much lower concentration than that found in saliva.

If an area of the body is sucked or licked, saliva may be transferred onto the skin and subsequently onto any items of clothing worn on this area of the body. Saliva staining, in the form of amylase may then be detected on skin swabs or items of clothing as long as the clothing or skin has not been washed. Cellular material will be shed, to varying degrees, with the saliva and as such it may be possible to obtain a DNA profile from an area of saliva staining.

12. The results of the scientific examinations conducted in this laboratory are as follows:

Not Current

APPENDIX 10

COMPLETE CASEWORK PREAMBLE - EXAMINATIONS BY QPS AND QHFSS

11. The following information is provided to assist in the understanding of the contents of this statement.

Forensic Biologist

As a forensic biologist, it is my 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 which are obtained from these samples are then compared with the DNA profiles obtained from an individual's reference sample.

Examinations

Unless otherwise stated, the examinations of items for biological material were conducted by officers within the QPS. Sub-samples from these items were forwarded to Queensland Health Forensic and Scientific Services (QHFSS) for the purposes of conducting DNA analysis.

Samples submitted to QHFSS for DNA analysis may include swabs, tape-lifts or small sections of material cut from an exhibit. Individual samples are typically submitted within small plastic tubes and are referred to as 'in-tube' samples.

It is my understanding that the QPS are responsible for item prioritisation, sample selection, selection of screening / sampling methods, application of anti-contamination and standard operating procedures (SOPs) on work undertaken on the items / samples prior to submission to QHFSS. As such, forensic biologists may not be able to provide information or opinion on the possible biological origin of any 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, notes are made at the time of the examination by the examining scientist and form part of the case file.

DNA Analysis Unit case files 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 the DNA Analysis Unit.

DNA Profiling

Please refer to the Appendix for an overview of DNA profiling.

Not Current

Reference Samples

One or more reference sample/s provided for this case have been profiled using the PowerPlex21 system, which tests twenty regions (loci) of DNA containing STRs, and an additional region which provides an indication of gender of the DNA source. All other item/s within this case have been profiled using the Profiler® Plus system (nine regions plus gender). Of the twenty regions of DNA that the PowerPlex21 system tests, nine of them are the same as those tested using the Profiler® Plus system. Comparisons made between the reference sample/s and all other item/s within the case, and any statistical analyses undertaken, have been made based on the nine regions of DNA common to both systems.

Unknown DNA Profiles

If DNA profiles are obtained which do not match any of the reference DNA profiles associated to the case, they are considered to be of unknown origin. Where possible, these DNA profiles are assessed for gender, and then assigned sequential numerical designations (eg. Unknown Male 1, Unknown Male 2). If it is not possible to assign gender, the term Unknown Person is applied. Please note that numerical designations may be applied prior to the availability of reference DNA profiles. This means that if a reference DNA profile is found to match a DNA profile designated as Unknown Male 1, then Unknown Male 1 will not be referred to in the statement.

Mixed DNA profiles

When more than one person has contributed DNA to a sample, the DNA profile obtained is referred to as a mixed DNA profile. The mixture of DNA can happen in many ways, however the resultant DNA profile can often be explained in terms of the following categories:

Major / minor mixtures – these generally occur when one person contributes more DNA to a sample than another person. It is possible to resolve these mixtures into individual contributions, referred to as major and minor DNA profiles.

Even mixtures – these generally occur when two (or more) people contribute DNA to a sample in approximately equal proportions. It is not possible to determine individual contributions to these mixtures, unless we can assume a contribution of DNA from a particular person (this is referred to as 'conditioning').

Conditioning can be performed on mixed DNA profiles obtained from samples taken from body surfaces, intimate swabs or clothing, where the person / owner is clearly identified through information provided to the laboratory. In these circumstances it is not unexpected to find DNA that could have originated from that person in the sample. Therefore if it is assumed that this person has contributed DNA to the mixed DNA profile, then the components of their DNA profile can be effectively subtracted from the mixture. This may leave a remaining DNA profile which can be used for comparison purposes.

Note: If the relevant information provided to the laboratory changes, for example regarding the ownership of an item of clothing, then the interpretation of the mixture may change in that it may no longer be appropriate to condition the mixture.

Complex mixtures - this is when the DNA profile contains an unknown number of contributors, and / or provides too limited an amount of information for meaningful comparison purposes. In some cases it may be possible to compare the reference DNA profile of a person with the DNA components within these complex mixtures. If it appears that the person's DNA profile is represented within the complex DNA profile, then this person can be described as not being excluded as a potential contributor of DNA. In other cases the mixed DNA profile may be so

Not Current

complex or incomplete that it may not be possible to draw any conclusions as to whether a person may have contributed DNA. In these instances, the complex DNA profile may be deemed unsuitable for comparison purposes.

Note: Additional complexity may arise when interpreting mixed DNA profiles where multiple potential contributors of DNA to the mixture are genetically related. This is due to the increased potential for related individuals to share genetic information.

Touch DNA / Transfer of DNA

When a person touches a surface, it is possible for their cellular material to be transferred onto that surface. This transferred cellular material can often be recovered 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.

The generation of a DNA profile will depend on many factors. These include the amount of cellular material transferred, the nature of the surface being touched and the amount of cellular material a person has available to transfer.

The persistence of any transferred cellular material on a surface will depend largely upon the nature of the surface and the conditions under which it has been kept in the time between deposition and recovery of the DNA. For example, cellular material could be lost from the surface by washing or mechanical action such as abrasion.

It therefore follows that the absence of a DNA profile from a touched surface does not necessarily mean that that person has not come into contact with it, as it is possible for a person to come into contact with a surface without a detectable amount of their DNA being transferred or recovered.

Blood stains

Potential blood stains 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

The presence of semen on an item can be indicated by the use of a presumptive chemical test which detects a major constituent of seminal fluid (Acid Phosphatase – AP). This constituent does, however, exist in other body fluids, such as vaginal secretions. Additional presumptive chemical testing (Prostate Specific Antigen – PSA / p30) can be undertaken and a positive reaction to both AP and PSA / p30 makes it highly likely that seminal fluid is present. The presence of semen can be confirmed via the microscopic identification of spermatozoa (sperm heads).

Samples may undergo a differential lysis extraction process which aims to separate spermatozoa and epithelial / cellular 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 the DNA Analysis Unit is for epithelial fractions from intimate female SAIK samples to be stored following a Differential Lysis Extraction process. This is primarily due to the fact that when the vast majority of these fractions are profiled, they are found to match the

Not Current

person from whom the sample was taken. Given the intimate nature of these samples, this finding is not unexpected. These epithelial fractions will be 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. Any semen which 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 likelihood 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.

The greater the delay between deposition and sampling, the less chance there is of finding semen. 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 which 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.

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 fluids and anal secretions, although usually at much lower concentration than that found in saliva.

If an area of the body is sucked or licked, saliva may be transferred onto the skin and subsequently onto any items of clothing worn on this area of the body. Saliva staining, in the form of amylase may then be detected on skin swabs or items of clothing as long as the clothing or skin has not been washed. Cellular material will be shed, to varying degrees, with the saliva and as such it may be possible to obtain a DNA profile from an area of saliva staining.

12. The results of the scientific examinations conducted in this laboratory are as follows:

Not Current

APPENDIX 11

COMPLETE PATERNITY PREAMBLE

10. The following information is provided to assist in the understanding of the contents of this statement.

Forensic Biology

As a Forensic Biologist, it is my role to report on the examination of items submitted in relation to this 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. Any DNA profiles which are obtained from these samples are then compared with the DNA profiles obtained from an individual's reference sample.

Examinations

The examinations described in this Statement of Witness were carried out by colleagues. The notes, which have been referred to in the preparation of this report, were made at the time of examination. All examinations were carried out in accordance with Standard Operating Procedures.

DNA Profiling

DNA is a complex chemical found in almost all cells in the human body. It carries genetic information which determines the physical and chemical characteristics of a person. The DNA system used at Queensland Health looks at 10 regions of DNA, 9 of which contain Short Tandem Repeats (STRs). The tenth region gives an indication as to the gender of the donor.

Two DNA components (alleles) are detected at each region of DNA tested. This total of 18 alleles, plus gender information, comprises an individual's DNA profile. Of the two alleles detected at each of the regions tested, one is inherited from an individual's biological mother, and the other component is inherited from an individual's biological father.

Reference Samples

One or more reference sample/s provided for this case have been profiled using the PowerPlex21 system, which tests twenty regions (loci) of DNA containing STRs, and an additional region which provides an indication of gender of the DNA source. All other item/s within this case have been profiled using the Profiler® Plus system (nine regions plus gender). Of the twenty regions of DNA that the PowerPlex21 system tests, nine of them are the same as those tested using the Profiler® Plus system. Comparisons made between the reference sample/s and all other item/s within the case, and any statistical analyses undertaken, have been made based on the nine regions of DNA common to both systems.

Parentage testing and Statistical calculations:

Not Current

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 mother is indeed the biological mother of the foetus/child, it is possible to determine which DNA components within the DNA profile of the child could have originated from her. The remaining DNA components within the DNA profile of the foetus/child must have originated from the biological father, and are called *obligate paternal alleles*.

If the DNA profile of a putative father **does not** contain the obligate paternal alleles in at least two of the DNA regions tested, then that person 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 that person is **not excluded** as a potential biological father of the foetus/child. This means that this putative father could indeed be the biological father.

Statistical analysis is then conducted to aid in the understanding of the strength of the evidence. The Paternity Index (PI) is a likelihood of two probabilities conditional upon different competing hypotheses;

1. The alleged father contributed the obligate paternal alleles observed in the DNA profile of the foetus/child

2. Another man chosen at random contributed the obligate paternal alleles observed in the DNA profile of the foetus/child.

The PI reflects how many times more likely it is to see the evidence (ie. Set of alleles) under the first hypothesis compared to the second hypothesis. The generally accepted minimum standard for an inclusion of paternity is a PI of 200 or greater (NATA Paternity Testing Technical Advisory Group, 2004).

(Adapted from Butler, J.M. (2005) Chapter 23, *Kinship and Parentage Testing in* Forensic DNA Typing, Biology, Technology, and Genetics of STR Markers, 2 Ed. Elsevier Academic Press: Burlington, MA 01803, USA.)

11. 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.

Not Current

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>.

Not Current

APPENDIX 12

QUALITY PARAGRAPHS

NB. These paragraphs are required to be entered into the preambles of statements containing results from DNAIQ extractions on the Automated Platforms during the period October 2007- July 2008. The particular category will depend on the investigation outcomes of each case.

Quality

Category A

Testing for this case has been conducted in a period where some results were the subject of an adverse event. An adverse event includes a deficient operation or function identified to have occurred within the automated extraction process utilised in testing during the period October 2007 to July 2008. Testing for this case was not the subject of any adverse result. An adverse result is a result which has been affected by an adverse event, whose integrity cannot be verified. This conclusion has been reached by conducting a review of the results and assessing a number of factors, including, but not limited to, the comparison of all other results from samples processed alongside this result, to detect whether the integrity of each sample can be verified. Retesting has been conducted on identified samples which have confirmed information in the original results.

Category B

Testing for this case has been conducted in a period where some results where the subject of adverse events. An adverse event includes a deficient operation or function identified to have occurred within the automated extraction process utilised in testing during the period October 2007 and July 2008. Within this case, the adverse event is demonstrated to have affected a result or results and the integrity cannot be verified. There was no remaining sample for retesting to be conducted. These results have therefore been reported as follows 'these samples did not pass our Quality System requirements at the DNA analysis stage and therefore the DNA profiling results relating to these samples cannot be reported'.

Category C

Testing for this case has been conducted in a period where some results were the subject of adverse events. An adverse event includes a deficient operation or function identified to have occurred within the automated extraction process utilised in testing during the period of October 2007 and July 2008. Testing for some samples within this case has been the subject of an adverse event. The cause of the adverse event was identified to have occurred within the automated extraction process. Portions of the sample remained available for further testing. Retesting has been conducted, using an alternative manual extraction method and all quality assurance checks were satisfactory. These samples have been reported as they have been assessed as no adverse event having been detected and the results have passed all quality assurance checks.

Not Current

APPENDIX 13

EVIDENTIARY CERTIFICATE WORKFLOW

Receive written request and clarify which samples are required to be included.

↓

Ensure that there is adequate time to complete audit trails and issue certificate at least 10 days before court date – negotiate with IO/DPP if required.
Timeframes approx. 4 weeks for Evidentiary Certificate alone, 6 weeks if requested at the same time as a statement.

↓

Create Evidentiary checklist using:
QIS2 30799: DNA Evidentiary Certificate Checklist

Follow instructions on Worksheet entitled: 'Instructions'
The minimum requirement is to check the electronic records of samples and batches in AUSLAB.

↓

Work through each sample and the relevant batches, looking at audit trail in AUSLAB to see if any issues have been raised. eg sample removed has not transferred yet, pos control is partial profile, failure of batch due to controls not working/OQI.
If you have examined the records relating to the receipt, storage and testing of the things covered by the Evidentiary Certificate, by 'checking' the boxes, you are confirming that the Quality Assurance Procedures relevant to the above at the time of testing were complied with.

If in examining the records, something needs to be addressed, notify your Senior Scientist and/or Team Leader to co-ordinate a possible investigation.

↓

Check storage audit trail for each sample, noting that there should be two final locations for most samples – one for spin basket and one for final amplified product. Ensure that throughout the audit trail, sample has been added and removed from particular location as it works its way through the process.

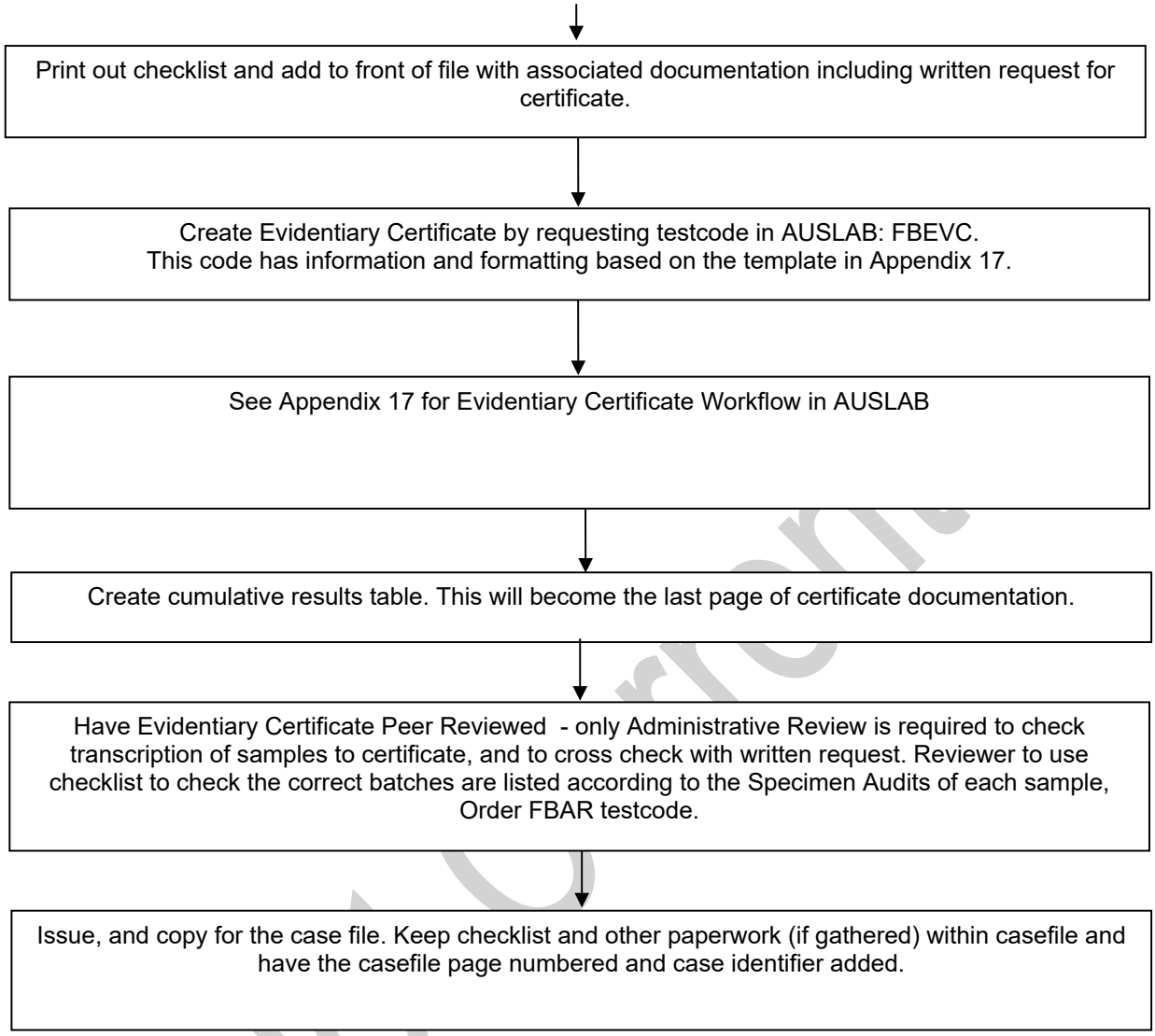
↓

As a minimum, AUSLAB audit trails can be checked for departures from the standard operating procedure. If required, the batch paperwork is scanned into the batches as 'log' files and can be checked by the following:

enter into batch → Shift F6 ('Files') → scroll to 'Log' → Export file to location to be retrieved → view .pdf

↓

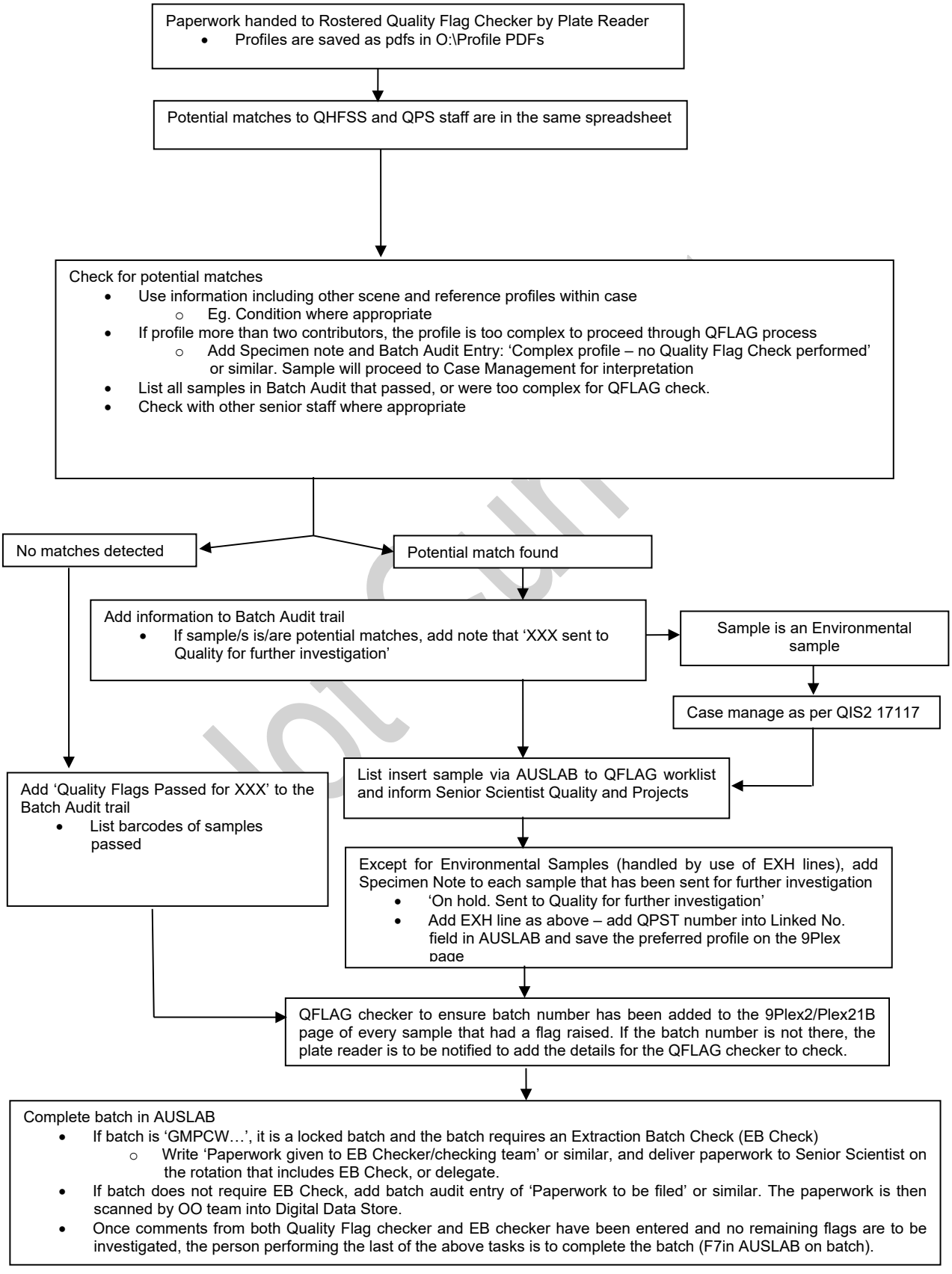
If the paperwork is not complete, get original paperwork correction signed and dated or whatever is required. If this staff member is on holidays, or no longer working in department, get their Senior to sign and date on their behalf.


Print out checklist and add to front of file with associated documentation including written request for certificate.
Create Evidentiary Certificate by requesting testcode in AUSLAB: FBEVC.
This code has information and formatting based on the template in Appendix 17.
See Appendix 17 for Evidentiary Certificate Workflow in AUSLAB
Create cumulative results table. This will become the last page of certificate documentation.
Have Evidentiary Certificate Peer Reviewed - only Administrative Review is required to check transcription of samples to certificate, and to cross check with written request. Reviewer to use checklist to check the correct batches are listed according to the Specimen Audits of each sample, Order FBAR testcode.
Issue, and copy for the case file. Keep checklist and other paperwork (if gathered) within casefile and have the casefile page numbered and case identifier added.

Not Current

APPENDIX 14

QUALITY FLAG CHECKING WORKFLOW



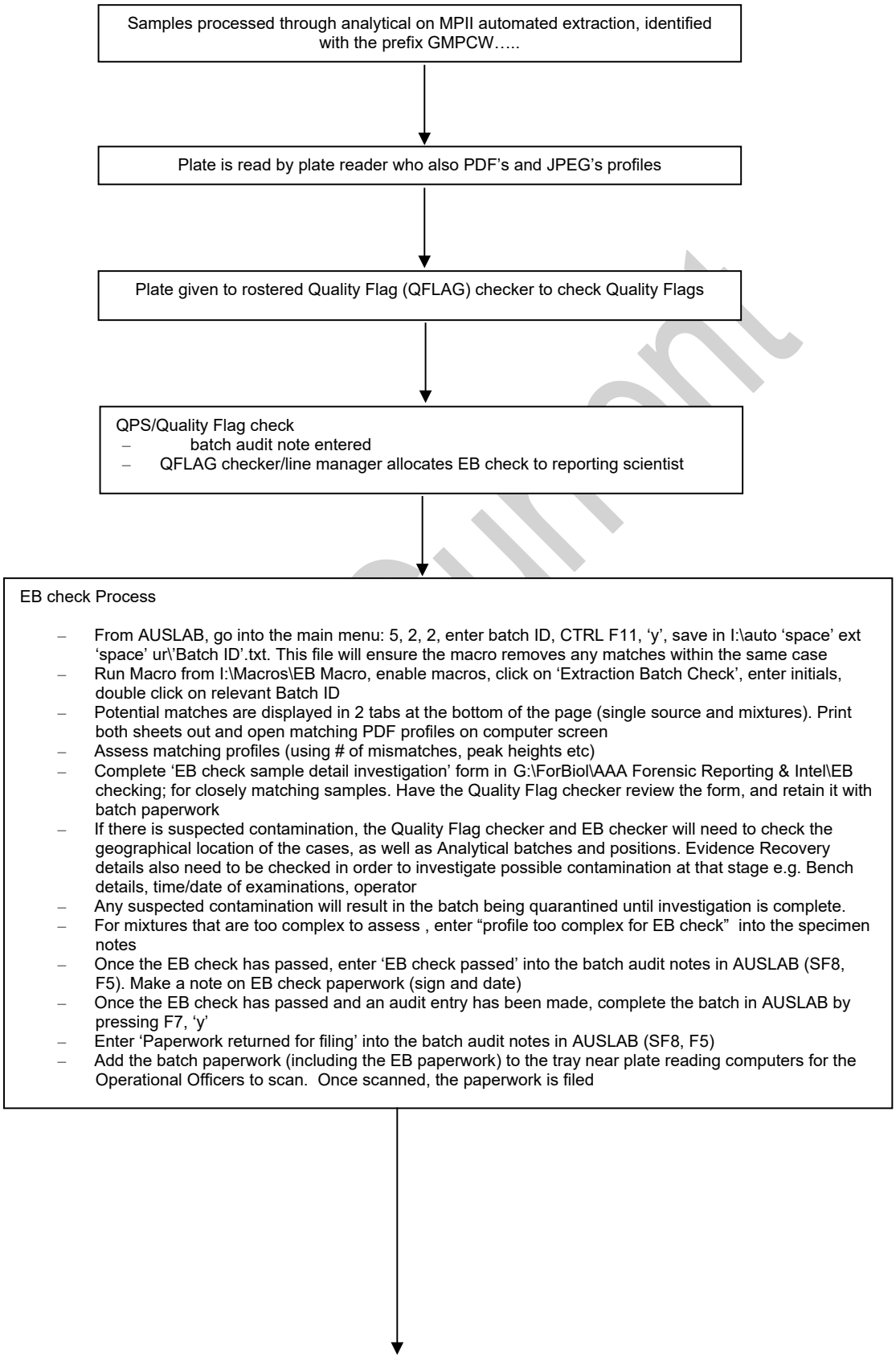
Notes on the Quality Flag Checking Process:

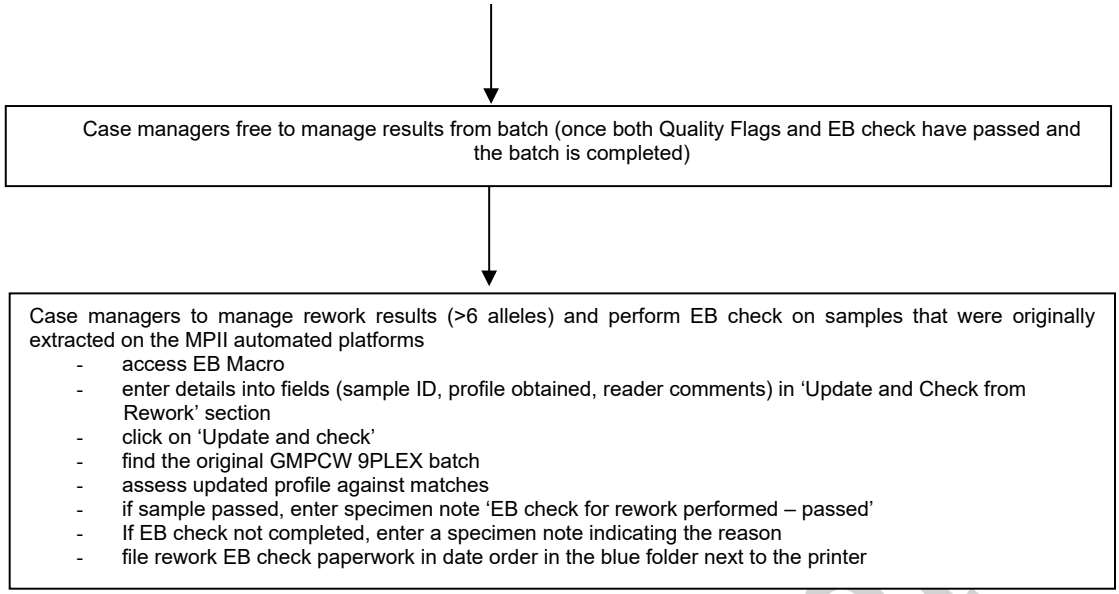
- Quality Flag Checking is to detect gross contamination that could have occurred at collection or during processing of the sample.
    - This includes single-source profiles, distinct major or minor profiles, or remaining contributions if the mixed profile has been conditioned.
- Due to the complexity of some DNA profiles, profiles that indicate at least three contributors (and therefore an unknown number of contributors) are generally not suitable for Quality Flag checking for the following reasons:
    - The number of contributors is not known and the often partial nature adds complexity.
    - At most, a person may not be able to be excluded as potential contributors and this interpretation may not be useful to the client as we cannot evaluate the significance of a possible inclusion by adding statistical weight.
- When profiles of at least three contributors are obtained, the Quality Flag Checker should note in the Batch Audit and the Specimen Notes:
    - 'Complex profile – no Quality Flag check performed' or similar wording
        - The profile will then proceed to case management for interpretation with case context.
- It may be possible for the higher RFU peaks (if demonstrating a pattern as such across the profile) to be QFLAG checked
    - If the peaks pass, write in the Batch Audit and Specimen Notes: 'Big peaks passed QFLAGs. Small peaks too complex for QFLAG checking' or similar wording
        - Refrain from using 'Major/Minor' terminology because the Case Manager may interpret the profile not to be a major/minor profile (vis. Powerplex 21 profiles).
- The macro that is applied to detect potential Quality Flags has a stringency of 13 alleles. This means, crime scene profiles with less than 13 alleles detected will not go through the macro and therefore will not be Quality Flag checked.
- When performing the Quality Flag task, the staff match table is colour coded for ease of interpretation.
    - The Crime Scene profile is in the column at far left. The QPS Elimination samples are in the next six columns
        - When an allele in the QPS elimination profile matches an allele found in the Crime Scene profile, the allele is coloured yellow.
        - When an allele in the QPS elimination profile is not found in the Crime Scene profile, the allele is coloured green.
    - When there are too many alleles in the Crime Scene profile to fit into the column, the alleles push data across the columns to the right
        - This is a data fault of the columns in AUSLAB
        - The alleles in the column immediately to the right are part of the profile in the column to the left and the Quality Flag checker should account for this in their comparisons
        - The colouring system is not affected. What this means is that even though the data is pushed into the adjacent column, the match/non-match determination of those alleles with the Crime Scene profile is not affected.

Not Current

APPENDIX 15

EXTRACTION BATCH CHECKING WORKFLOW (EB Checking)





EB Macro Notes:

- The Extraction Batch macro is performed before results are case managed and released to the QPS. It allows for the detection of contamination between samples that we extracted on the same automated MPII extraction batch. These batches are identified by GMPCW…..
- It compares profiles from different cases that have greater than 6 alleles against each other.
- Matches are assessed by the reporting scientist, considering both samples as the potentially contaminating and contaminated profiles.
- The EB macro divides and displays any potential matches into single source and mixtures, in two separate tabs.
- The profile highlighted in white is the profile that the profiles underneath have matched to.
- The macro displays matching loci in different colours: green indicates that there are at least 2 matching alleles, yellow indicates 1 matching allele, light orange indicates a mismatch at the entire loci, and bright orange indicates a mismatch at Amelogenin.
- The EB check can be performed at any desk. The profile highlighted in white is to be printed off, and the profiles matching to it can be displayed on the computer screen so that comparisons can be made.
- Once samples have been reworked, the reworked result needs to be checked against the batch the sample was originally extracted on. If the 9plex result is used as the reported profile; or the rework result is the same, similar, has less information or is too complex, a rework EB check is not necessary. This is assessed by the case manager, and a specimen note added with the reason the EB check was not performed.

Not Current

DNA EVIDENTIARY CERTIFICATE (and APPENDIX v5)

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 …

10. 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.

Not Current

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.

Not Current

APPENDIX 1

Procedural overview for the DNA Analysis Unit,
Queensland Health Forensic and Scientific Services (QHFSS)

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.
For details of the current ISO/IEC 17025 Field Application Document, Forensic Science, Supplementary requirements for accreditation, please refer to the NATA website:
http://www.nata.asn.au/publications

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 DNA Analysis Unit of Queensland Health Forensic and Scientific Services (QHFSS)

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.

Not Current

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.

Not Current

DNA (STR) profiling systems available at the DNA Analysis Unit, Queensland Health Forensic and Scientific Services (QHFSS)

Table 1: Profiler® Plus multiplex system, list of loci:

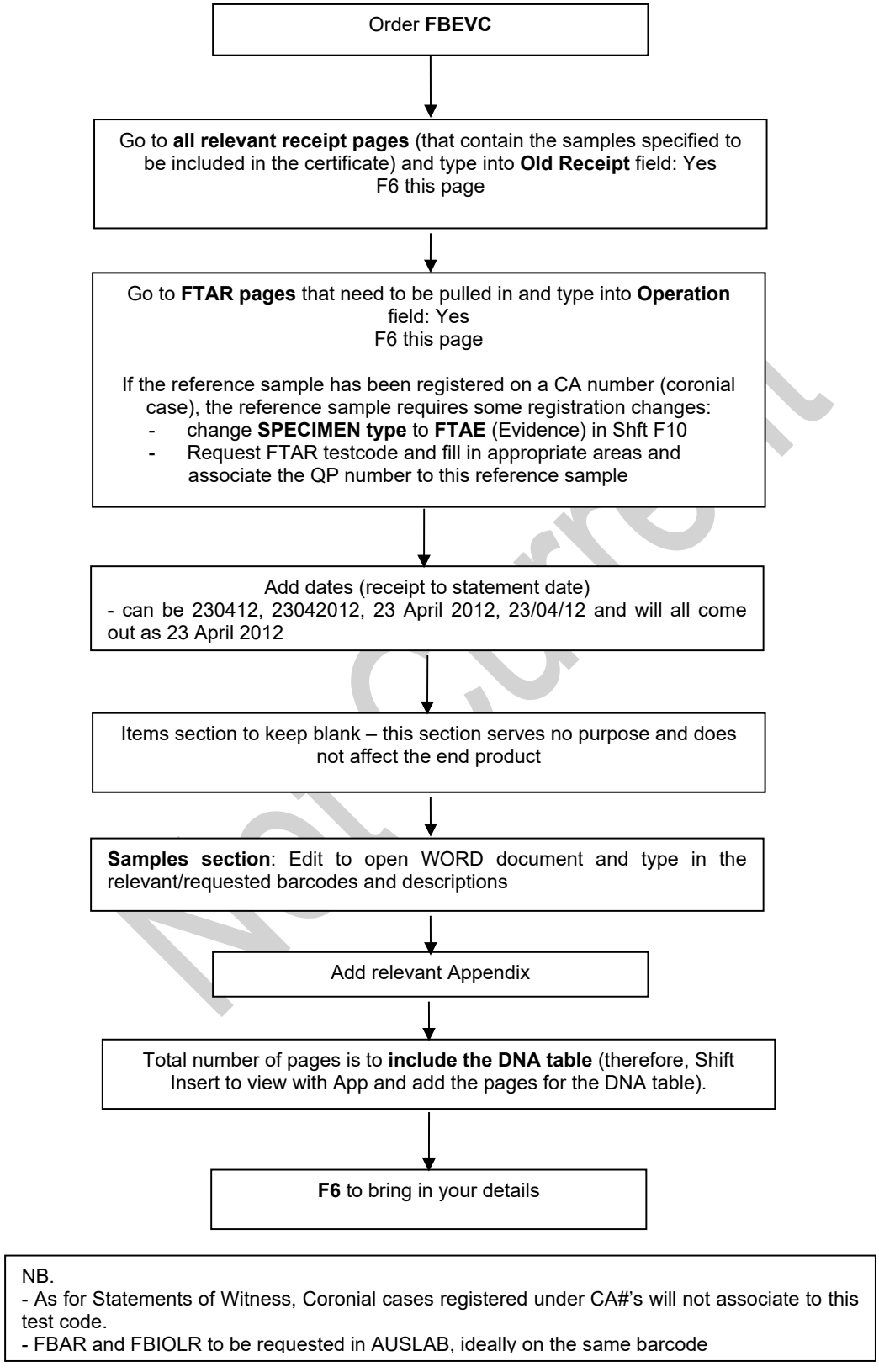
Abbreviated Name	Scientific Name	Chromosomal Name
D3	D3S1358	3
vWA	HUMVWFA31/A	12
FGA	HUMFIBRA	4
Amel	AMELOGENIN	Sex X and Y
D8	D8S1179	8
D21	D21S11	21
D18	D18S51	18
D5	D5S818	5
D13	D13S317	13
D7	D7S820	7

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

Not Current

DNA EVIDENTIARY CERTIFICATE WORKFLOW IN AUSLAB



Not Current

Forensic and Scientific Services
HSSA | Health Services Support Agency

Minutes
Forensic Reporting and Intelligence Team Meeting

Chairperson:	Emma Caunt	**Date and**	10:00am 22/08/13
Venue:	FSS CR102	**Secretariat:**	Emma Caunt
Meeting Purpose:	Fortnightly team meeting	**File Location:**	G:\ForBiol\DNA Analysis Team Meetings\Forensic Reporting and Intelligence Team\2013\Apr-Jun
Attendees:	Penny Taylor, Robert Morgan, Angela Adamson, Rhys Parry, Ingrid Moeller, Matthew Hunt, Kylie Rika, Deborah Nicoletti, Adrian Pippia, Sharon Johnstone, Josie Entwistle, Lisa Benstead, Emma Caunt Anne Finch, Angelina Keller, Amanda Reeves,		
Guests:	Kirsten Scott, Allan McNevin,		
Apologies:			
Absent:	Claire Gallagher, Alicia Quartermain, Tim Gardam, Shannon Merrick, Susan Brady, Jacqui Wilson, Justin Howes, Helen Williams,		

1.0 PREVIOUS MINUTES ENDORSED

Previous meeting held (insert date of last meeting) were accepted by XX seconded by XX

2.0 CONFLICTS OF INTEREST

Any conflicts of interest need to be noted at the beginning of the meeting.

3.0 BUSINESS ARISING FROM PREVIOUS MINUTES

Refer "Action Table" for business arising from previous minutes – Page 4

4.0 STANDING AGENDA ITEMS

Item 4.1:

Subject: **Court Reports**

Discussion: JMW – [redacted], [redacted], [redacted]
EJC – [redacted]
AJR – [redacted]
DRN – [redacted], [redacted]

Item 4.2:

Subject: **Articles of Interest**

Discussion: None

ACTION:

Responsibility:

Due Date/Status:	
Item 4.3:	
Subject:	**Workplace Health and Safety**
Discussion:	None
ACTION:	
Responsibility:	
Due Date/Status:	
Item 4.4:	
Subject:	
Discussion:	
ACTION:	
Responsibility:	
Due Date/Status:	

NEW BUSINESS

Item 5.1:	
Subject:	**Case management process improvement**
Discussion:	A working party for improving case management processes has been established – ARM, JMW, KDS. Jacqui is the point of contact if you have any suggestions.
ACTION:	
Responsibility:	**All Scientists**
Due Date/Status:	
Item 5.2:	
Subject:	**Batch audit entries**
Discussion:	These must be read and noted without exception. If you can think of a more efficient way of being provided with the information please let me know. Please don't be complacent with these as important information may be missed. It is the responsibility of the case manager/reporter to determine whether a result is reportable. The responsibility does not lie with analytical.
ACTION	
Responsibility:	**All Scientists**
Due Date/Status:	
Item 5.3:	
Subject:	**N-2 (PAF)**
Discussion:	Please remind case managers to be aware of N-2 and that there currently isn't a threshold for the removal of peaks, and that it (and N+2) may be observed at the following loci in PP21 - D1, D6, D13, vWA, D21, D7, D5, D12 and D19 (refer page 12 of QIS#31389).
Responsibility:	**All Scientists**
Due Date/Status:	
Item 5.4:	
Subject:	**Allele sizing (PJT)**
Discussion:	In the Analytical meeting Allan discussed the issue of excess samples affecting the size standard peaks. The way it was detected was an interstate mismatch on NCIDD where NSW got a 20 and we got a 19.3.
ACTION:	
Responsibility:	**All Scientists**
Due Date/Status:	

Item 5.5:	
Subject:	**AUSLAB issues (PAF)**
Discussion:	Faults that have been previously addressed and solved are re-occurring in Auslab. 1 - Batches when completed are creating two identical batches (e.g. Completing a Genemapper batch and then creating two duplicate JPEG batches) 2 - Samples failing to allocate to batches (currently occurring with RRCW2 returned samples and may occur with other reworks*) - you may find this occurring with OQI#34817 samples * audit trail will say sample is on an outstanding batch (as the audit trail is created before allocation occurs), check if your sample is on the outstanding batch through 5, 2, 1 and if it isn't then go to SF10 and delete testcode and then go back in to SF7 to re-order testcode. 3 - Batches that are completed are staying on the Outstanding Batch list. As mentioned in the last FRIT meeting by Lisa, can you please CC Lisa, Anne and/or Tom in on any correspondence to LISS regarding any faults that you log/register. This allows the Auslab Working Party to keep track of what jobs are being logged by the laboratory.
ACTION:	
Responsibility:	**All Scientists**
Due Date/Status:	
Item 5.6:	
Subject:	**Statement wording**
Discussion:	See G:\ForBiol\AAA Forensic Reporting & Intel\AAA_Reporting guidelines\PP21 and STRmix case mgt\ Example Statement Wording_Aug 2013 Given the no. of times we issue statements without evidence, it is thought that the original wording that was proposed will be understood better without clarification, even more so than other formats including ones that see the use of a table. The wording has been softened slightly by replacing the use of 'did' and 'did not' with 'has' and 'has not'. Wording has been checked by Duncan Taylor (FSSA) and Jo Bright (ESR). There is still a degree of poetic licence with statement wording as not all profiles will fit into these categories. However, this is the format that all reporters should be using.
ACTION:	
Responsibility:	**All Scientists**
Due Date/Status:	
Item 5.7:	
Subject:	**Number of contributors and reference samples**
Discussion:	This discussion was passed to other jurisdictions to see what everybody else is doing. There are a mixture of views. BSAG has now passed this to StatSWG for resolution, however it is noted that a resolution may not be possible. In the mean time, there will be some meetings to make a local decision as to how we are going to deal with this so that everybody is doing the same thing. If you have any strong opinions, please let myself or your senior know so that your opinion can be included in the discussions.
ACTION:	
Responsibility:	**All Scientists**
Due Date/Status:	

6.0	NEW BUSINESS – FOR NOTING
Item 6.1:	**Originally tabled <<insert date>>**
Subject:	
Discussion:	
ACTION:	
Responsibility:	
Due Date/Status:	
Item 6.2:	**Originally tabled <<insert date>>**
Subject:	**N/A**
Discussion:	
ACTION:	
Responsibility:	
Due Date/Status:	

7.0	CLOSURE
Meeting Closed at: 11:30am	

8.0	NEXT MEETING	
Date: Jan /13	**Time:** 10:30am	**Venue:** CR102

Action Register

Minutes Reference	Item Number	Subject / Discussion	Action	Action Officer	Due Date	Status

Accepted Manuscript

Title: Developmental validation of STRmix™, expert software for the interpretation of forensic DNA profiles

Author: Jo-Anne Bright Duncan Taylor Catherine McGovern Stuart Cooper Laura Russell Damien Abarno John Buckleton

PII: S1872-4973(16)30076-X
DOI: http://dx.doi.org/doi:10.1016/j.fsigen.2016.05.007
Reference: FSIGEN 1517

To appear in: *Forensic Science International: Genetics*

Received date: 25-1-2016
Revised date: 9-5-2016
Accepted date: 10-5-2016

Please cite this article as: Jo-Anne Bright, Duncan Taylor, Catherine McGovern, Stuart Cooper, Laura Russell, Damien Abarno, John Buckleton, Developmental validation of STRmix™, expert software for the interpretation of forensic DNA profiles, Forensic Science International: Genetics http://dx.doi.org/10.1016/j.fsigen.2016.05.007

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

ACCEPTED MANUSCRIPT

Developmental validation of STRmix™, expert software for the interpretation of forensic DNA profiles

Jo-Anne Bright[1], Duncan Taylor[2,3], Catherine McGovern[1], Stuart Cooper[1], Laura Russell[1], Damien Abarno[2], John Buckleton[1]

1. ESR, Private Bag 92021, Auckland 1142, New Zealand
2. Forensic Science South Australia, 21 Divett Place, Adelaide, SA 5000, Australia
3. School of Biological Sciences, Flinders University, GPO Box 2100 Adelaide SA, Australia 5001

Jo-Anne Bright[a], Duncan Taylor[b,c], Catherine McGovern[a], Stuart Cooper[a], Laura Russell[a], Damien Abarno[b], John Buckleton[a]

[a]ESR, Private Bag 92021, Auckland 1142, New Zealand

[b]Forensic Science South Australia, 21 Divett Place, Adelaide, SA 5000, Australia

[c]School of Biological Sciences, Flinders University, GPO Box 2100 Adelaide SA, Australia 5001

Highlights

- The developmental validation of STRmix™ following the 2015 SWGDAM Guidelines for the Validation of Probabilistic Genotyping Systems is described
- Performance of the software is discussed with respect to sensitivity, specificity, precision, accuracy, and reproducibility

ACCEPTED MANUSCRIPT

Abstract

In 2015 the Scientific Working Group on DNA Analysis Methods published the SWGDAM Guidelines for the Validation of Probabilistic Genotyping Systems [1]. STRmix™ is probabilistic genotyping software that employs a continuous model of DNA profile interpretation. This paper describes the developmental validation activities of STRmix™ following the SWGDAM guidelines. It addresses the underlying scientific principles, and the performance of the models with respect to sensitivity, specificity and precision and results of interpretation of casework type samples. This work demonstrates that STRmix™ is suitable for its intended use for the interpretation of single source and mixed DNA profiles.

Keywords: DNA mixtures; Probabilistic genotyping; Continuous method; Validation; STRmix.

Introduction

The dominant method for forensic DNA analysis involves the amplification of short tandem repeats using PCR. Amplified products are separated via capillary electrophoresis (CE). Fluorescently labelled tags are used to colour code the markers or loci. A laser excites the primer tags as the different lengths of DNA travel through the capillaries of the electrophoresis instrument, which emit a signal that is recorded. The signals are visualised as peaks in a graph of fluorescence versus time, known as an electropherogram (epg). The height of the peaks is approximately proportional to the initial amount of DNA template and is measured in relative fluorescent units (rfu). In this way height can be used as an approximation of DNA quantity or template.

Manual techniques for DNA profile interpretation are heuristically based and may be difficult to apply consistently between laboratories, individual scientists and even a single scientist. Variable decisions often occur early in the manual interpretation process and can even occur at allele assignment. Divergence in these choices can have significant downstream consequences [2, 3]. Phenomena such as stutter (artifactual amplicons produced as a consequence of the PCR process), allelic drop-in (the presence of low amounts of extraneous DNA) and dropout (which is a consequence of low template and/or degraded DNA and

ACCEPTED MANUSCRIPT

results in partial DNA profiles) [4] are all considered at profile analysis and interpretation. Interpretation of DNA profiles is also complicated by mixed samples (the presence of DNA from more than one individual).

The interpretation of an epg or evidentiary DNA profile should initially be undertaken 'blind'; in isolation of the person of interest's (POI) reference DNA profile, and where possible avoiding contextual effects [5, 6]. Comparison with reference profiles of any POI or other relevant evidentiary profiles is undertaken after profile interpretation. Traditionally there are three primary conclusions that can be drawn: *cannot exclude* (or *inclusion*), *can exclude*, or *inconclusive* which is sometimes also called *uninterpretable* [7]. It is desirable when an association is reported (cannot exclude or inclusion) to present the evidence with the associated statistical weight [7]. When the evidence profile originates from a single individual, the weight of evidence can be presented as a match probability. This is an assignment of the probability that a random person might match the crime scene stain given the observation of that crime stain profile. A favoured alternative to the match probability, which can be extended to use for mixed DNA profiles, is the likelihood ratio (*LR*). The *LR* considers the probability of obtaining the evidence profile(s) given two competing propositions, usually aligned with the prosecution case and defence case. The *LR* is used throughout Australasia and the UK and is used in some laboratories within the US and Europe for criminal forensic work to express the weight of evidence. The *LR* is accepted to be the most relevant and powerful statistic to calculate the weight of the evidence and is the only method recommended by the International Society for Forensic Genetics (ISFG) for ambiguous profiles [8]. Ambiguous profiles include all mixtures and single source profiles where dropout and drop-in are a consideration.

Known shortcomings of traditional methods of DNA profile interpretation have led to the development of improved models that factor in the probability of dropout [9-13]. The drop model (also known as the semi-continuous method) can optionally incorporate a probability for dropout, Pr(*D*), and/or a probability for drop-in, Pr(*C*). Semi-continuous methods do not use peak heights when generating possible genotype sets and do not model artifacts such as stutter. Continuous methods make assumptions about the underlying behaviour of peak heights across all profiles to evaluate the probability of a set of peak heights in a given profile. These methods are designed to be used in expert systems and reduce the requirement for the manual assignment of peaks as allelic within evidence profiles, and hence reduce the opportunity for inconsistency in interpretation to occur. The calculations are sufficiently complex that software is needed. STRmix™ is one such continuous method that employs a fully continuous approach for DNA profile interpretation (http://strmix.esr.cri.nz/ [14]).

In 2015 the Scientific Working Group on DNA Analysis Methods published the SWGDAM Guidelines for the Validation of Probabilistic Genotyping Systems [1]. The developmental validation of a probabilistic genotyping system has been described by SWGDAM as "the acquisition of test data to verify the functionality of the system, the accuracy of statistical calculations and other results, the appropriateness of analytical and statistical parameters, and the determination of limitations" [1].

The developmental validation of STRmix™ was initially undertaken in 2012 following the requirements outlined within the FBI Quality Assurance Standards [15] by analysts at Forensic Science South Australia (FSSA) and the Institute of Environmental Science and Research Limited (ESR; http://www.esr.cri.nz/). FSSA is the South Australian State Forensic Science Laboratory and is accredited by the National Association of Testing Authorities, Australia. ESR is the New Zealand Government Crown Research Institute that undertakes forensic services for the NZ Police. ESR forensic DNA laboratories are accredited by the Laboratory Accreditation Board of the American Society of Crime Laboratory Directors (ASCLD/LAB) under the International Testing Program (ISO 17025).

ACCEPTED MANUSCRIPT

Within this paper we describe the developmental validation activities undertaken for STRmix™ following the SWGDAM recommendations [1]. Each of the guidelines is discussed in turn under their recommendation number.

Guideline 3.1 Publication of underlying scientific principles

All significant portions of the statistical algorithms and underlying scientific principles behind STRmix™ have been published in peer reviewed scientific literature. Within Table 1 we provide a summary of these models and algorithms and their references aligned with the software version in which they were introduced.

STRmix™ uses the quantitative information from an electropherogram (epg) such as peak heights (O), to calculate the probability of the profile given all possible genotype combinations (S_i). A value, or weight (w_i), is assigned to the normalised probability density $p(O|S_i)$. STRmix™ assigns a relative weight to the probability of the epg given each possible genotype combination at a locus. The weights across all combinations at that locus are normalised so that they sum to one. Therefore, a single unambiguous genotype combination at any locus would be assigned a weight of one.

STRmix™ describes the fluorescence observed in one or more epgs using a number of models that describe various properties of DNA profile behaviour. These are described as mass parameters and include a template for each contributor, a locus specific amplification efficiency for each locus, a replication efficiency for each PCR replicate, and a degradation for each contributor. This biological model is described in Bright et al. [16]. Profile degradation is modelled as exponential [17, 18]. Drop-in is optionally modelled as a gamma distribution following Puch-Solis [19]. In addition, STRmix™ employs a per allele stutter model, the parameters of which are based on empirical data [16, 20, 21].

Posterior distributions of mass parameters are sampled from using Markov chain Monte Carlo (MCMC). In general, MCMC is a numerical method used, in this case, to approximate an integral (typically multi-dimensional) of the observed data across all parameters. MCMC methods sample from the posterior distribution of the desired integral. It does so by using Markov chains that have the posterior distribution as their equilibrium distribution. These chains 'walk' around in a memoryless fashion using an acceptance-rejection criterion to determine whether to take a step or not. At each step that the chain accepts the integrand value, it is counted towards the integral. At each step that the chain rejects the integrand value at that proposed point, the current point is counted towards the integral. The rejection-acceptance rule used within STRmix™ is called the Metropolis-Hastings algorithm [22, 23]. The chain will then propose new steps in its search for a state that provides a reasonably high contribution to the integral until it finds a state which it will accept and move to. The statistical algorithms within STRmix™ are described in Taylor et al. [14].

STRmix™ does not use the reference profiles during profile deconvolution unless a reference from a known contributor is available (for example the complainant's DNA on their intimate samples collected as part of an investigation into a sexual assault). Where a reference profile is available from a person of interest (POI) a likelihood ratio may be calculated. It is the ratio of the probability of the observed crime stain (O) given each of two competing hypotheses, H_p and H_d, and given all the available information, I. Mathematically, we express this as:

$$LR = \frac{\Pr(O \mid H_p, I)}{\Pr(O \mid H_d, I)}$$

The likelihood ratio is calculated in STRmix™ incorporating values for F_{ST} (theta) using the subpopulation model of Balding and Nichols in 1994 [24], referred to as recommendation 4.2

ACCEPTED MANUSCRIPT

in the 1996 National Research Council report (NRCII) [25]. As a continuous extension to the classic incorportation of a theta value (which is typically a fixed value) STRmix™ can consider a distribution for theta. Propositions within STRmix™ are flexible. The defence proposition aligns with exclusion of the person of interest and typically considers an unknown, unrelated individual within a selected population. Where appropriate, alternate propositions are calculated under the defence propositions such as a sibling, parent, child or cousin of the person of interest [26]. Additionally STRmix™ can provide an *LR* based on the unifying theory. This is where rather than specifying either an unrelated individual or a nominated relative (sibling, parent etc.) under the defence propositon, all members of the population, including possible relatives of the POI can be considered by taking into account their prior probabilities based on population properties.

If one or more contributors is known to be present (i.e. conceded by both parties) then this information can be provided to STRmix™ at the deconvolution stage in order to assist in the deconvolution of the remaining questioned contributors. This assumption of a known contributor is then carried forward to the *LR* calculation. If a reference profile is not available from a person of interest, the profile may be compared directly with a database of known individuals [28] to identify investigative leads.

STRmix™ uses the highest posterior density (HPD) method for calculating an *LR* distribution, from which a quantile can then be chosen in order to report a bound of the probability density distribution [29, 30]. Within STRmix™ versions 2.3 onwards, the variability due to MCMC, the sampling variation inherent in generating allele frequency databases and the variability in F_{ST} (theta) can be estimated.

Guideline 3.2 Sensitivity and specificity studies

With respect to interpretation methods, sensitivity is defined as the ability of the software to reliably resolve the DNA profile of known contributors within a mixed DNA profile for a range of starting DNA template. The log(*LR*) for known contributors (H_p true) should be high and should trend to 0 as less information is present within the profile. Information includes the amount of DNA from the contributor of interest, conditioning profiles (for example the victim's profile on intimate samples), PCR replicates and decreasing numbers of contributors. Specificity is defined as ability of the software to reliably exclude known non contributors (H_d true) within a mixed DNA profile for a range of starting DNA template. The *LR* should trend upwards to neutral as less information is present within the profile. This is shown diagrammatically in Figure 1.

Specificity and sensitivity within STRmix™ were tested by calculating the *LR* for a number of GlobalFiler™ mixtures for both known contributors and known non-contributors [38]. Two, three and four contributor mixtures were constructed in varying proportions and amplified with varying amounts of template DNA as described in Table 2.

ACCEPTED MANUSCRIPT

Each sample was amplified in triplicate giving a total of 93 samples. Profiles were interpreted using STRmix™ v1.08 and *LR*s calculated for the known contributors and 186 non contributors. The propositions considered were:

H_p: The DNA originated from the person of interest and N-1 unknown contributors

H_d: The DNA originated from N unknown individuals

Where N was the number of contributors within the profile.

The plots of $\log_{10}(LR)$ versus DNA in the PCR (pg) produced for these comparisons are reproduced in Figures 2 through 6. The *LR*s produced from comparisons to known contributors (sensitivity tests) are signified by a blue point and those produced from comparisons to known non-contributors (specificity tests) are signified by a red point. A minimum value for $\log_{10}(LR)$ of -30 was used, and any *LR*s obtained that fell below this were given the value of -30. The lines on figures are given only as a visual indication of trends in the scattered results. The polygons seen give a visual indication of the spread of the *LR*s.

The plots in Figures 2 through 6[1] clearly demonstrate the sensitivity of STRmix™ for these mixtures by inspection of the spread of blue points. They show the range of expected *LR* values for contributors given the amount of input DNA (guideline 3.2.1.2). Type I errors (incorrect rejection of a true hypothesis) are clearly identified as blue points *below* the horizontal line of $\log_{10}(LR) = 0$. As expected, this is dependent on the amount of DNA per contributor and the number of contributors to a profile (guideline 3.2.1.1).

The plots also demonstrate the specificity of STRmix™ by inspection of the red points. The per contributor amount for H_d true contributors was taken as the average of the known contributors (guideline 3.2.2.2). Type II errors (failure to reject a false hypothesis) are clearly identified as reds points *above* the horizontal line of $\log_{10}(LR) = 0$. As for sensitivity tests, this depends on the amount of DNA within the profile and number of contributors (guideline 3.2.2.1). A series of much larger simulations (over 100 million *LR*s in total) exploring the specificity of STRmix™ and comparing it to theoretical expectations was carried out in [39]. This work found close alignment with expected and observed specificity from STRmix™ results.

The *LR* distributions for H_p true and H_d true are very well separated at high template for two contributor mixtures. As the number of contributors increased and the template lowered the two distributions converged on $\log_{10}(LR) = 0$. At high template STRmix™ correctly and reliably gave a high *LR* for true contributors and a low *LR* for false contributors. At low template or high contributor number STRmix™ correctly and reliably reported that the analysis of the sample tends towards uninformative or inconclusive.

There are some arguments [1-3] that a single point estimate of the *LR* as given in Figures 2 through 6 is actually the best and most theoretically sound estimate to give if the goal was an even handed and probabilistic treatment of uncertainty. In DNA profile interpretation we typically deliberately give an underestimate. In our own casework we predicate this with the words “at least” by which we mean that the number reported is either below or very near the bottom of the plausible range. Our experience suggests that this is done because of the desire by the courts and forensic scientists to avoid overstating the evidence. Over time the avoidance of overstatement has changed into what is probably a very considerable and

[1] Reprinted from Forensic Science International: Genetics, Volume 11, Duncan Taylor, Using continuous DNA interpretation methods to revisit likelihood ratio behaviour. Forensic Science International: Genetics, Pages 144-53, Copyright 2014, with permission from Elsevier.

ACCEPTED MANUSCRIPT

deliberate understatement. This has been facilitated, we believe, because DNA can afford this understatement given the magnitude of our likelihood ratios.

Sensitivity and specificity studies however have a scientific component to them and it may be desirable to use the best estimate available for these. If these studies are used to formulate decisions such as assigning terms to a verbal scale then it should be noted that they refer to the point estimate and not the lower bound. This has an additional and possibly undesirable consequence that if the verbal scale is calibrated from the sensitivity and specificity plots and then this scale is applied to the lower bound, the scale itself now possesses an element of conservativeness.

There is no specific SWGDAM guideline regarding error rate but it is one of the Daubert standards regarding the admissibility of expert evidence in the US [40], with acknowledgement that these guiding factors are neither exclusionary nor mandatory [41]. With respect to forensic DNA evidence, the concept of error rates and false inclusions[2] are similar and often confused. False inclusions would come under the specificity guideline of SWGDAM (guideline 3.2).

Our preferred procedure when using STRmix™ is that the analyst assesses whether a person of interest is excluded prior to either their assessment of the results of software calculations or interpretation of the profile using the software at all. Following this procedure, STRmix™ is being continually checked against human expectations and hence is being continually validated.

The number of *LR*s >1 is largely determined by the sample. Factors include the number of contributors and template. Considerable research has been undertaken that allows informed statements to be made about the false inclusion rate for any given sample [14, 28, 38, 42].

The *LR* is an assessment of the weight of evidence. It is developed by considering two propositions: one aligned with the prosecution and an alternative. *LR*s >1 support the prosecution proposition and those lower than one support the alternative.

To highlight the matter, consider that we make up a DNA mixture and hence we know the donors. Consider that this mixture is made from Smith and Brown. If we test the proposition that it contains Smith we expect a high *LR*. Suppose the *LR* is a billion. Is this correct? It is larger than one and as such that part is correct, but is a billion too large or too small or just right? The problem is that we do not have the 'true answer' and this cannot be obtained by any method.

False exclusions or false inclusions need to be interpreted in an *LR* framework. A false exclusion most nearly corresponds with an *LR* markedly less than one when H_p is true. A false inclusion most nearly corresponds with an *LR* markedly greater than one when H_d is true. *LR*s near one are best described as uninformative and this may be the correct indication of the value of the profile even for comparisons with true or false donors if the information present in the profile is limited.

When we consider a possible error rate for STRmix™ this must be balanced against the error rate for the entire DNA analysis process which can cause false inclusions and exclusions independent of the program. A false inclusion occurs when:

[2] Note that the terms 'false inclusion' and 'false exclusion', whilst commonly used, imply an error has occurred, when in reality the probability has been assigned as expected in accordance with theory. A better term would be 'support for a false proposition'; however we retain the terms 'false inclusion/exclusion' for general understanding.

ACCEPTED MANUSCRIPT

- A non-donor has the correct alleles by chance, in total or in large part, to explain the mixture.

It is very improbable that operator error (such as the inclusion of artifacts) or false information about a known contributor would cause a false inclusion.

The rate of false inclusion is increased in situations where the true DNA donor is a close relative of the POI[3]. Higher order mixtures, say four contributors, increase the chance of false inclusions. Depending on the type of profile and proportion of DNA corresponding to the POI, replication and the correct use of known contributors can reduce the chance of false inclusions (refer Figures 5 and 6). In addition, more loci used in the analysis will reduce the chance of false inclusion.

A false exclusion occurs when:

- The PCR reaction runs sufficiently poorly that the peak or stutter heights give misleading information, or
- A non-contributor is assumed to be present, or
- There is an operator error, notably inclusion of an artifact in the peak information used by STRmix™ at interpretation. An artifactual peak that has been retained within the input file will become part of the information used by STRmix™ to build genotype combinations. This will result in genotype combinations containing the artefact which will not align with the "true" genotypes of contributors to the profile. If the POI aligns with one of these altered (false) genotypes, this might result in a false exclusion.

There are a number of factors within STRmix™ under the control of the operator or the laboratory that affect errors. Most significantly are the two variance terms. If these are set too low they increase false exclusions. Set too high they increase false inclusions. These variances are set during a laboratory's internal validation by modelling the observed variation in allelic and stutter peak heights within a set of single source profiles of varying quality [31]. There are a number of diagnostics output by STRmix™ that allow a human check of the results including the genotypic weights ($p(O|S_j)$), the posterior mean of the variance terms and summary statistics of the MCMC (discussed later).

False inclusions and false exclusions may occur as a result of a combination of specific software, multiplex and operator factors. These are measurable. The most significant factors affecting them are the number of contributors, the number of known contributors, template levels, and the multiplex used. These factors are wrapped up in the *LR* in a way that the chance of producing an *LR* equal to or larger than the one in any particular case (LR_{case}) is less than $1/LR_{case}$. This relationship has been tested in trials of over 120 million cases of simulated false contributors and has always held [39].

The fraction of false donors exceeding LR_{case} has been termed the *p*-value [43-45] and it has been convincingly argued that they do not replace the *LR* [46]. Nor is the *p*-value a direct measure of the false inclusion rate since an *LR* for a false donor less than LR_{case} but still much larger than one would be considered a false inclusion.

[3] Exploratory experimental work (ongoing) undertaken in conjunction with USACIL and the FBI suggests that STRmix™ can handle most of these situations.

ACCEPTED MANUSCRIPT

We have no realistic way of measuring the false exclusion rate except to say that we have no undiagnosed instances of false exclusion.

The pink data within Figures 2 through 6 are the $\log_{10}(LR)$ values for non-donors. Any red data points above the line support H_p and may therefore be considered false inclusions. These data, which are towards the low template end, are slightly above the $\log_{10}(LR) = 0$ line, and are usually likelihood ratios between 1 and 1,000 ($\log_{10}(LR)$ 0 to 3). We term these low grade false inclusions since the *LR*s are low and near neutrality or only slightly to the inclusionary side. They occur when the false donor has the correct alleles for inclusion and hence they are a property of DNA rather than a consequence of the software not performing. There are no modelling improvements that could ever be made which will eliminate all *LR*s that falsely favour inclusion. This is because the phenomenon causing these results is not a modelling phenomenon, but is due to the available biological data. With any interpretation method there is a modelling component (including probability of dropout and drop-in) that will affect the magnitude of the *LR*, and this could mean the difference between a false inclusion and correct exclusion for a particular non-donor.

Uncertainty in the number of contributors

The determination of the effect of incorrectly assigning the number of contributors to a profile on the interpretation is not explicitly a requirement of developmental validation within the SWGDAM guidelines however this is something the STRmix™ development team has explored. The true number of contributors to a profile is always unknown. Analysts are likely to add contributors in the presence of an artifact, high stutter, or forward stutter peak. The assumption of one fewer contributor than that actually present may be made when contributors are at very low levels, are affected by peak masking and are dropping out (or visible below the analytical threshold), and in profiles where DNA is from individuals with similar profiles at the same concentrations.

The effect of the uncertainty in the number of contributors within STRmix™ has previously been reported for a number of profiles with *N* and *N*+1 assumed contributors, where *N* is the known number of contributors [28, 42]. The inclusion of an additional contributor beyond that present in the profile had the effect of lowering the *LR* for trace contributors within the profile. STRmix™ adds the additional (unseen) profile at trace levels which interacts with any known trace contribution, diffusing the genotype weights and lowering the *LR*. There was no significant effect on the *LR* of the major or minor contributor within the profiles.

Separately, the effect of underestimating the number of contributors to a profile (*N* versus *N*-1) has been investigated. Assigning the number of contributors as *N*-1 (where *N* is the known number of contributors) may result in an exclusionary *LR* for a known contributor. This occurs as STRmix™ is more likely to favour an incorrect genotype as it had to account for profiling information that does not explain the data accurately.

Guideline 3.2.3. Precision

STRmix™ assigns a relative weight to the probability of the epg given each possible genotype combination at a locus. These weights are determined by Markov chain Monte Carlo (MCMC) methods. The results of no two analyses will be completely the same using a stochastic system like MCMC. This is a phenomenon that is relatively new to forensic DNA interpretation, which up until this point has always had the luxury of, at least theoretically,

ACCEPTED MANUSCRIPT

completely reproducible interpretation results. The reproducibility of *LR*s calculated using STRmix™ has previously been explored by Bright et al. [35, 48].

The main cause of high variability within STRmix™ is non-convergence with the MCMC. Strictly, Markov chains do not converge. They explore the sampling space forever until they are told to stop. What we mean when we say Markov chains have reached convergence is that all chains are sampling from, and remain in, the 'same' high probability space.

Non-convergence is caused by the MCMC chains not being run for a sufficient number of accepts. The MCMC process starts with a number of iterations termed the 'burn-in'. Accepted genotypes from the burn-in process are not counted as they are likely to start at a low probability location. At the completion of burn-in the MCMC progresses to post burn-in. STRmix™ is set to run for a user defined number of burn-in and post burn-in accepts. STRmix™ uses accepts as a method of controlling how long the MCMC runs rather than total iterations. The reason for this is that by ensuring a defined number of accepts is obtained there is some degree of automatic scaling, whereby more complicated problems (with lower acceptance rates) will automatically run for more iterations, without the need for user intervention.

Non-convergence can be diagnosed using the Gelman-Rubin statistic [49, 50]. A high Gelman-Rubin statistic in conjunction with other diagnostics may be an indication of non-convergence. The solution to non-convergence is to run the problem for longer, i.e. for more MCMC accepts. We typically multiply the number of burn-in and post burn-in accepts by 10.

Putting aside non-convergence, there will always exist a level of MCMC run to run variability. This is simply due to the fact that the analysis is based on random number generation to function, which as the name suggests, is random. Ideally this variability in some output value is small in comparison to the size of the value itself and hence its impact on interpretation is minimal, and in some instances can be taken into account. Variation in *LR*s produced from STRmix™ analyses will depend on both the sample and the run parameters. Sample specific factors that affect precision include:

1. Number of contributors to a DNA profile
2. Quality/intensity of the DNA profile
3. Number of replicates available for analysis
4. The probability of the observed data given the genotype of the POI as a contributor (commonly referred to as the 'fit' of the POI)
5. The amount of STR information available in the profile.

STRmix™ run specific parameters that affect precision include

1. Number of iterations the MCMC has run
2. The number of Markov chains used
3. The step size of the Markov chain (termed the random walk standard deviation, RWSD).

The RWSD is a metaparameter that describes the standard deviation of the normal distributions from which the step size for each continuous parameter is drawn. We describe this metaparameter in more detail below. The effect of these run specific parameters on the variability of the *LR* is discussed in detail below.

ACCEPTED MANUSCRIPT

Number of MCMC chains and accepts

Increasing the number of either accepts or moves and adjusting the step size (the RWSD) can reduce but not totally remove the variation. There is, however, an associated runtime cost. Hence a trade-off between reproducibility and runtime must be struck.

The variation in the calculated *LR* due to sample factors and run specific parameters in STRmix™ has been explored for a number of different profiles with varying numbers of contributors and quality. Eight profiles were generated 'in silico'. These included one, two, three and four contributor profiles, in various template (high and low level) and proportions, in the GlobalFiler™ kit configuration. Each profile was interpreted in STRmix™ v2.3.07 ten times giving 80 runs in a batch. For each batch, a different combination of number of chains, burn-in and post burn-in accepts were trialled. In total, sixteen different chain/iteration combinations were tested generating data for over 1200 profile deconvolutions. The data was analysed to determine which chain/iteration combination resulted in the best reproducibility whilst also considering the impact on run time. A summary of the number of chain and accepts combinations considered is provided in Table 3.

A summary of the point estimate and 1st percentile (taking into account sampling variation in allele proportions and weights) of the distribution of $\log_{10}(LR)$ value (called the $\log_{10}(LR)$ and $\log_{10}$(HPD) respectively) for each of the ten replicates is provided in Appendix 1 (ordered by run parameter set) and Appendix 2 (ordered by profile). In addition summary statistics including the Gelman-Rubin diagnostic and posterior means of the allele and stutter variance constants are provided.

Inspection of the results in Appendix 1 and 2 show that as the profile is interpreted using more Markov chains and higher numbers of accepts, STRmix™ analyses are more likely to converge to the same parameter values, resulting in more reproducible *LR*s. The number of chains, total number of burn-in and post burn-in accepts and number of contributors all had an effect on run times. Consequently some interpretations were not completed after reviewing the wider results.

The *LR* for the two GlobalFiler™ single source profiles under all run configuration was identical. Due to the peak heights of these profiles dropout was not considered, resulting in a single genotype combination at each locus with weights equalling one. This was the expected result. The two person mixtures all gave *LR*s within one order of magnitude across all run configurations. There was an increase in observed *LR* variability within the three and four person mixtures with lower numbers of chains and lower total iterations.

A summary of the distribution of the $\log_{10}(LR)$ and $\log_{10}$(HPD) for ten replicates of the eight GlobalFiler™ profiles using eight chains with 50,000 burn-in accepts and 400,000 post burn-in MCMC accepts is provided in Figure 7.

Random walk standard deviation

At each iteration, the MCMC will have a particular set of values stored that describe the profile. When proposing new values for the next MCMC iteration the values will be chosen close to the current set of values. The distance of the step-size is based on a normal distribution with a mean set to the current value and a variance that dictates step-size. This is known as a Gaussian random walk. In a Gaussian walk the size of the step for any given variable is sampled randomly from $\sim N(0, sd^2)$. The size of sd^2 is dependent on the parameter and is tuned by the RWSD. Setting the RWSD too high will result in the values

ACCEPTED MANUSCRIPT

for the mass parameters that are used to describe the profile differing significantly between steps. This will allow the Markov chain to explore much more posterior topography but will result in many rejected iterations, where parameters have been chosen that do not describe the profile adequately, resulting in longer run times. It may also have the effect of requiring additional iterations to ensure fine scale posterior topography is adequately explored. A RWSD that is set too small will mean the larger scale topography may not be explored sufficiently resulting in a decrease in precision and, potentially, accuracy. While this suggests that values for RWSD which are either too high or too low can have determimental outcomes, in practise the MCMC can accommodate a broad range of values with little negative effect, but some potentially positive. A demonstration of the effect of varying the RWSD on the $\log_{10}(LR)$ for the four contributor high and low template GloabFiler™ profile is given in Figure 8. The profile was interpreted ten times each using three different values for the RWSD: 0.01, 0.005 and 0.0001. Interpretations were undertaken using eight chains with 50,000 burn-in accepts and 400,000 post burn-in MCMC accepts within STRmix™ version 2.4.02.

Inspection of Figure 8 shows that reproducible *LR*s (within one order of magnitude) were generated using both 0.01 and 0.005. The run times using a RWSD of 0.005 were significantly less however than when using 0.01. The *LRs* assigned using a RWSD of 0.0001 were highly variable indicating STRmix™ had not likely explored the probability space sufficiently. On balance the RWSD value of 0.005 afforded a reproducible LR with a low run time.

We have demonstrated that at least 50,000 burn-in and 400,000 post burn-in accepts across eight chains and a RWSD of 0.005 are suitable MCMC run parameters leading to reproducible *LR*s (within one order of magnitude) for many different types of profile. These settings are likely to be excessive for many one, two and some three person profiles. They will be sufficient for the remaining three and most four person profiles. Decreasing the number of accepts may mean that STRmix™ has not converged and, even with convergence, more variability is expected. Increasing the number of accepts has been shown to help with reproducibility for more complex profiles and will certainly mean higher run times. A summary of the approximate run times for different profiles interpreted using STRmix™ v2.4.02 on a laptop(Windows 7 64 bit, Intel Core i7-5600U CPU, 2.6 GHz, 16 GB RAM) are given in Table 4.

In calculating the *LR*, the numerator is the weighted sum of the probability of fewer genotype sets than the denominator. In many cases the numerator may have only one term. Since the denominator is the weighted sum across the probability of many genotype sets it has a stability to variation in the *LR*. However the numerator of the *LR* is more sensitive and this effect is at its greatest when the weight for the numerator genotype set(s) is low. This is most obvious for profiles where the inclusion of a POI requires an improbable peak height variability (observed as large heterozygote balances or dropout) i.e. where the fit of the POI to the profile is poor, or when the inclusion of the POI requires one or more drop-in events to have occurred (which will also increase *LR* variability due to allele proportion uncertainty).

We have demonstrated that higher order mixtures and profiles with low template and/or poor quality lead to a decrease in precision (replication in *LR* across replicates runs). As a general guide, we have observed that if the overall *LR* is greater than 1 and one or more of the locus *LR* values are less than or equal to 1, the POI is likely to have a poor fitting genotype to the observed data at these loci. In these cases the MCMC can be run at 10 or more times the

ACCEPTED MANUSCRIPT

default number of accepts and/or by increasing the RWSD in order to ensure improved precision.

In general, using the default settings as described above, when comparing a POI who is a good fit to the observed profile the difference between the smallest and largest *LR* is small in relation to the size of the *LR*. For profiles where an unlikely stochastic effect has occurred, or the POI is a poor fit to the profile then the difference between the largest and smallest *LR* may be higher but again small in relation to the *LR*. In the 1200 dataset described above (Appendix 2) the largest differences between the smallest and largest log(*LR*) using the recommended run settings was 1.3 fold. For profiles where an unlikely stochastic effect occurred, or the POI was a poor fit to the profile then the difference in log(*LR*) values can be above one. These situations can be minimised or eliminated via policies that suggest increasing iterations based on the profile data.

Reproducibility

Reproducibility is often stated as one of the main principles of the scientific method. A value is reproducible if there is a high degree of agreement between *LR*s run on the same input in different locations by different people. Reproducibility is one component of the precision of a measurement or test method. The other component is repeatability which is the degree of agreement of *LR*s on the same input by the same observer in the same laboratory.

Reproducibility is not intended to mean "exactly the same". Reproducibility means that the results are very similar within the limits of measurement or they lead to the same conclusion. In any real world application we must accept measurements to a degree of resolution and models of a limited level of complexity, or we must accept that the property we are measuring has a degree of variability. A level of uncertainty can exist in a measurement (or model) and yet the measurement can still be informative. In fact science and statistics rely on this fact.

If the same or a different operator interpreted the same input file using STRmix™ with the same random number seed[4] they would obtain exactly the same answer. So why then do we not set the seed and obtain exactly the same answer each time? Strangely this is dishonest repeatability. It would give a false impression of perfect precision. We prefer to give a true measure of our precision.

For very simple situations we can manually calculate the value of the *LR* from the mixture deconvolution part of the software. For the remaining situations, which comprise the vast majority of situations, we can predict limits and patterns but not exact values (for example by referring to plots such as those in Figures 2 through 6). If we retain the concept of a correct, but unknowable, answer, and we plot the output from STRmix™ against these limits the patterns can be assessed to draw conclusion about the function of the STRmix™ models.

Guideline 3.2.4. Case-type Samples

[4] No computer code can actually produce a truly random number. When you tell a computer to generate a sequence of random numbers it draws upon an algorithm that generates what looks like (to humans) as being random, but will eventually start repeating itself. If a computer was told to generate a set of 1000 random numbers twice then it would generate two lists of 1000 seeming random looking numbers, but the lists would be identical. The way to get around this is by providing the algorithm with a random starting value (or 'seed').

ACCEPTED MANUSCRIPT

The mixtures described in section 3.2.3 above (Precision) include a range of profile types typically encountered in casework. These profiles include single source and mixed DNA profiles containing up to four contributors generated for both Identifiler™ and GlobalFiler™ profiles. In addition, the developmental validation of STRmix™ involved the testing of a number of profiles generated using other kits and different capillary electrophoresis instruments (3130 and 3500) including ProfilerPlus®, PowerPlex® 21, Fusion, MiniFiler™, SGMPlus™ (profiles amplified at 34 cycles) and NGM Select™ (data not shown). Back stutter is explicitly modelled in all versions of STRmix™ and version 2.4 introduces to modelling of forward stutter. The profiles included contributors with shared alleles. STRmix™ models the variability of single peaks. The variance of this model is determined by directly modelling laboratory data. This is undertaken within STRmix™ using the Model Maker function.

Mock samples versus casework

Three experiments have previously been reported comparing the use of mock case samples and casework samples, or single source and mixed DNA profiles, to form interpretation policies [31, 51, 52]. None of the studies found any obvious difference between these sets. This may be the expectation from theory. Peak height is approximately linearly proportional to the number of template molecules sampled. The standard deviation in that peak height is proportional to the square root of the number of template molecules [53, 54].

If we posit that casework has degradation and inhibition effects not modelled with mock samples then we need to see how that would affect the peak heights and their variability. Degradation effectively reduces template from the starting extract but whatever number of quality template molecules survive this number is still the primary explanatory variable for peak height and relative variation. Therefore if 50% of the template was degraded we would expect this to behave similarly to a mock sample with half the template.

The effect of inhibition is more difficult to predict. Inhibitors may bind to the single stranded DNA or to the polymerases or any other co-factor. If they are simply removing template from the reaction then they would act the same as degradation. In any case what we tend to observe is that a whole locus or sets of loci amplify poorly and all peaks are lowered [55]. We could easily see how the relative variability might remain the same. STRmix™ explicitly models locus specific amplification efficiencies (LSAE). The LSAE model reflects the observation that even after template DNA amount, degradation and variation in peak height within loci are modelled, the peak heights between loci are still more variable than predicted, resulting in poorer amplification of some loci possibly due to inhibition. The variance of the LSAE model is determined by directly modelling laboratory data (see [31]). LSAE values for each STRmix™ interpretation appear within the results. We can demonstrate the relationship of LSAE values to average peak heights (APH) via a simple plot. The LSAE values should mimic the average peak heights of the locus if degradation is minimal, otherwise you will see a trend across sets of loci within dye colours according to molecular weight. This is demonstrated for one single source Identifiler™ profile in Figure 9. The differences in APH and LSAE in this figure are due to overall profile degradation which is modelled separately.

We have described above the theoretical expectations from the interpretation of inhibited and degraded profiles using STRmix™. Separately, we have interpreted a number of DNA profiles derived from various mock crime samples such as cigarette butts, bloodstains on wood, touched items and worn clothing. Inspection of the diagnostics from these STRmix™ interpretations including degradation and LSAE values align with our expectations (data not shown).

ACCEPTED MANUSCRIPT

Guideline 3.2.6. Accuracy

There is a subset of profiles where the expected answer may be replicated relatively easily by hand. By comparing the software output with the expected answer, the performance and limitations of the software may be examined. An understanding of the models behind the methods is essential for this process. Examples of where we can predict the answer include single source profiles, mixtures where the profile of a major contributor is unambiguous (major/minor) and mixtures of two contributors in equal proportions (balanced). STRmix™ has been shown to give the expected result in each case [48].

Functionality has been installed within STRmix™ to facilitate validation and performance checks. This includes the extended output and set seed functions. The extended output contains all of the parameters and calculated probabilities for each iteration within a run. The 'set seed' function turns off the random processes within STRmix™ and allows direct comparison of runs within and between different versions of the software. STRmix™ is built in two separate parts that communicate via a text file. The first part runs the MCMC, the second the *LR* calculation. Hence, in some version releases it is possible to test one part using an old output from the other part variously using the set seed or checks of the extended output to allow the direct comparison of outputs and lessen the validation load.

The following functionality and outputs from STRmix™ were verified by hand as part of the developmental validation tasks for each commercial version:

1. Expected allele and stutter heights given mass parameters
2. Expected peak heights of drop or 'Q' alleles given mass parameters
3. Probabilities given expected and observed peak heights and varying analytical thresholds
4. Locus specific amplification efficiency calculations
5. Summation of probabilities for each allele in a locus and across a profile
6. Summation of probabilities across multiple replicate profiles
7. Informed priors on mixture proportion
8. *LR* values where there are no assumed contributors
9. *LR* values for propositions with assumed contributors
10. *LR* values with varying theta values
11. Relatives calculations (where a relative is considered as an alternate contributor under H_d)
12. Sampling from the Beta distributions for theta
13. *LR* stratified point estimates
14. *LR* highest posterior density (HPD) interval values
15. Gaussian walk
16. Gelman-Rubin statistic, ESS, weight resampling
17. Drop-in function
18. Database search functionalities
19. Model maker.

The comparison of expected heights, probability and *LR* values was conducted in MS Excel or by comparison to results generated in the r_{HPD} package written by Professor James Curran in R [56].

The likelihood ratios calculated using STRmix™ have been compared to two probabilistic genotyping methods employing semi-continuous models and two binary methods of profile interpretation [48, 57]. Where a profile was able to be fully resolved or for single source

ACCEPTED MANUSCRIPT

profiles where dropout was not a consideration (weight, w_i, equals one at each locus) the *LR* between STRmix™ and the semi-continuous methods were comparable where they were using the same population genetics model. For mixed DNA profiles, generally STRmix™ resulted in higher *LR*s for ground truth known trials as continuous models use more of the profiling information (for example peak height information) compared with semi-continuous and binary interpretation methods.

Conclusion

Within this paper we describe the exercises undertaken as part of STRmix™ developmental validation following the SWGDAM guidelines for the validation of probabilistic genotyping software [1]. This work demonstrates that STRmix™ is suitable for its intended use for the interpretation of single source and mixed DNA profiles including profiles of a complex and low level nature.

A number of different parameters within STRmix™ that are known to affect *LR* reproducibility were investigated. We have interpreted over 1200 profiles and conclude that at least 50,000 burn-in and 400,000 post burn-in accepts across eight Markov chains and a RWSD of 0.005 are suitable STRmix™ run parameters leading to reproducible *LR*s (within one order of magnitude) for many different types of profile.

Having undertaken both internal and developmental validations following the SWGDAM guidelines we find them a good template within which to work. Recommendations 3.2.5 (control samples) and 3.2.6.2 (analysis of raw data files) are not applicable to STRmix™.

Acknowledgements

The authors would like to thank Johanna Veth (ESR), John Simich (Erie County, NY), Shawn Monpetit (San Diego, CA), Bjorn Sutherland (ESR) and two anonymous reviewers for their helpful comments that greatly improved this paper.

References

[1] Scientific Working Group on DNA Analysis Methods (SWGDAM). Guidelines for the Validation of Probabilistic Genotyping Systems. 2015.
[2] Budowle B, Onorato AJ, Callagham TF, Manna AD, Gross AM, Guerreri RA, et al. Mixture Interpretation: defining the relevant features for guidelines for the assessment of mixed DNA profiles in forensic casework. Journal of Forensic Sciences. 2009;54:810-21.
[3] Gill P, Buckleton J. Commentary on: Budowle B, Onorato AJ, Callaghan TF, della Manna A, Gross AM, Guerrieri RA, Luttman JC, McClure DL. Mixture interpretation: Defining the relevant features for guidelines for the assessment of mixed DNA profiles in forensic casework. J Forensic Sci 2009;54(4):810-21. Journal of Forensic Sciences. 2010;55:265-8.
[4] Buckleton JS, Triggs CM, Walsh SJ. DNA Evidence. Boca Raton, Florida: CRC Press; 2004.
[5] Dror IE, Charlton D, Peron AE. Contextual information renders experts vulnerable to making erroneous identifications. Forensic Science International. 2006;156:74-8.
[6] Thompson WC. Painting the target around the matching profile: the Texas sharpshooter fallacy in forensic DNA interpretation. Law, Probability and Risk. 2009;8:257-76.
[7] Scientific Working Group on DNA Analysis Methods (SWGDAM). SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories. 2010.

ACCEPTED MANUSCRIPT

[8] Gill P, Brenner CH, Buckleton JS, Carracedo A, Krawczak M, Mayr WR, et al. DNA commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures. Forensic Science International. 2006;160:90-101.
[9] Haned H. Forensim: An open-source initiative for the evaluation of statistical methods in forensic genetics. Forensic Science International: Genetics. 2011;5:265-8.
[10] Haned H, Gill P. Analysis of complex DNA mixtures using the Forensim package. Forensic Science International: Genetics Supplement Series. 2011;3:e79-e80.
[11] Balding DJ, Buckleton J. Interpreting low template DNA profiles. Forensic Science International: Genetics. 2009;4:1-10.
[12] Lohmueller K, Rudin N. Calculating the weight of evidence in low-template forensic DNA casework. Journal of Forensic Sciences. 2013;58(s1):s234-59.
[13] Mitchell AA, Tamariz J, O'Connell K, Ducasse N, Budimlija Z, Prinz M, et al. Validation of a DNA mixture statistics tool incorporating allelic drop-out and drop-in. Forensic Science International: Genetics. 2012;6:749-61.
[14] Taylor D, Bright J-A, Buckleton J. The interpretation of single source and mixed DNA profiles. Forensic Science International: Genetics. 2013;7:516-28.
[15] FBI Quality Assurance Standards for Forensic DNA Testing Laboratories. 2011.
[16] Bright J-A, Taylor D, Curran JM, Buckleton JS. Developing allelic and stutter peak height models for a continuous method of DNA interpretation. Forensic Science International: Genetics. 2013;7:296-304.
[17] Bright J-A, Taylor D, J.M. C, Buckleton JS. Degradation of forensic DNA profiles. Australian Journal of Forensic Sciences. 2013;45:445-9.
[18] Buckleton J, Kelly H, Bright J-A, Taylor D, Tvedebrink T, Curran JM. Utilising allelic dropout probabilities estimated by logistic regression in casework. Forensic Science International: Genetics. 2014;9:9-11.
[19] Puch-Solis R. A dropin peak height model. Forensic Science International: Genetics. 2014;11:80-4.
[20] Brookes C, Bright J-A, Harbison S, Buckleton J. Characterising stutter in forensic STR multiplexes. Forensic Science International: Genetics. 2012;6:58-63.
[21] Bright J-A, Curran JM, Buckleton JS. Investigation into the performance of different models for predicting stutter. Forensic Science International: Genetics. 2013;7:422-7.
[22] Hastings WK. Monte Carlo sampling methods using Markov chains and their applications. Biometrika. 1970;57:97--109.
[23] Metropolis N, Rosenbluth AW, Rosenbluth MN, Teller AH, Teller E. Equations of state calculations by fast computing machines. Journal of Chemical Physics. 1953;21:1087-91.
[24] Balding DJ, Nichols RA. DNA profile match probability calculation: how to allow for population stratification, relatedness, database selection and single bands. Forensic Science International. 1994;64:125-40.
[25] National Research Council Report: The evaluation of forensic DNA evidence. Washington DC: National Academy Press; 1996.
[26] Taylor D, Bright J-A, Buckleton J. Considering relatives when assessing the evidential strength of mixed DNA profiles. Forensic Science International: Genetics. 2014;13:259-63.
[27] Taylor D, Bright J-A, Buckleton J, Curran J. An illustration of the effect of various sources of uncertainty on DNA likelihood ratio calculations. Forensic Science International: Genetics. 2014;11:56-63.
[28] Bright J-A, Taylor D, Curran J, Buckleton J. Searching mixed DNA profiles directly against profile databases. Forensic Science International: Genetics. 2014;9:102-10.
[29] Taylor D, Bright JA, Buckleton J, Curran J. An illustration of the effect of various sources of uncertainty on DNA likelihood ratio calculations. Forensic Science International: Genetics. 2014;11:56-63.

ACCEPTED MANUSCRIPT

[30] Triggs CM, Curran JM. The sensitivity of the Bayesian HPD method to the choice of prior. Science & Justice. 2006;46:169-78.
[31] Taylor D, Buckleton J, Bright J-A. Factors affecting peak height variability for short tandem repeat data. Forensic Science International: Genetics. 2016;21:126-33.
[32] Bright J-A, Curran JM. Investigation into stutter ratio variability between different laboratories. Forensic Science International: Genetics. 2014;13:79-81.
[33] Kelly H, Bright J-A, Buckleton JS, Curran JM. Identifying and modelling the drivers of stutter in forensic DNA profiles. Australian Journal of Forensic Sciences. 2013;46:194-203.
[34] Taylor D, Bright J-A, McGoven C, Hefford C, Kalafut T, Buckleton J. Validating multiplexes for use in conjunction with modern interpretation strategies. Forensic Science International: Genetics. 2016;20:6-19.
[35] Bright J-A, Stevenson KE, Curran JM, Buckleton JS. The variability in likelihood ratios due to different mechanisms. Forensic Science International: Genetics. 2015;14:187-90.
[36] Taylor D, Bright JA, Buckleton J. The 'factor of two' issue in mixed DNA profiles. Journal of Theoretical Biology. 2014;363:300-6.
[37] Taylor D, Buckleton J, Bright J-A. Does the use of probabilistic genotyping change the way we should view sub-threshold data? Australian Journal of Forensic Sciences. 2015:DOI:10.1080/00450618.2015.1122082.
[38] Taylor D. Using continuous DNA interpretation methods to revisit likelihood ratio behaviour. Forensic Science International: Genetics. 2014;11:144-53.
[39] Taylor D, Buckleton J, Evett I. Testing likelihood ratios produced from complex DNA profiles. Forensic Science International: Genetics. 2015;16:165-71.
[40] Daubert et al v Merrell Dow Pharmaceuticals Inc., 509 US 579 (1993). 1993.
[41] Kumho Tire Co. Ltd et al. v. Carmichael et al. In: Court USS, editor. 526 US 1371999.
[42] Bright J-A, Curran JM, Buckleton JS. The effect of the uncertainty in the number of contributors to mixed DNA profiles on profile interpretation. Forensic Science International: Genetics. 2014;12:208-14.
[43] Dørum G, Bleka Ø, Gill P, Haned H, Snipen L, Sæbø S, et al. Exact computation of the distribution of likelihood ratios with forensic applications. Forensic Science International: Genetics. 2014;9:93-101.
[44] Gill P, Haned H. A new methodological framework to interpret complex DNA profiles using likelihood ratios. Forensic Science International: Genetics. 2013;7:251-63.
[45] Haned H, Dorum G, Egeland E, Gill P. On the meaning of the likelihood ratio: is a large number always an indication of strength of evidence? 25th Congress of the International Society for Forensic Genetics. Melbourne, Australia2013.
[46] Kruijver M, Meester R, Slooten K. p-Values should not be used for evaluating the strength of DNA evidence. Forensic Science International: Genetics.16:226-31.
[47] Taylor D, Buckleton J. Do low template DNA profiles have useful quantitative data? Forensic Science International: Genetics. 2015;16:13-6.
[48] Bright J-A, Evett IW, Taylor D, Curran JM, Buckleton J. A series of recommended tests when validating probabilistic DNA profile interpretation software. Forensic Science International: Genetics. 2015;14:125-31.
[49] Gelman A, Rubin DB. Inference from Iterative Simulation Using Multiple Sequences. Statistical Science. 1992;7:457-511.
[50] Gelman A, Carlin JB, Stem HS, Rubin DB. Bayesian data analysis. New York: Chapman & Hall; 1995.
[51] Bright J-A, McManus K, Harbison S, Gill P, Buckleton J. A comparison of stochastic variation in mixed and unmixed casework and synthetic samples. Forensic Science International: Genetics. 2012;6:180-4.

ACCEPTED MANUSCRIPT

[52] Bright J-A, Turkington J, Buckleton J. Examination of the variability in mixed DNA profile parameters for the Identifiler(TM) multiplex. Forensic Science International: Genetics. 2009;4:111-4.
[53] Gill P, Curran J, Elliot K. A graphical simulation model of the entire DNA process associated with the analysis of short tandem repeat loci. . Nucleic Acids Research. 2005;33:632-43.
[54] Weusten J, Herbergs J. A stochastic model of the processes in PCR based amplification of STR DNA in forensic applications. Forensic Science International: Genetics. 2012;6:17-25.
[55] Bright J-A, Cockerton S, Harbison S, Russell A, Samson O, Stevenson K. The effect of cleaning agents on the ability to obtain DNA profiles using the Identifiler™ and PowerPlex® Y multiplex kits. Journal of Forensic Sciences. 2011;56:181-5.
[56] R Development Core Team. R: A language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing; 2004.
[57] Bille TW, Weitz SM, Coble MD, Buckleton JS, Bright J-A. Comparison of the performance of different models for the interpretation of low level mixed DNA profiles. ELECTROPHORESIS. 2014;35:3125-33.

Figure Captions

Figure 1. A diagram showing the desired performance of a method of mixture interpretation.

Figure 2 *LR*s produced for two person mixtures

Figure 3 *LR*s produced for three person mixtures

Figure 4 *LR*s produced for four person mixtures

Figure 5 *LR*s produced for four person mixtures using three replicate amplifications

Figure 6 *LR*s produced for four person mixtures using three replicate amplifications and assuming three out of the four known contributors in each analysis

Figure 7: $\text{Log}_{10}(LR)$ (○) and $\log_{10}(\text{HPD})$ (◊) of ten replicate interpretations of different GlobalFiler™ profiles, interpreted using eight chains with 50,000 burn-in accepts and 400,000 post burn-in MCMC accepts

Figure 8: $\text{Log}_{10}(LR)$ of ten replicate interpretations of the high template (blue bars) and low template (grey bars) four person GlobalFiler™ profiles, interpreted using eight chains with 50,000 burn-in accepts and 400,000 post burn-in accepts and varying RWSD. Runtime (in minutes) is indicated by the black lines, which correspond to the right hand vertical axis.

Figure 9: Plot of APH (bars) and LSAE value (line) for each locus ordered by molecular weight for a single source Identifiler™ profile

Tables

ACCEPTED MANUSCRIPT

Table 1: A summary of the scientific principles, the STRmix™ version in which they were introduced and their publications

Algorithms, scientific principles and methods	Version introduced	Refe
Allele and stutter peak height variability as separate constants within the MCMC	V2.0	[14]
Peak height variability as random variables within the MCMC	V2.3	[31]
Model for calibrating laboratory peak height variability	V2.0	[31]
Application of a Gaussian random walk to the MCMC process	V2.3	Des
Modelling of back stutter by regressing stutter ratio against allelic designation	V2.0	[16,
Modelling of back stutter by regressing stutter ratio against *LUS*	V2.3	[16,
Modelling of forward stutter	V2.4	[34]
Modelling of allelic drop-in using a simple exponential or uniform distribution	V2.0	[14]
Modelling of allelic drop-in using a Gamma distribution	V2.3	[19]
Modelling of degradation and dropout	V2.0	[17]
Modelling of the uncertainties in the allele frequencies using the HPD	V2.0	[30]
Modelling of the uncertainties in the MCMC	V2.3	[29,
Database searching of mixed DNA profiles	V2.0	[28]
Familial searching of mixed DNA profiles	V2.3	[26]
Relatives as alternate contributors under the defence proposition	V2.3	[26]
Modelling expected stutter peak heights in saturated data	V2.3	[34]
Taking into account the ‘factor of two’ in *LR* calculations	V2.3	[36]
Model for incorporating prior beliefs in mixture proportions	V2.3	[37]

Table 2: A summary of the experimental set up

Sample	Mixture proportions for contributor				Total DNA added to PCR (pg)
	One	Two	Three	Four	
1-3	0.50	0.50	-	-	400,200,50
4-6	0.33	0.67	-	-	
7-9	0.20	0.80	-	-	
10-11	0.17	0.83	-	-	
13-15	0.09	0.91	-	-	
16-18	0.33	0.33	0.33	-	
19-21	0.50	0.33	0.17	-	
22-26	0.25	0.25	0.25	0.25	400,200,50,20,10
27-31	0.40	0.30	0.20	0.10	

ACCEPTED MANUSCRIPT

653 Table 3: Summary of run parameters (chains, burn-in and post burn-in accepts) undertaken
654 to interpret the sixteen profiles in order to explore the precision of STRmix™.

Set	Chains	Burn-in accepts	Post burn-in accepts
1	4	50,000	150,000
2	4	500,000	200,000
3	4	50,000	2,000,000
4	4	500,000	2,000,000
5	8	50,000	400,000
6	8	500,000	400,000
7	8	50,000	4,000,000
8	8	500,000	4,000,000
9	16	50,000	800,000
10	16	500,000	800,000
11	16	50,000	8,000,000
12	16	500,000	8,000,000
13	20	50,000	1,000,000
14	20	500,000	1,000,000
15	20	50,000	10,000,000
16	20	500,000	10,000,000

655

656

657 Table 4: Approximate time taken to complete interpretation of various GlobalFiler™ profile
658 types within STRmix™ (hours:minutes:seconds), 8 chains with 50,000 burn-in and 400,000
659 post burn-in MCMC accepts, and RWSD of 0.005.

Number of contributors	High template profile	Low template profile
Single contributor	0:00:12	0:00:12
Two contributors	0:00:34	0:01:13
Three contributors	0:16:52	0:16:42
Four contributors	1:53:37	1:42:50

660

661

662

663

664

665

666

667

#107

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

Queensland Government

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	14/12/2012		1st Issue

Document sign off

This document has been **approved** by:

Name	Position	Signature	Date
Cathie Allen	Managing scientist	[redacted]	17.12.12.

Approval provided verbally on 6.12.12.

This document has been **endorsed** by:

Name	Position	Signature	Date
Justin Howes	Team Leader FRIT	[redacted]	14.12.12

Name	Position	Signature	Date
Paula Brisotto	Team Leader ER&Q	[redacted]	14-12-12

Name	Position	Signature	Date
Sharon Johstone	Senior Scientist Intell Team	[redacted]	14/12/12

Name	Position	Signature	Date
Amanda Reeves	Senior Scientist Reporting 1	[redacted]	14/12/12

Name	Position	Signature	Date
Emma Caunt	A/Senior Scientist Reporting 2	[redacted]	14/12/12

Name	Position	Signature	Date
Adrian Pippia	A/Senior Scientist ER	[redacted]	14-12-12

Name	Position	Signature	Date
Allan McNevin	Senior Scientist Analytical	[redacted]	14/12/2012

Name	Position	Signature	Date
Thomas Nurthen	Senior Scientist Q & P	[redacted]	17/12/2012

Contents

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 DNA Analysis Unit. A limit of reporting threshold of 40RFU will be adopted for analysis of extracted DNA samples amplified at either 25µL or 12.5µL total PCR volumes.

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 0.5ng, 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 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)
- 1.5mL 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, 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 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.
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 4.6) 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 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

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 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 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

[(2.0µl 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 AmpFℓSTR® Profiler Plus® and AmpFℓSTR® 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

$$\mathbf{LOD = \mu_{PK} + 3\sigma_{PK}}$$

The limit of reporting (LOR) also known as the analytical threshold (AT) was calculated from Equation 2[8].

Equation 2

$$\mathbf{LOR = \mu_{PK} + 10\sigma_{PK}}$$

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 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 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, 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 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	2.41	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**	**23.40**
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

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.

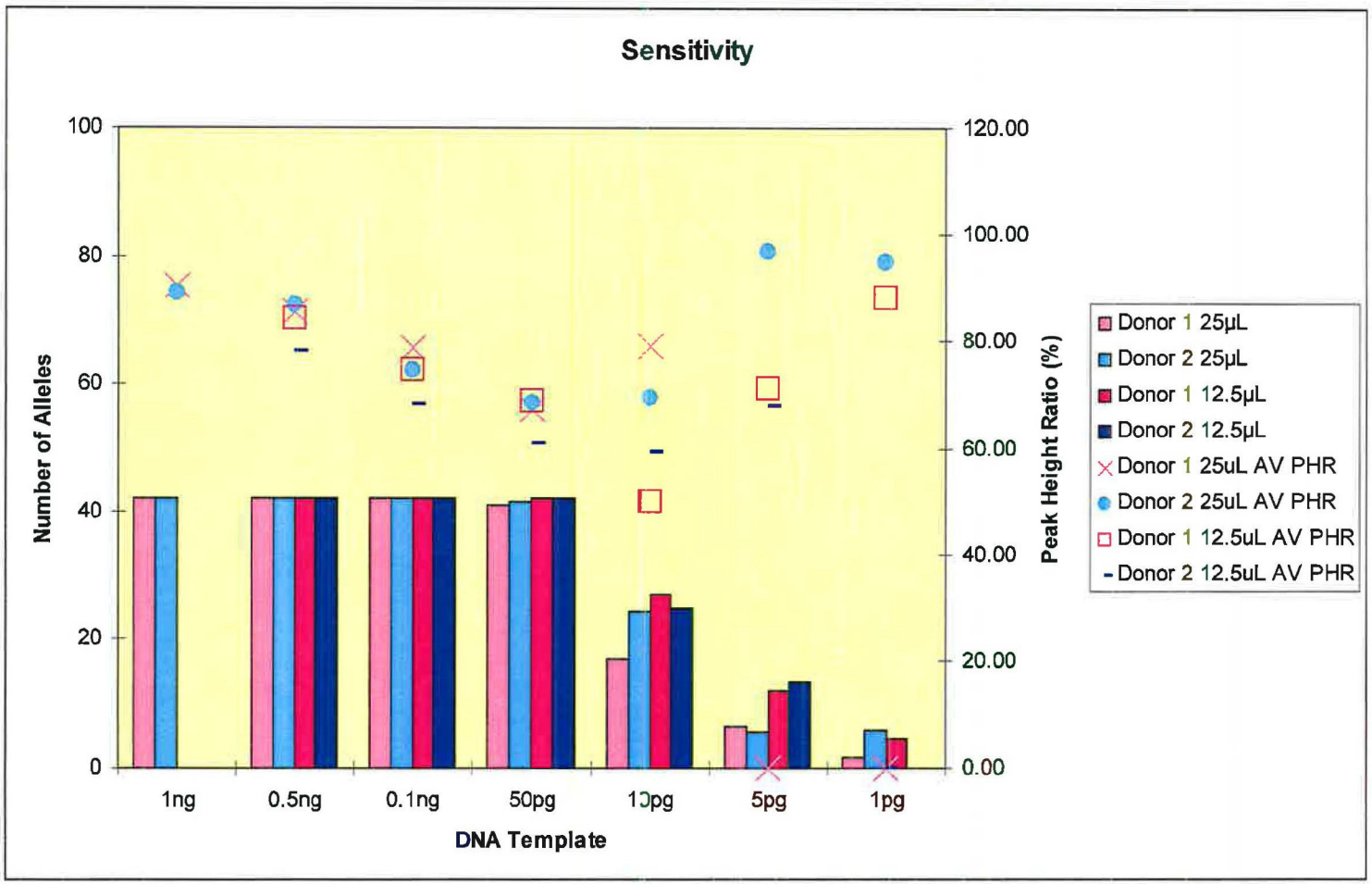


Figure 1 - Average number of alleles for each donor at each DNA template at amplification volumes of 25µL and 12.5µL. AV PHR = Average Peak Height Ratio

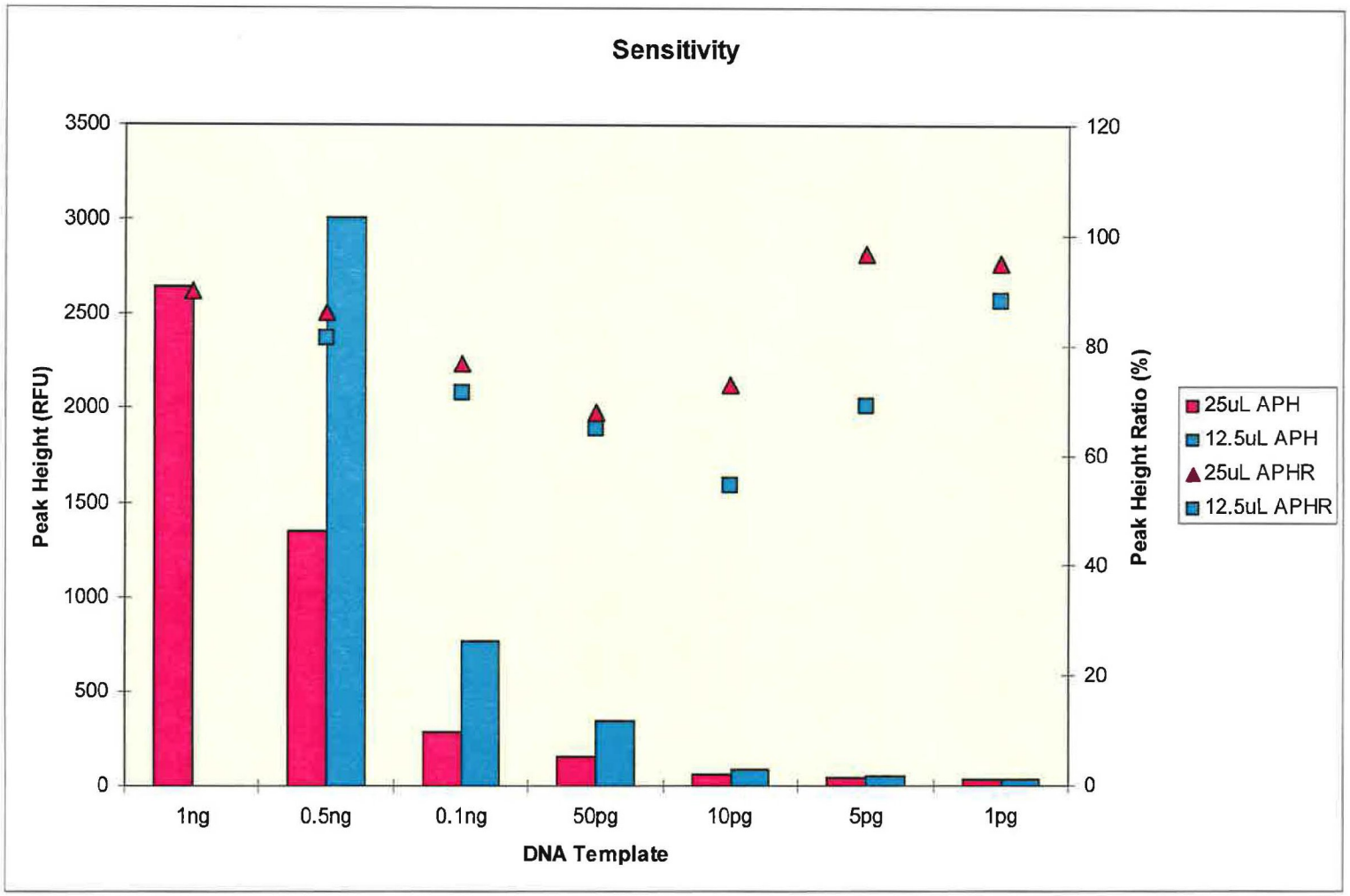


Figure 2 Average peak height and average peak height ratio for each DNA template

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.

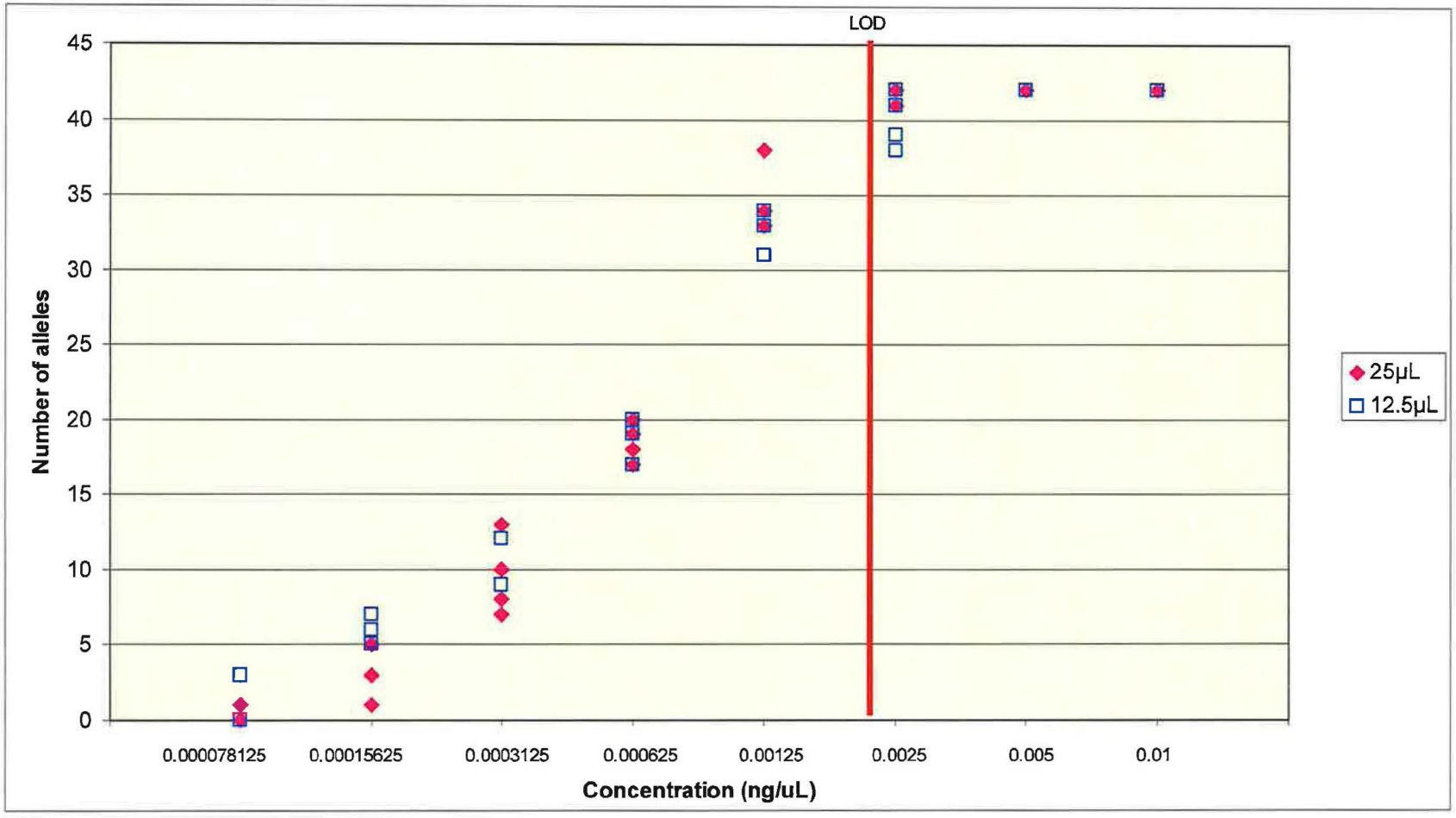


Figure 3 - Comparison of sample concentration vs allele count for 25µL and 12.5µL total PCR volumes.

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.

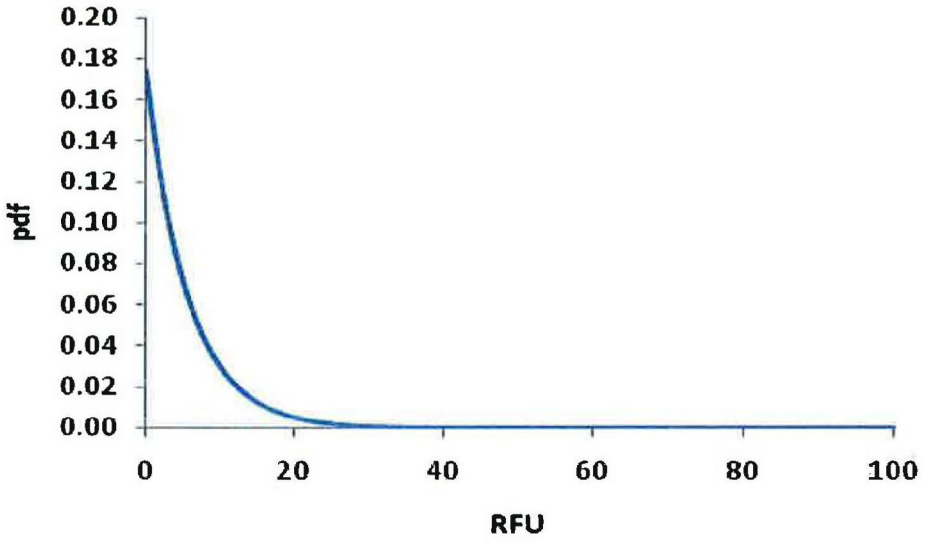


Figure 4 - Probability of Drop in for 25µL total PCR volume.

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.

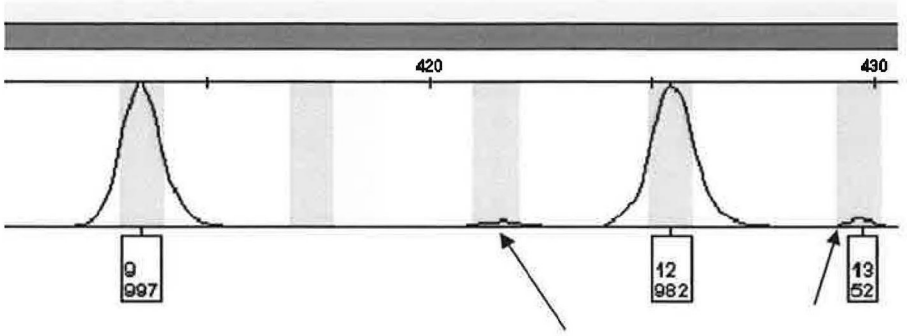


Figure 5 - Example of stutter and over stutter.

Promega supplied a stutter text file (using $\mu + 3\sigma$[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 (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 17.

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.

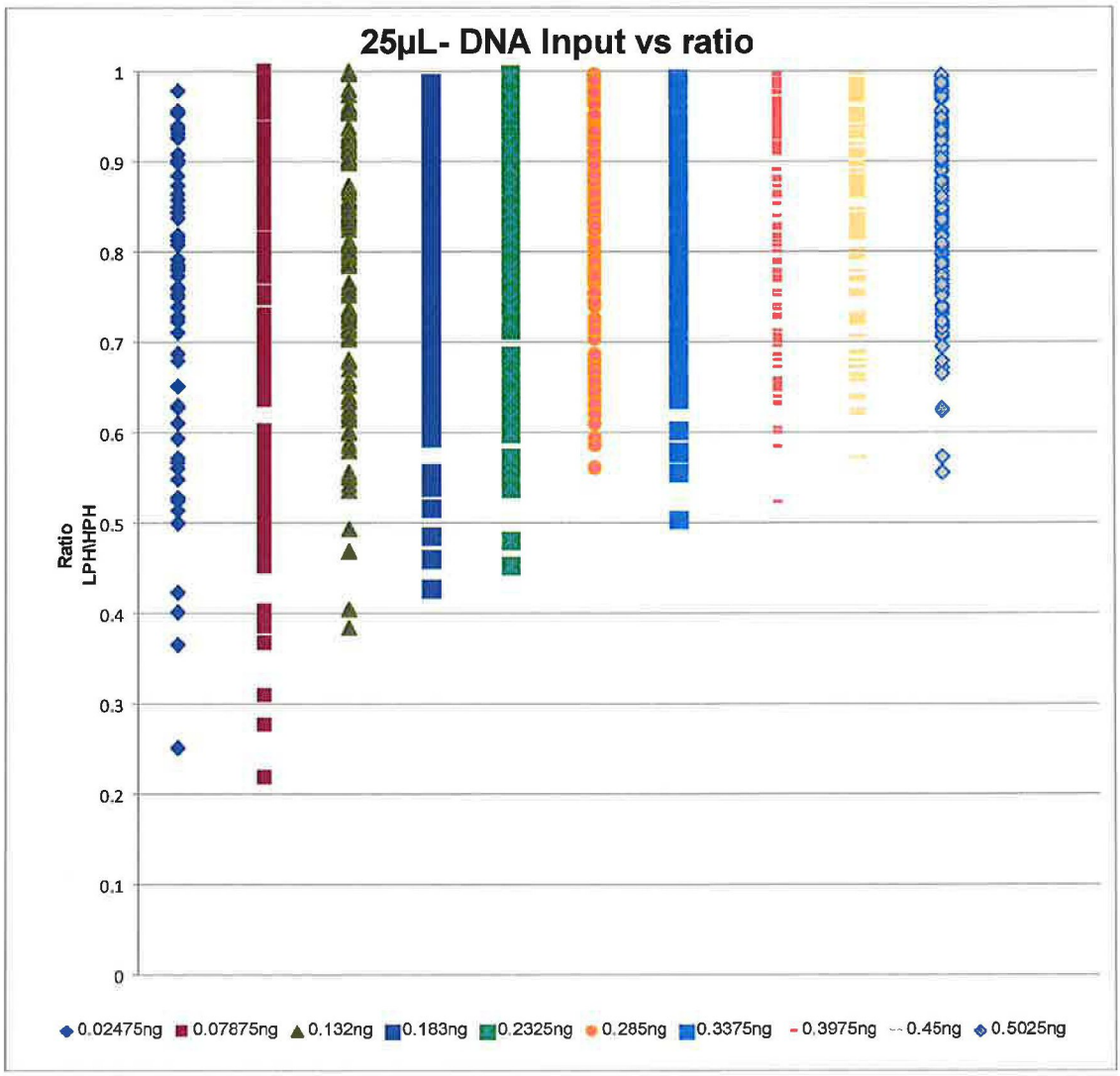


Figure 6 - 25µL total PCR volume, Peak balance vs total input DNA

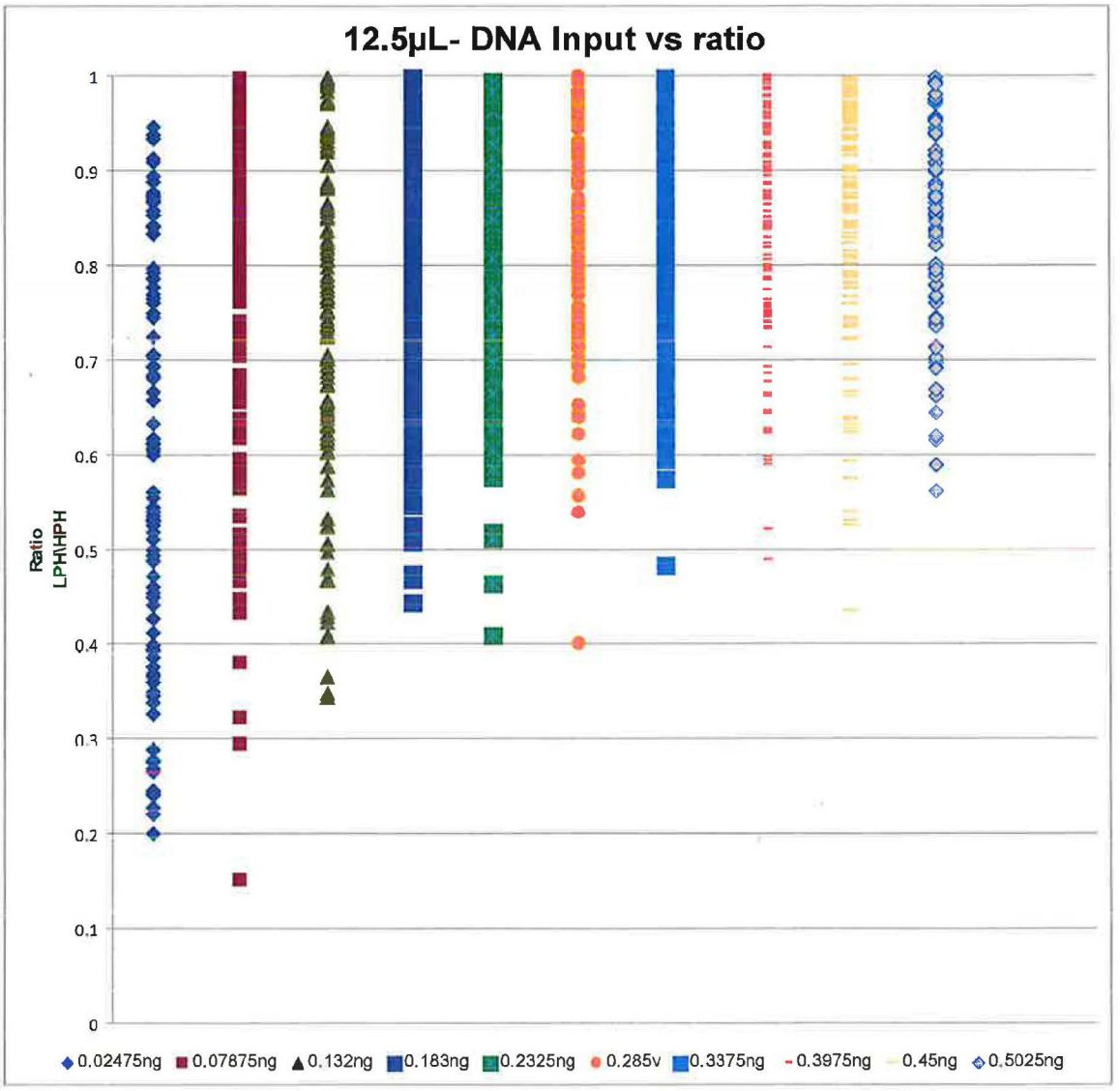


Figure 7 - 12.5µL Total PCR volume - Peak balance vs total input DNA.

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

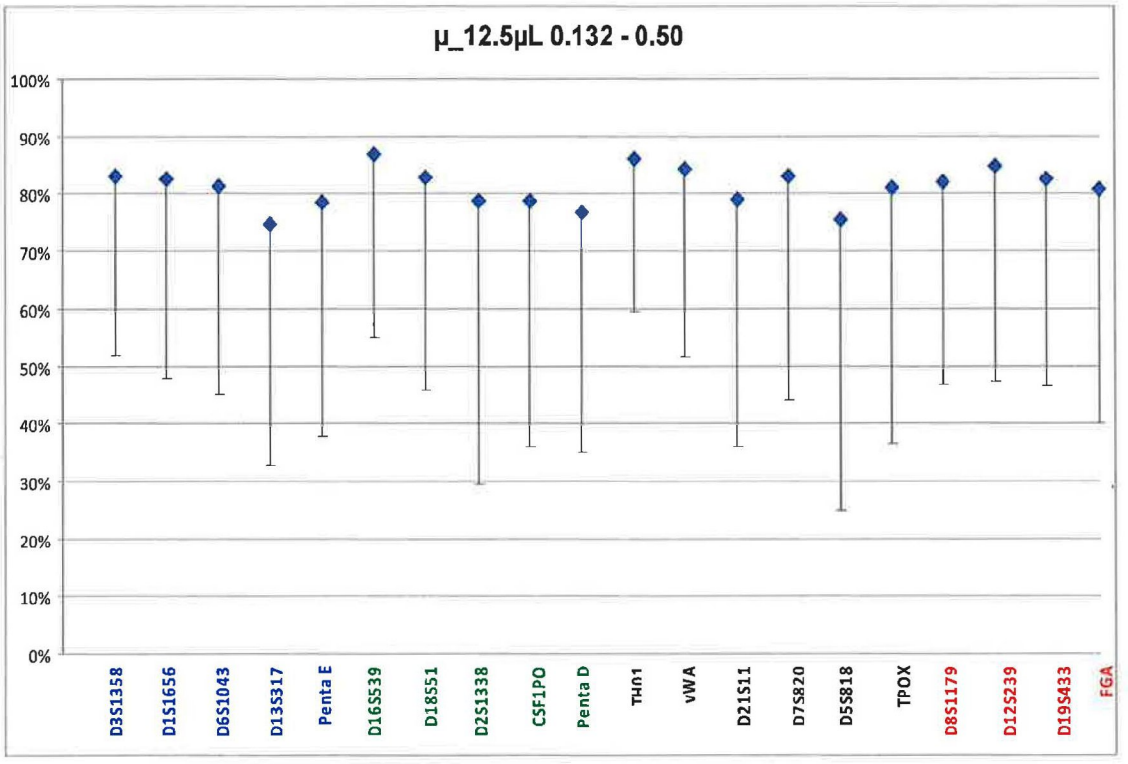


Figure 8 - 12.5µL total PCR volume µPHR per Loci

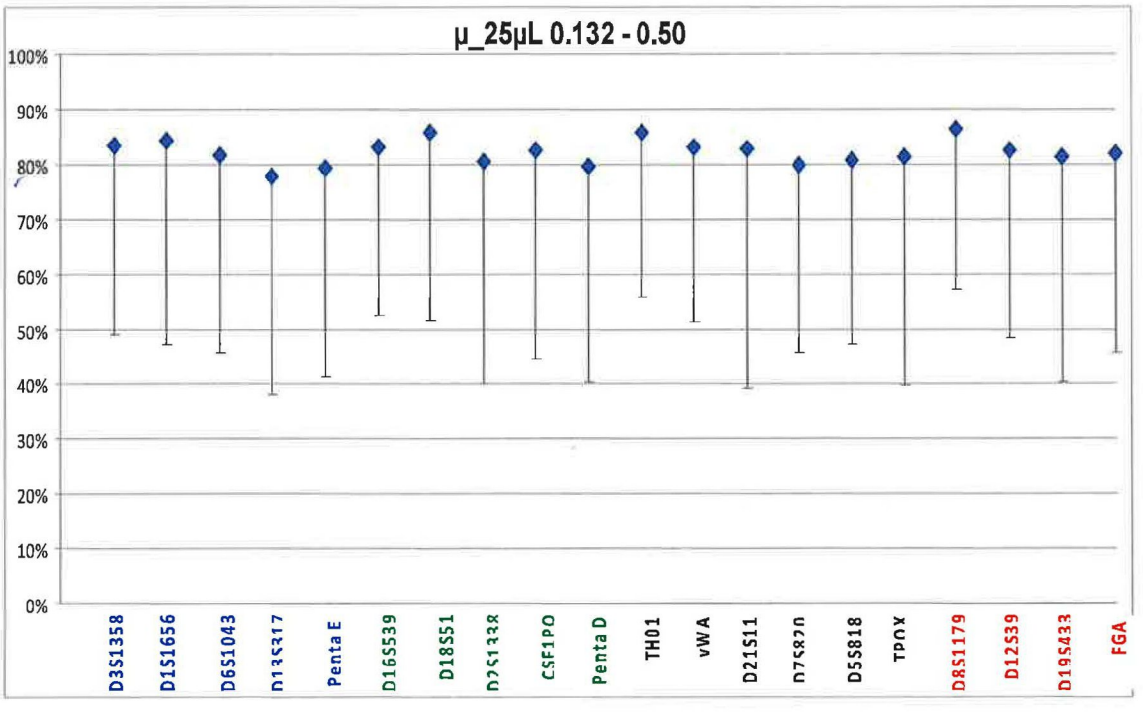


Figure 9 - 25µL total PCR volume µPHR per Loci

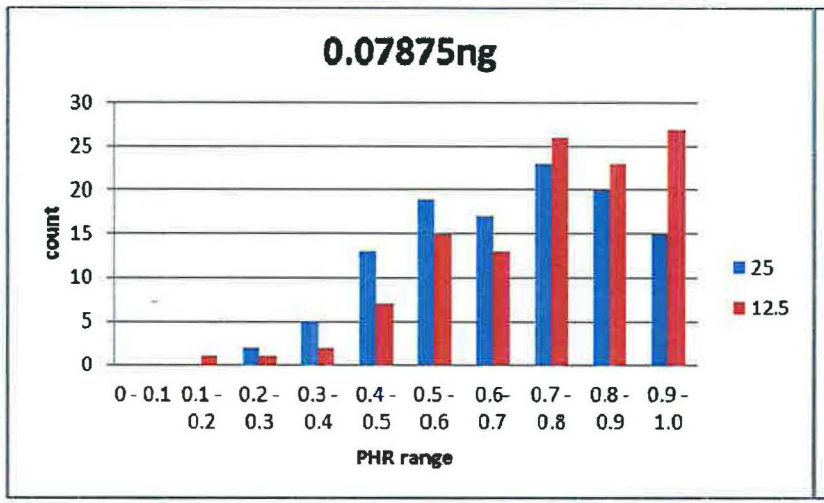


Figure 10 - The count of allele pairs per 0.1 PHR bin for 0.02475ng.

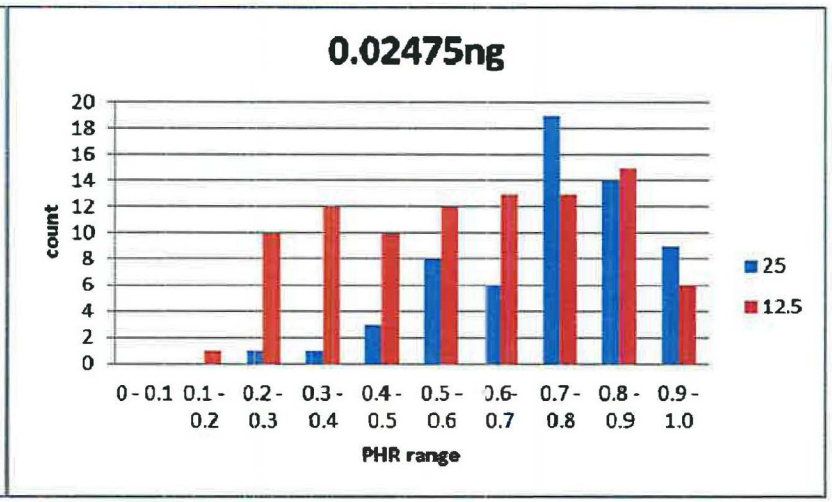


Figure 11 - The count of allele pairs per 0.1 PHR bin for 0.07875ng.

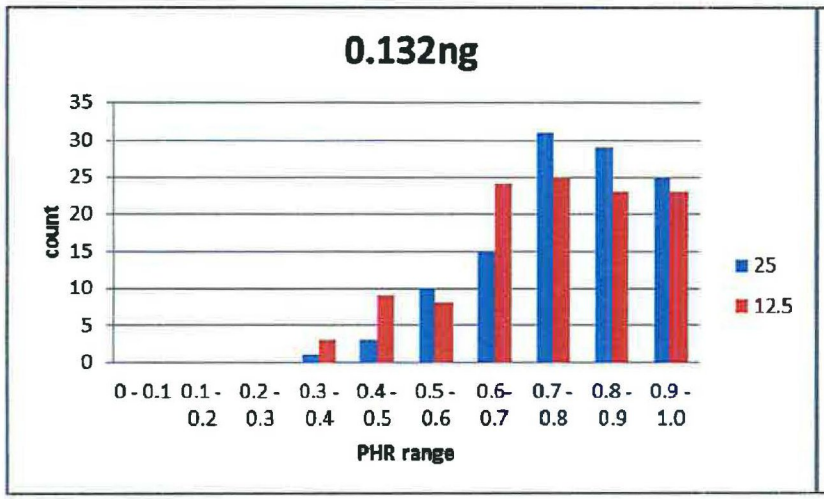


Figure 12 - The number of allele pairs per 0.1 PHR bin for 0.132ng.

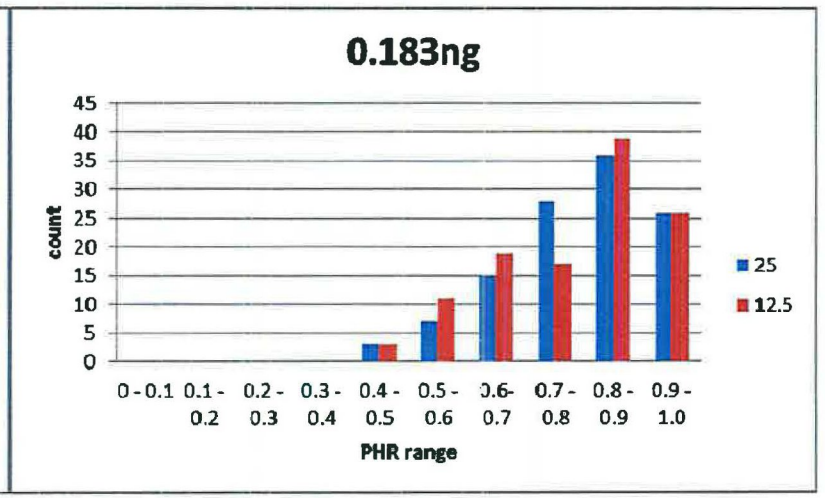


Figure 13 - The count of allele pairs per 0.1 PHR bin for 0.183ng.

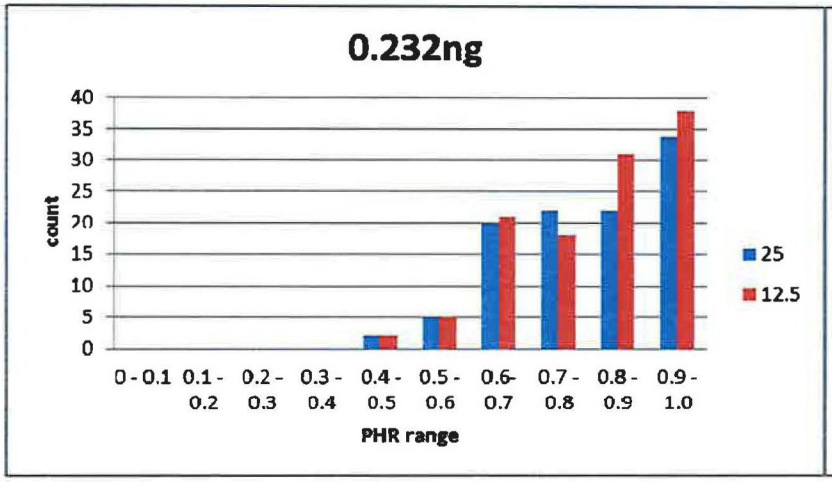


Figure 14 - The count of allele pairs per 0.1 PHR bin for 0.232ng.

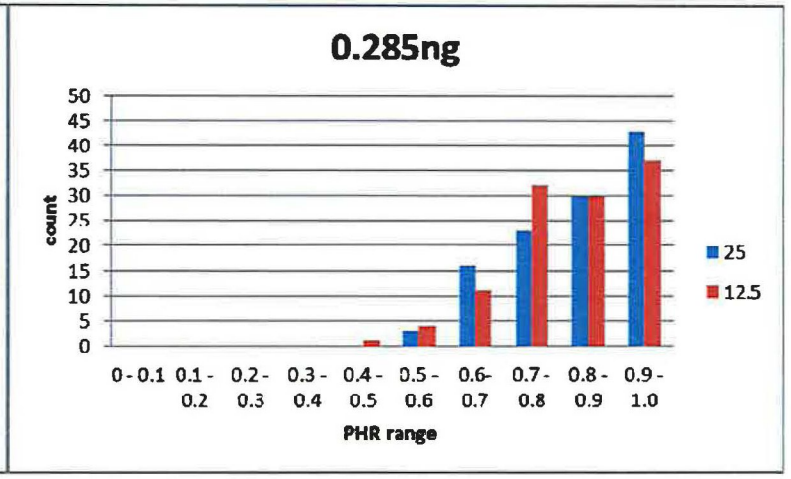


Figure 15 - The number of allele pairs per 0.1 PHR bin for 0.285ng.

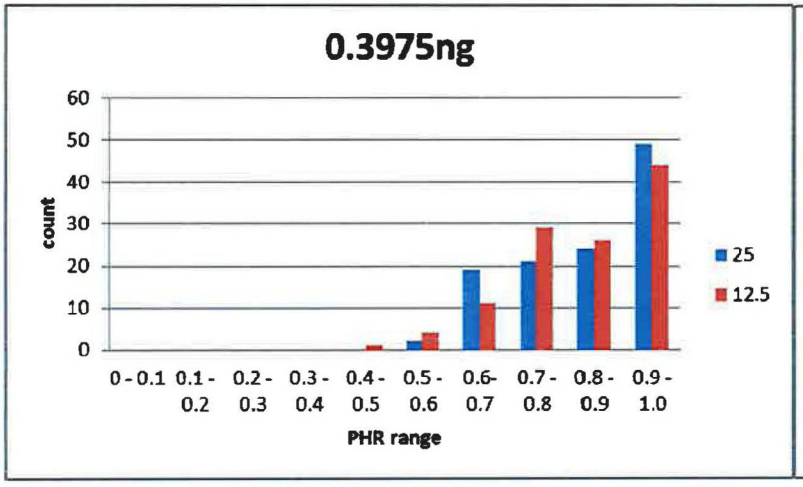


Figure 16 - The count of allele pairs per 0.1 PHR bin for 0.3375ng.

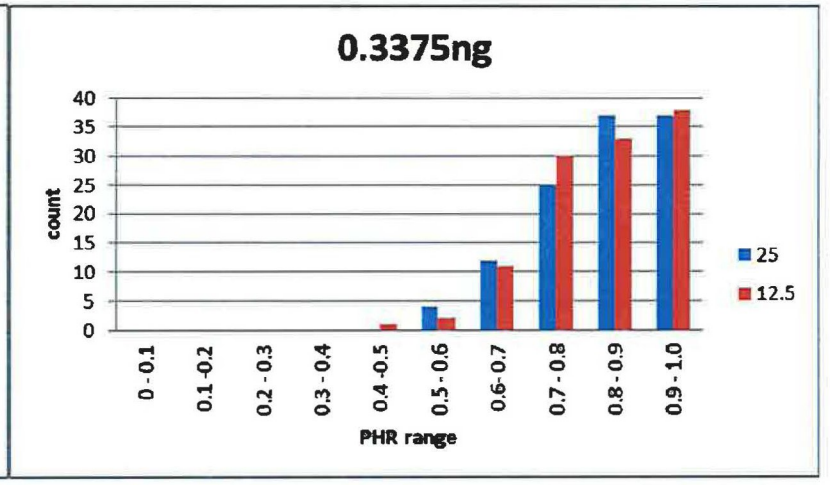


Figure 17 - The count of allele pairs per 0.1 PHR bin for 0.3975ng.

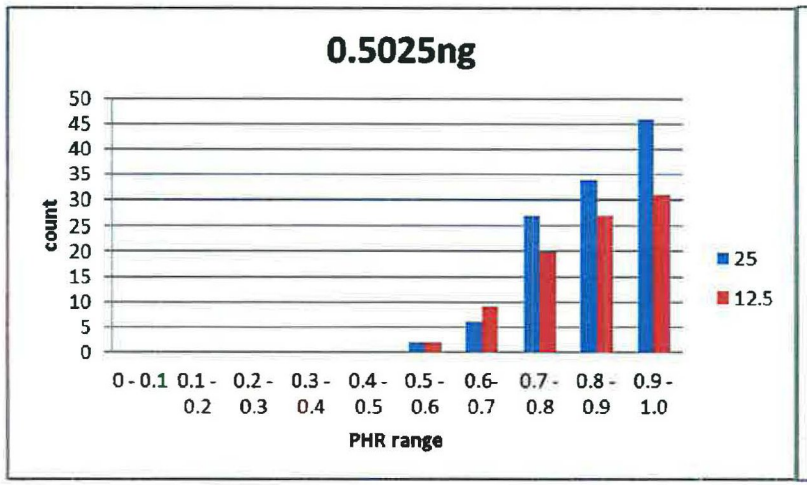


Figure 18 - The count of allele pairs per 0.1 PHR bin for 0.45ng.

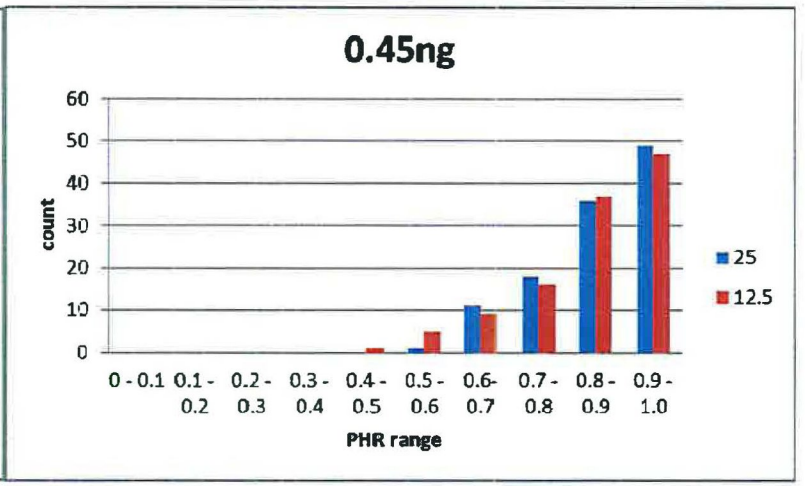


Figure 19 - The count of allele pairs per 0.1 PHR bin for 0.5025ng.

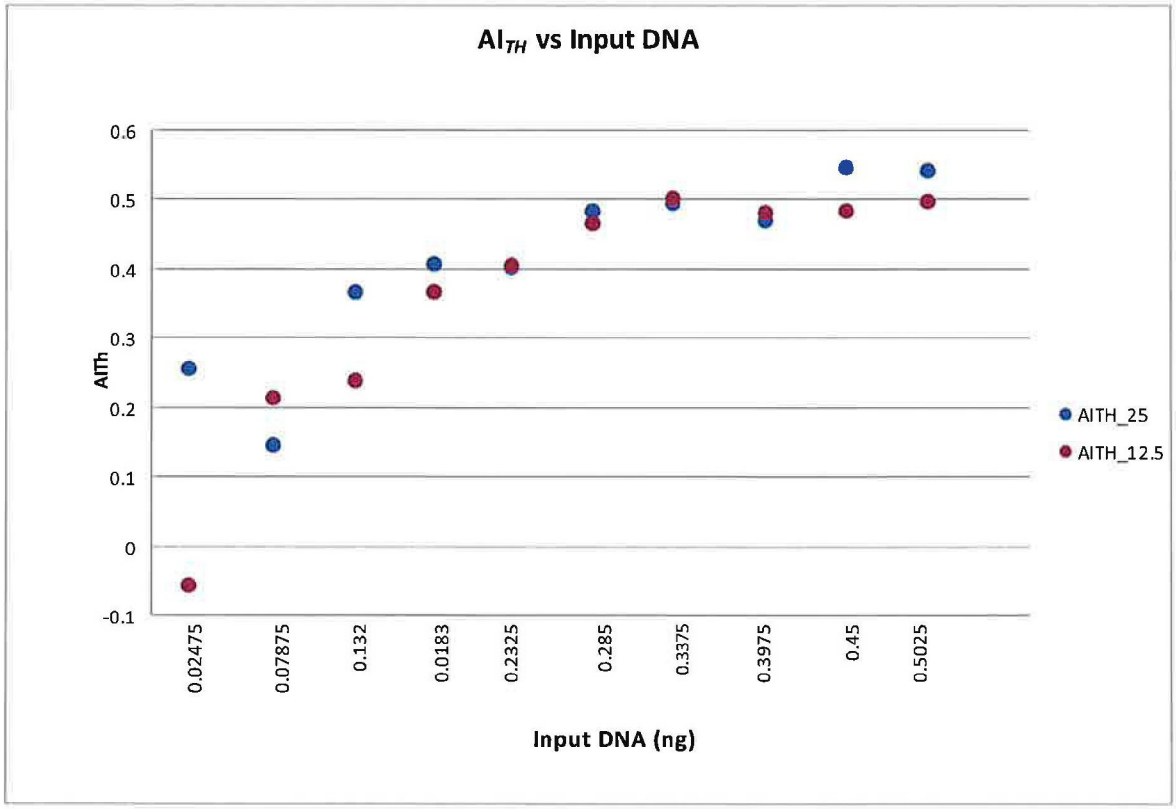


Figure 20 - Calculated AI_{TH} vs DNA template

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.

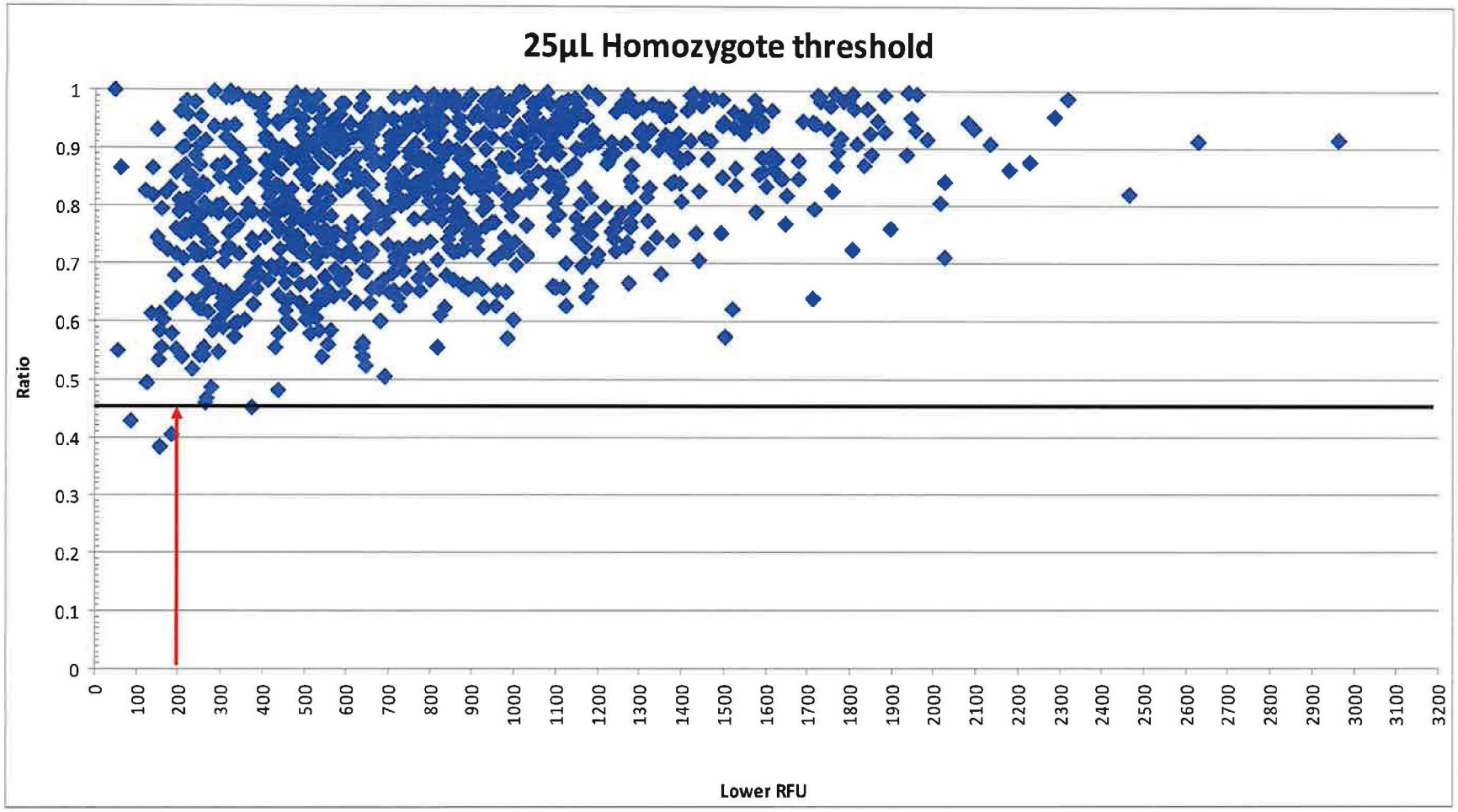


Figure 21 - Plot of the peak height ratio vs RFU of lower peak for 25µL. The black horizontal line is the AI_{TH}. The red vertical line is set to encompass the majority of points that fall below the AI_{TH}.

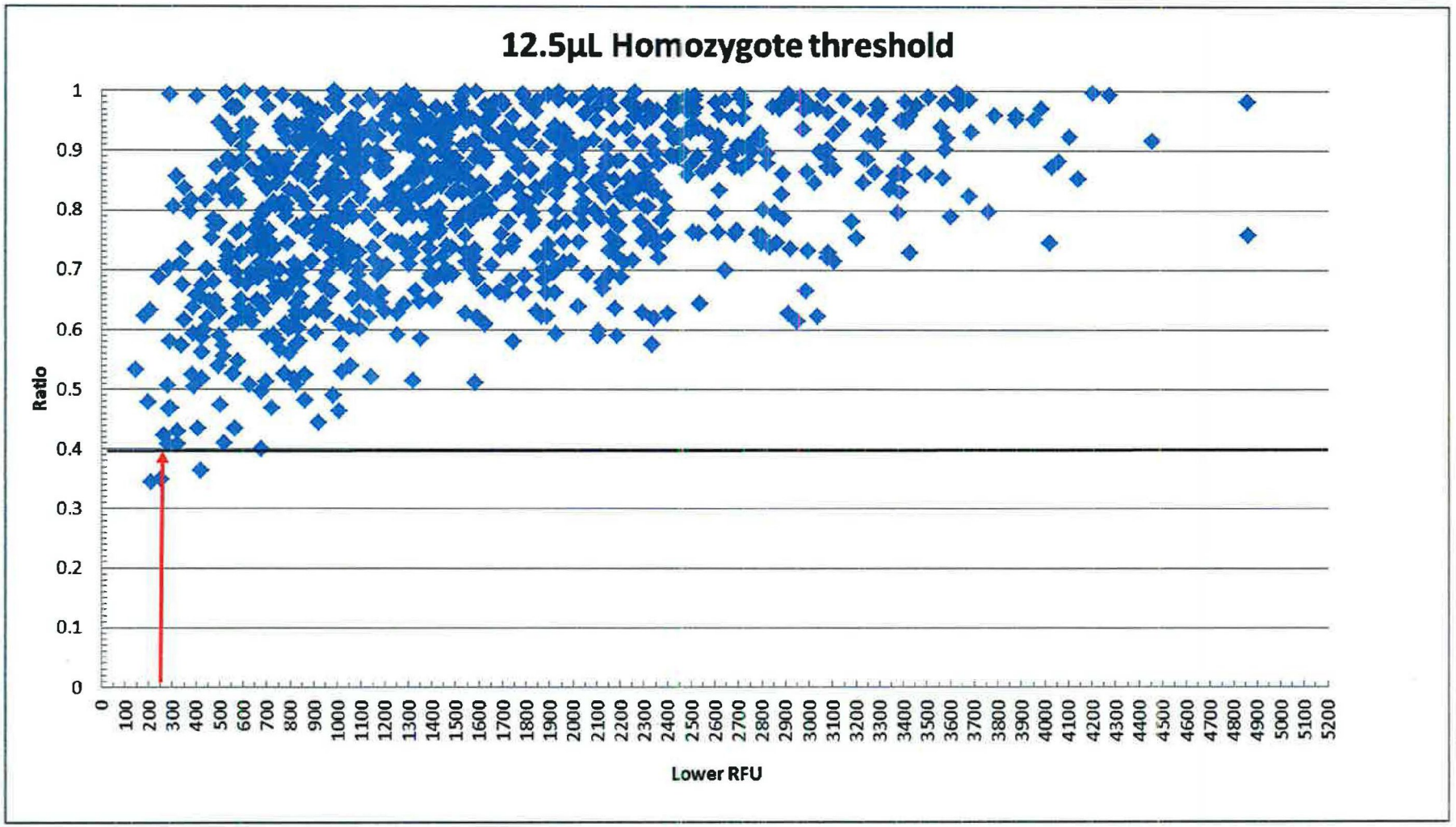


Figure 22 - Plot of the peak height ratio vs RFU of lower peak for 12.5µL. The black horizontal line is the AI_{TH}. The red vertical line is set to encompass the majority of points that fall below the AI_{TH}

[redacted]

WIT.0016.0104.0050

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.

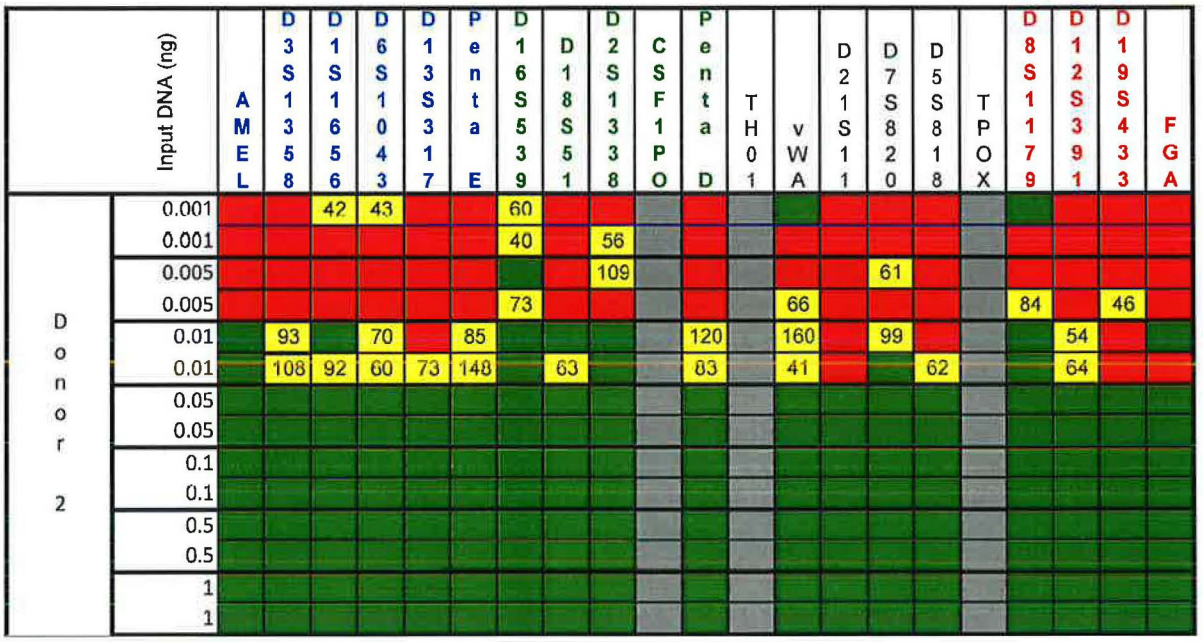
The data for the 25µL amplification shows 62 drop out events occurred across both donors from dilutions 0.001ng to 0.05ng. Figure 24 shows the highest peak height (RFU) where a heterozygous pair dropped out was at 160RFU for the 0.01ng dilution for donor 2 amplified at 25µL total PCR volume.

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

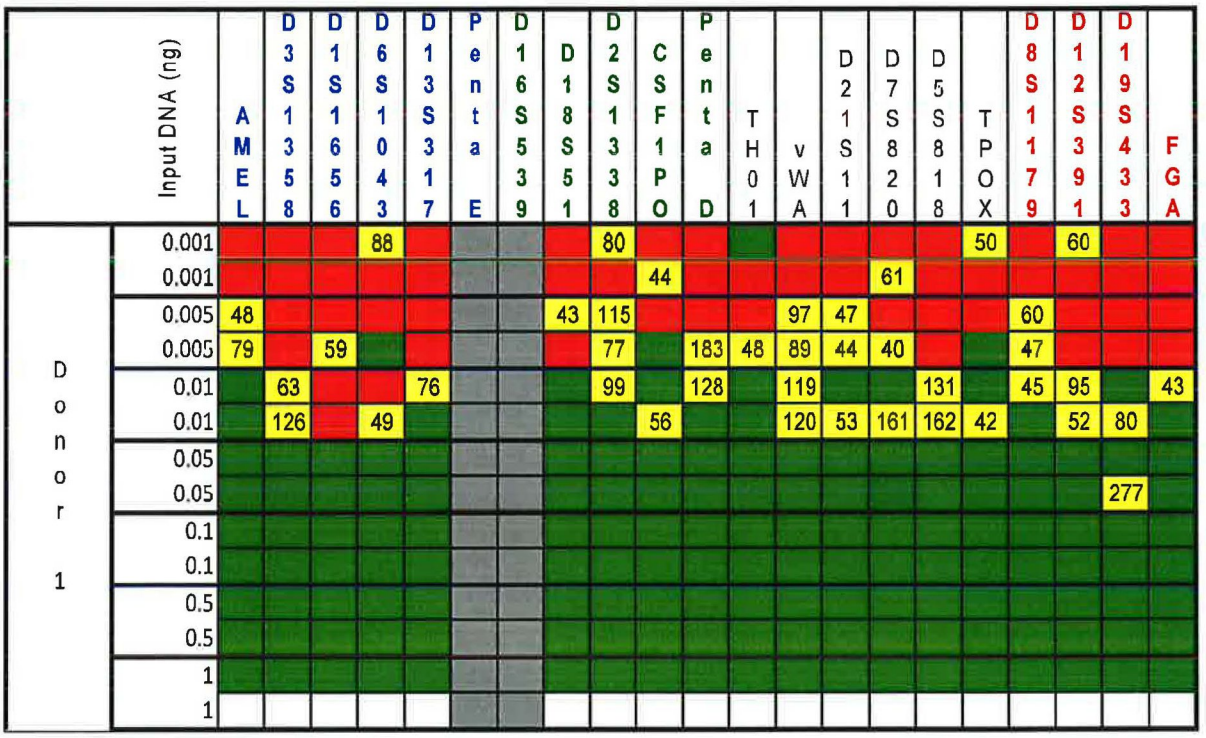
	Input DNA (ng)	AMEL	D3S1358	D1S1656	D6S1043	D13S317	Penta E	D16S539	D18S51	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX	D8S1179	D12S391	D19S433	FGA
Donor 1	0.001										54											
	0.001								43													
	0.005	83												50		96					69	
	0.005	41		46		61								46				54	70			
	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



Donor 2	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
	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



Donor 1	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
	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

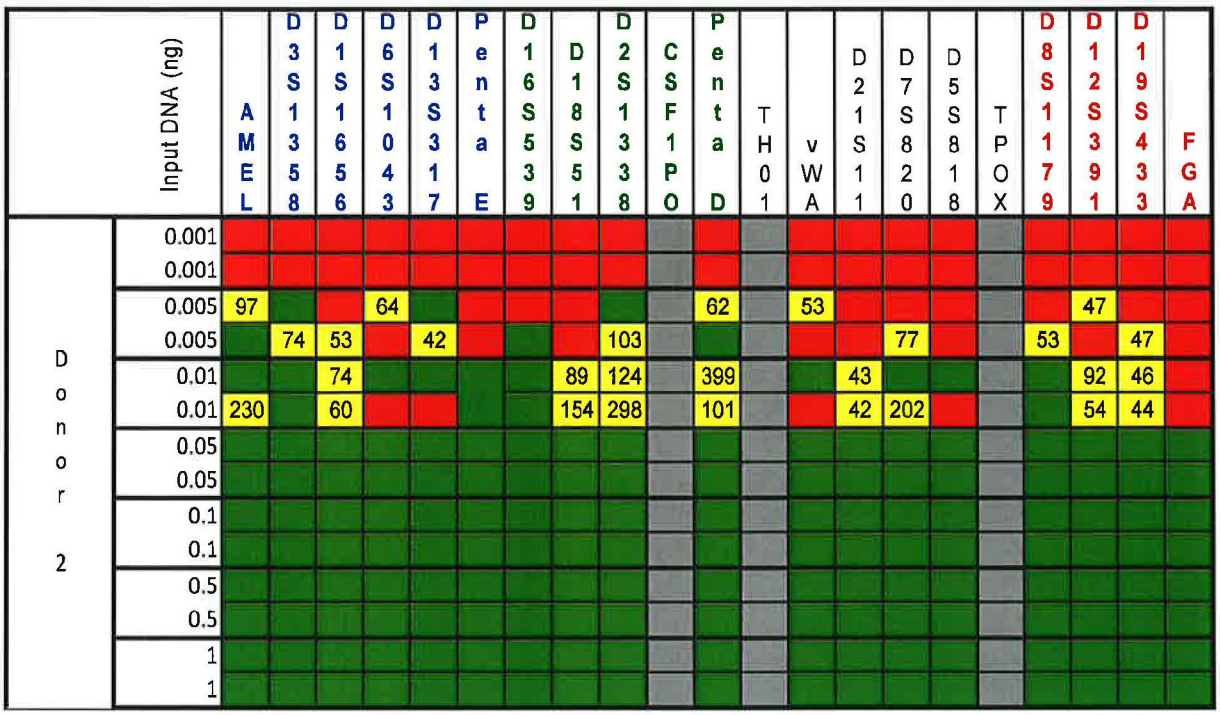


Figure 26 - Heat Map – Donor 2 - 12.5µL total PCR volume

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

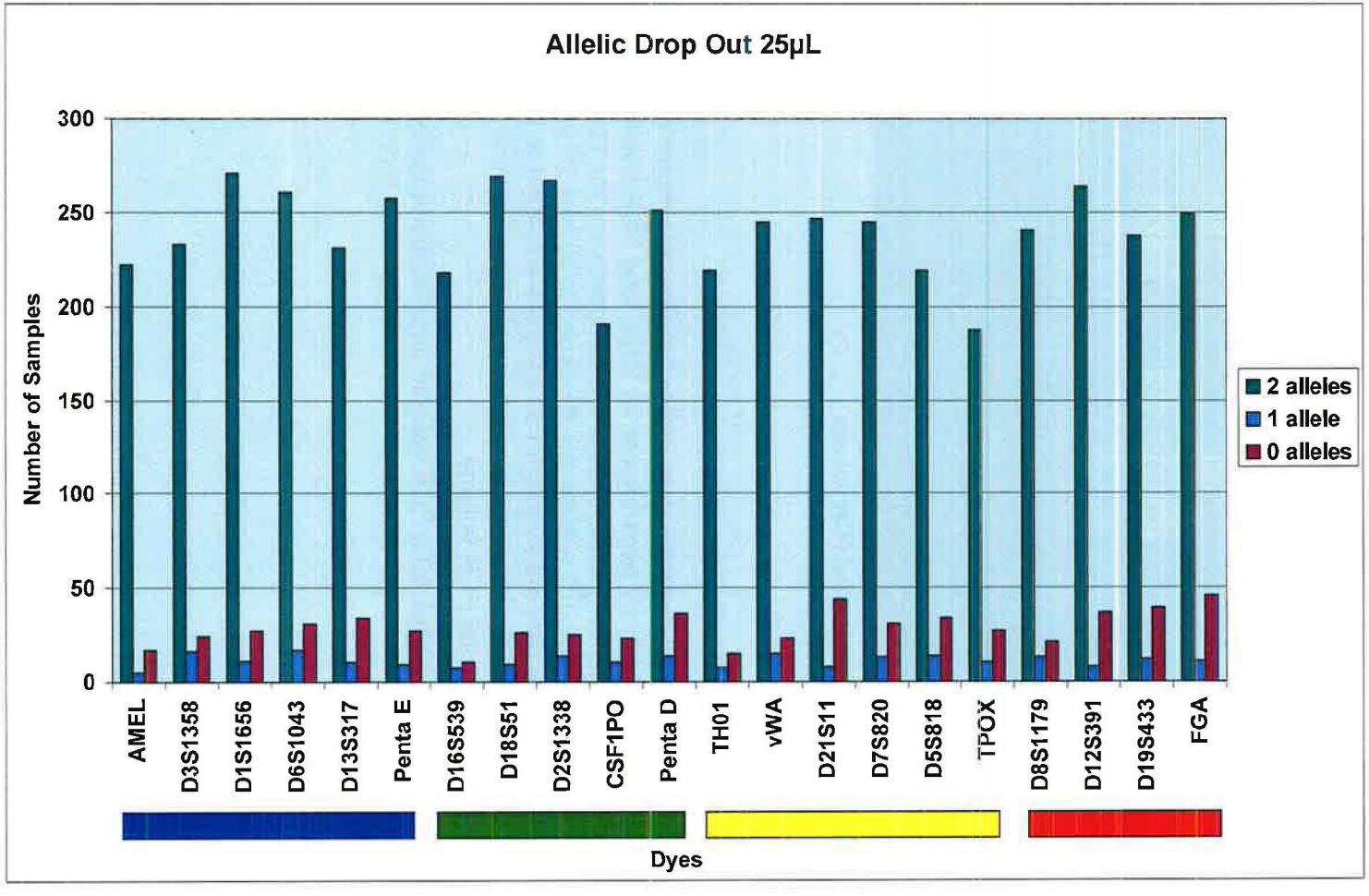


Figure 27 - Dropout events for samples amplified at 25µL

WIT.0016.0104.0054

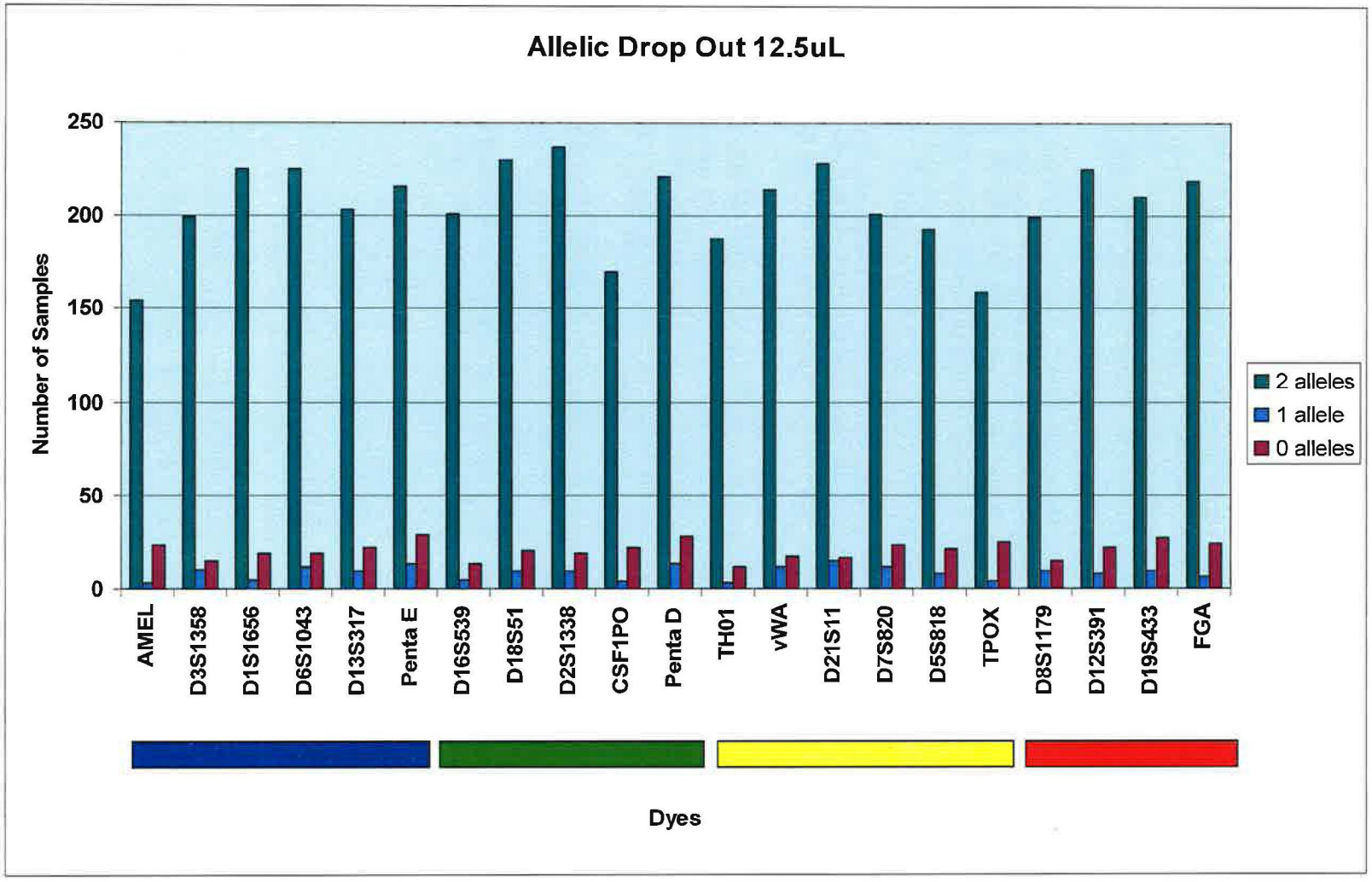


Figure 28 - Dropout events for samples amplified at 12.5µL

WIT.0016.0104.0055

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.

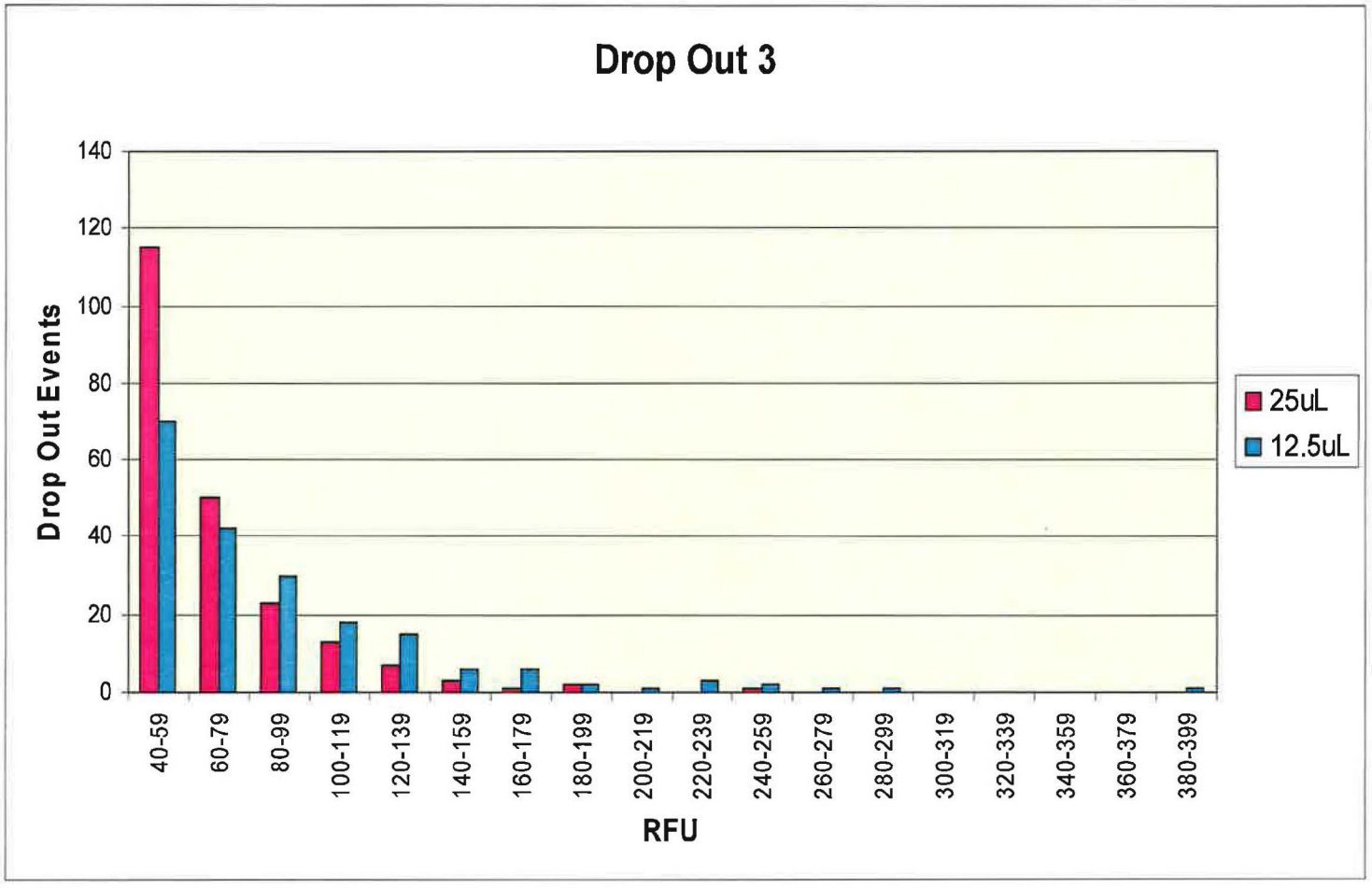


Figure 29 - Number of drop out events seen within peak height ranges at 25µL and 12.5µL amplifications

WIT.0016.0104.0057

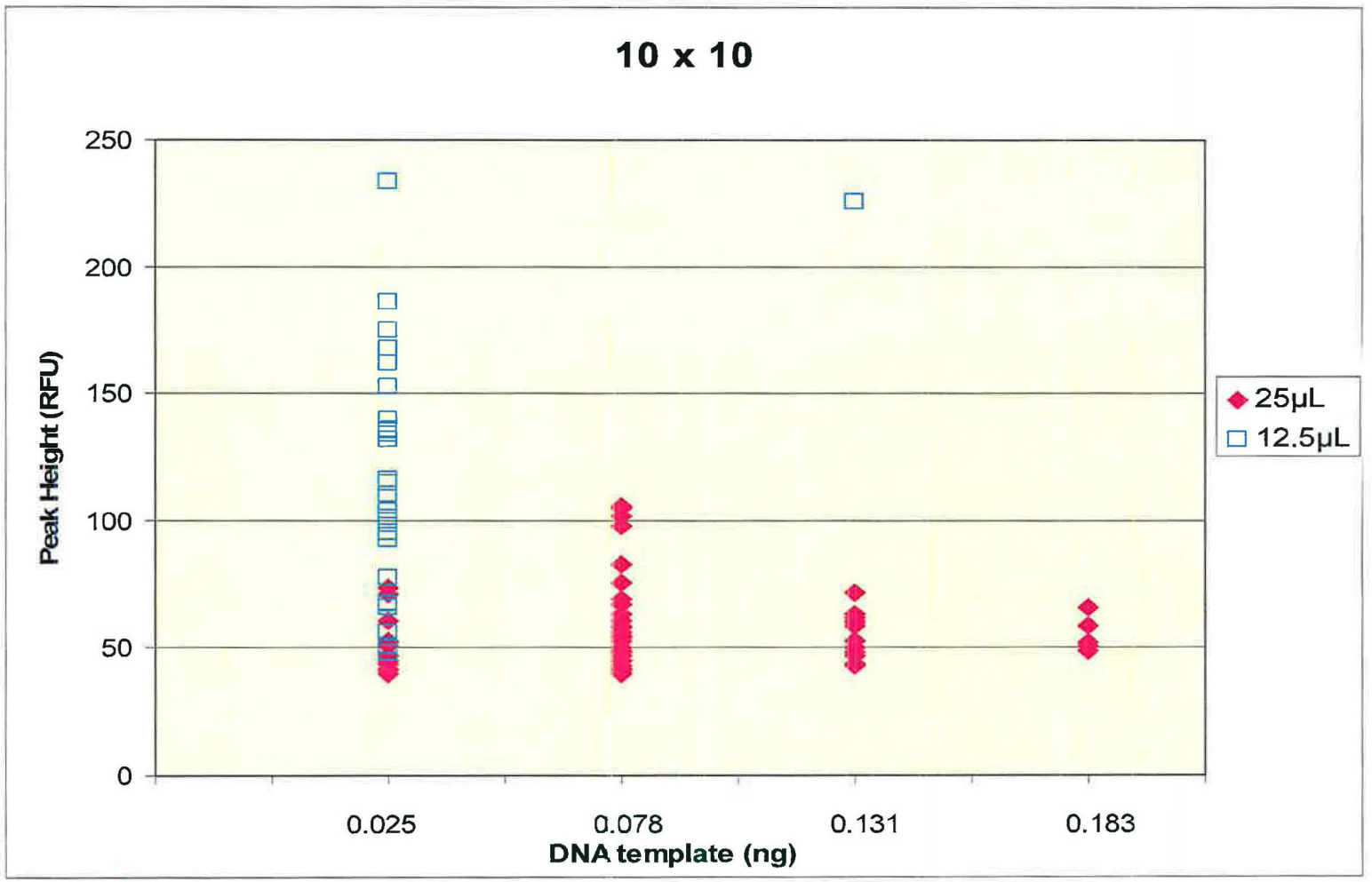


Figure 30 - Peak heights where the heterozygote pair has dropped out at different DNA templates for 12.5uL and 25uL using the baseline data (10 x10)

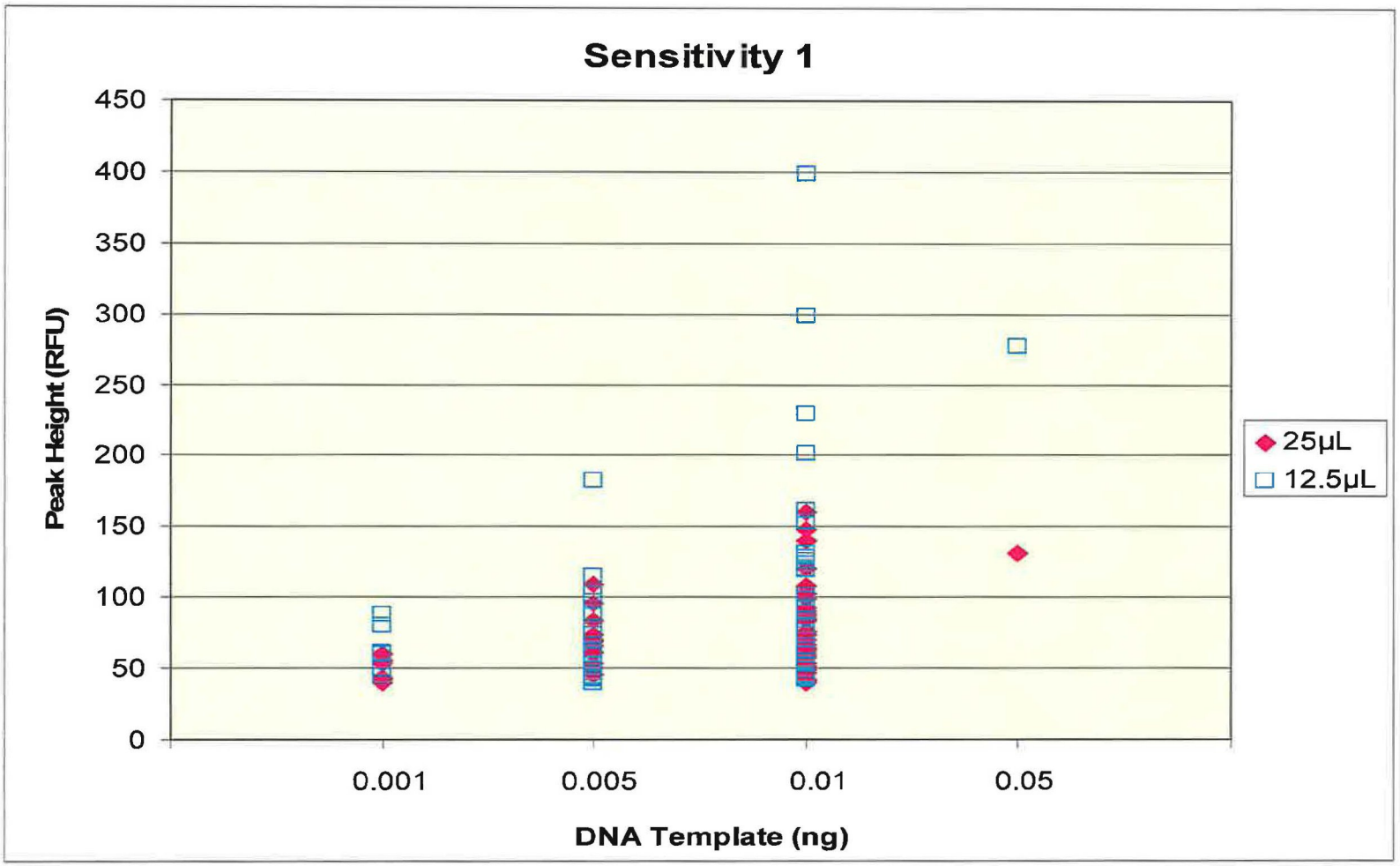


Figure 31 - Peak heights where the heterozygote pair has dropped out at different DNA templates for 12.5uL and 25uL using sensitivity 1 data

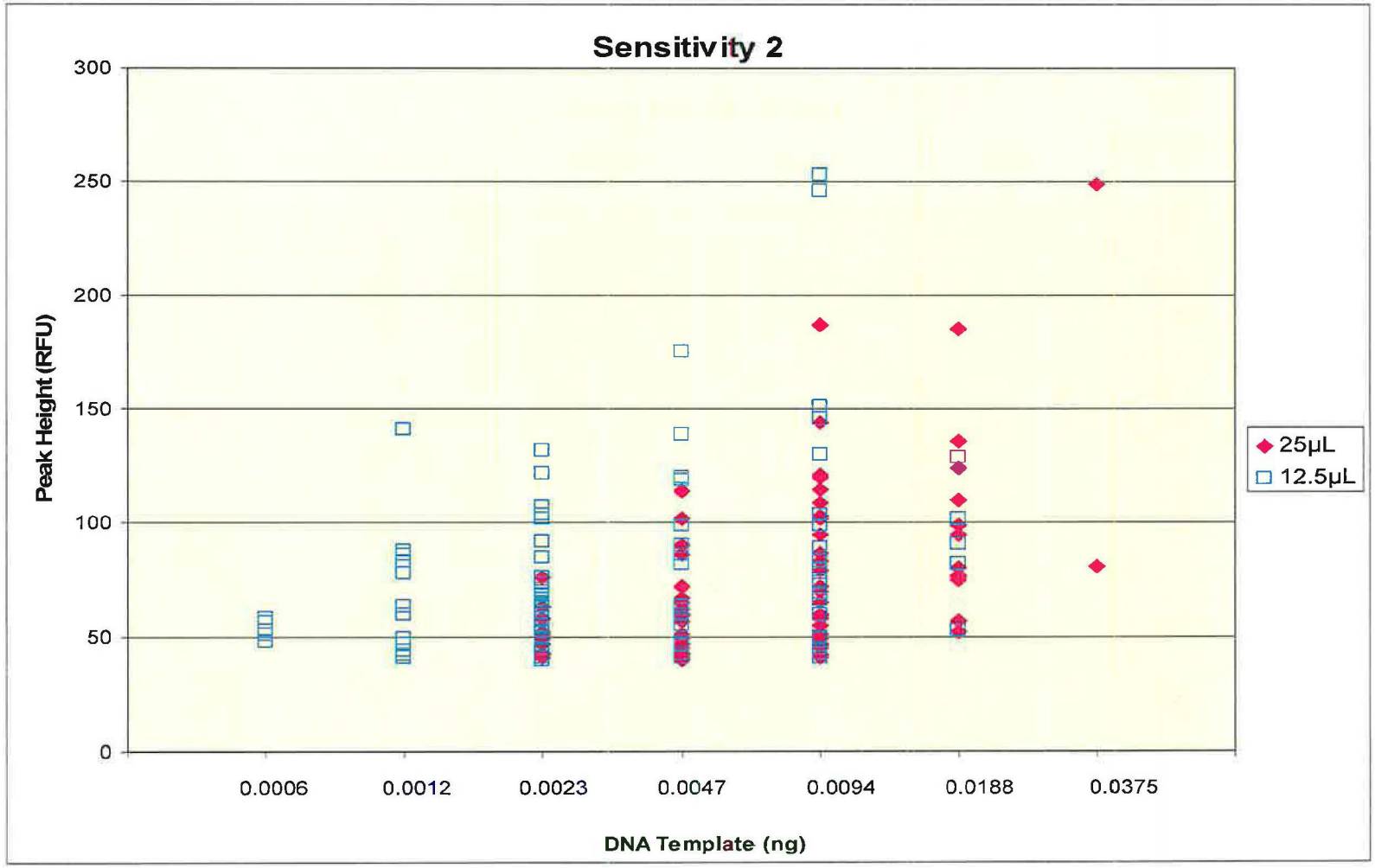


Figure 32 - Peak heights where the heterozygote pair has dropped out at different DNA templates for 12.5uL and 25uL using sensitivity 2 data

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 or re-amplify at 25µL total PCR volume.
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.

9 References

1. Rakay, C.A., J. Bregu, and C.M. Grgicak, *Maximizing allele detection: Effects of analytical threshold and DNA levels on rates of allele and locus drop-out.* Forensic Science International: Genetics, 2012. **6**(6): p. 723-728.
2. BSAG, *BSAG Verification Plan for the new DNA marker set.* 2011.
3. STATSWG, *STATSWG recommendations for the interpretation of DNA.* 2011.
4. Promega, *PowerPlex 21 System Technical Manual.* 2011.
5. Applied_Biosystems, *AmpFℓSTR® Profiler Plus® PCR Amplification Kit User's Manual.* 2006.
6. Applied_Biosystems, *COfiler® PCR Amplification Kit User Bulletin.* 2006.
7. Whatman, *Applying and Preparing Buccal Cell Samples on FTA Cards for DNA Analysis*, in *Whatman FTA Protocol BD03.*
8. Gilder, J.R., et al., *Run-Specific Limits of Detection and Quantitation for STR-based DNA Testing.* Journal of Forensic Sciences, 2007. **52**(1): p. 97-101.
9. Mathieson, M., Weber, C., McNevin A., Nurthen T. & Allen, C., *PART 1 - Project#69- Project Plan for Sensitivity and Amplification volume determination using Promega PowerPlex® ESI17 System, Promega PowerPlex® ESX17 System and Applied Biosystems AmpFℓSTR® NGM SElect™*, D. Analysis, Editor. 2011.
10. Bright, J., *Variability in PowerPlex® 21 stutter ratios across Australian laboratories.* 2012.
11. SWGDAM, *SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories.* 2010, Scientific Working Group on DNA Analysis Methods (SWGDAM).
12. Gilder, J., et al., *Magnitude-dependent variation in peak height balance at heterozygous STR loci.* International Journal of Legal Medicine, 2011. **125**(1): p. 87-94.
13. Leclair, B., et al., *Systematic analysis of stutter percentages and allele peak height and peak area ratios at heterozygous STR loci for forensic casework and database samples.* J Forensic Sci, 2004. **49**(5): p. 968-80.
14. Weber, C., McNevin, A., Muharam, I., & Ientile, V., *Peak Height and Allelic Imbalance Thresholds.* 2008, Forensic and Scientific Services. p. 15.
15. Promega, *Internal Validation of STR systems.* 2006, Promega Corporation. p. 15.
16. Bright, J.B., J., *Analysis of the Australian Caucasian Sub-Population Data for the PowerPlex® 21 Autosomal short tandem repeat Loci.* 2012.
17. Bright, J.B., J., *Analysis of the Australian Aboriginal and Asian Sub-Population Data for the PowerPlex® 21 Autosomal short tandem repeat Loci.* 2012.

18. Leibelt, C., et al., *Identification of a D8S1179 primer binding site mutation and the validation of a primer designed to recover null alleles.* Forensic Science International, 2003. **133**(3): p. 220-227.

19. Kline, M., Junkins, B., & Rodgers, S.,, *Non-Amplifcation of vWA Allele.* Journal of Forensic Sciences, 1998. **43**(1): p. 250.

20. Ricci, U., et al., *A Single Mutation in the FGA Locus Responsible for False Homozygosities and Discrepancies Between Commercial Kits in an Unusual Paternity Test Case.* Journal of Forensic Sciences, 2007. **52**(2): p. 393-396.

21. Butler, J. *Data Interpretation & Statistical Analysis.* in *Topics and Techniques for Forensic Analysis.* 2012. New York City,NY,US: NIST.

22. Butler, J., Coble, MD, Cotton, RW, Grgicak, CM, & Word, CJ. *MIXTURE INTERPRETATION: Using Scientific Analysis.* in *22nd International Symposium on Human Identification.* 2011. Washington, DC, US: NIST.

23. Gill P, P.-S.R., Curran J., *The low-template-DNA (stochastic) threshold--its determination relative to risk analysis for national DNA databases.* Forensic Science International: Genetics, 2009. **3**(2): p. 104-111.

24. Kirkham, A., et al., *High-throughput analysis using AmpFISTR® Identifiler® with the Applied Biosystems 3500xl Genetic Analyser.* Forensic Science International: Genetics, 2013. **7**(1): p. 92-97.

25. Gaines ML, W.P., Valentine JA, & Brown CL,, *Reduced Volume PCR Amplification Reactions Using the AmpFℓSTR® Profiler Plus ™ Kit.* J Forensic Sci,, 2002. **47**(6).

26. Barbaro, A., P. Cormaci, and S. Votano, *Direct PCR by the AmpFISTR NGM™ kit for database purpose.* Forensic Science International: Genetics Supplement Series, 2011. **3**(1): p. e103-e104.

27. Laurin, N., A. De Moors, and C.J. Frégeau, *New validated analytical process for convicted offender samples submitted to the Canadian National DNA Data Bank.* Forensic Science International: Genetics Supplement Series, 2011. **3**(1): p. e25-e26.

28. Oostdik, K., et al., *Developmental validation of the PowerPlex® 18D System, a rapid STR multiplex for analysis of reference samples.* Forensic Science International: Genetics, 2013. **7**(1): p. 129-135.

29. Lancaster, K.A., McNevin, A., & Nurthen, T., *Verification of Applied Biosystems 7500 Real Time PCR System.* 2010.

30. Cowen, S., et al., *An investigation of the robustness of the consensus method of interpreting low-template DNA profiles.* Forensic Science International: Genetics, 2011. **5**(5): p. 400-406.

31. Goodwin, W., Linacre, A., & Hadi, S., *An Introductionto Forensic Genetics.* 2011: Wiley.

32. Butler, J., M. , *Forensic DNA Typing: Biology, Technology and Genetics of STR Markers.* 2005: Academic Press.

33. Butler, J.M., *Fundamentals of Forensic DNA Typing.* 2010: Academic Press.

34. Ensenberger, M.G., et al., *Developmental validation of the PowerPlex 16 HS System: an improved 16-locus fluorescent STR multiplex.* Forensic Sci Int Genet, 2010. **4**(4): p. 257-64.

35. Alaeddini, R., S.J. Walsh, and A. Abbas, *Forensic implications of genetic analyses from degraded DNA—A review.* Forensic Science International: Genetics, 2010. **4**(3): p. 148-157.

36. Hill, C.R., et al., *Concordance and population studies along with stutter and peak height ratio analysis for the PowerPlex® ESX 17 and ESI 17 Systems.* Forensic Science International: Genetics, 2011. **5**(4): p. 269-275.

37. Kelly, H., et al., *Modelling heterozygote balance in forensic DNA profiles.* Forensic Science International: Genetics, 2012. **6**(6): p. 729-734.

38. Krenke, B.E., et al., *Validation of a 16-locus fluorescent multiplex system.* J Forensic Sci, 2002. **47**(4): p. 773-85.

39. Benschop, C.C.G., et al., *Low template STR typing: Effect of replicate number and consensus method on genotyping reliability and DNA database search results.* Forensic Science International: Genetics, 2011. **5**(4): p. 316-328.

40. Bright, J., Buckelton, J., & Taylor, D., *Estimation of STRmix parameters for Queensland Health Scientific Services v1.05.* 2012.

41. Word, C.J. *Peak Height Ratios.* in *21st International Symposium on Human Identificaiton.* 2010. San Antonio, Tx, US: NIST.

42. Sgueglia, J.B. *Developing Thresholds, Protocols and Validation Studies Using the New SWGDAM Guidelines.* in *AAFS 2011 Workshop #17.* 2011. Chicago, IL, US: NIST.

43. Cotton, R. *Amplification Variation and Stochastic Effects.* in *21st International Symposium on Human Identification.* 2010. San Antonio, TX, US.

44. Buckleton J., T., C.M., & Walsh, S.J., *Forensic DNA evidence Interpretation.* 2004: CRC.

45. Hlinka, V., Muharam, I., & Allen, C., *Extended internal retrospective validation of the ABI PRISM 7000/Quantifiler system.* 2006.

46. Hlinka, V., Muharam, I., & Allen, C., *Extended internal prospective validation of the ABI PRISM 7000/Quantifiler system.* 2006.

10 Appendix A - Index to Supplementary data

10.1 Procedure for Creating a Dilution Series

10.1.1 Project#102 Serial dilutions final.xls

10.2 PowerPlex 21 bins

10.2.2 PowerPlex_21_IDX_v1.1

10.3 Sub-Population Datasets

10.3.1 Aboriginal-Torres Straits Results.xls

10.3.2 Caucasian results.xls

10.3.3 PP21_SEAsian_Population data.xls

10.4 Concordance

10.4.1 CONCORDANCE SAMPLES.xls

10.4.2 CTS 2003-2012 concordance comparison.xls

10.5 Baseline Determination

10.5.1 Baseline 3130xl A Half.xls

10.5.2 Baseline 3130xl B Half.xls

10.5.3 Baseline 3130xl A_rerun.xls

10.5.4 Baseline 3130xl B_rerun.xls

10.5.5 Baseline_3130xlA.xlsx

10.5.6 Baseline_3130xlB - original.xlsx

10.5.7 Baseline_3130xlA-original.xlsx

10.5.8 Baseline_3130xlB.xlsx

10.6 Sensitivity 1

10.6.1 Comparing Full v Halfv2.xls

10.7 Sensitivity 2

10.7.1 Low quant values.xls

10.8 Drop In

10.9 Stutter

10.10 Peak Balance

10.10.2 Alth_Homoth_summary.xls

10.11 Drop out 1

10.12 Drop out 2

10.13 Drop out 3

10.14 Mixture Studies

10.14.1 Mixtures_val_2012.xls

[redacted]

Procedure for Case Management

Not Current

Not Current

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	All information relating to a particular case. This can include all case histories, receipts, communication with clients, examination notes, Analytical data, results and reports.
Examining Scientist	Scientist/s who has/have examined exhibits for a case in accordance with 17142 (Examination of Items) and related standard operating procedures.
Case Managing Scientist	Scientist/s who has/have been involved in the assessment of results and compilation of the case file in preparation for statement writing or peer review.
Reporting Scientist	Scientist who is responsible for writing a Statement of Witness outlining the results of a case and for presenting evidence in a court of law.
DRMU	DNA Results Management Unit – A QPS Unit that transfers the EXR/EXH and LKR results from the Forensic Register to QPRIME. They also perform quality checks on the validity of the information/results received.
SSLU	Scientific Services Liaison Unit – A unit within Forensic and Scientific Services that acts as a liaison between Investigating Officers, other external clients and DNA Analysis.
QPS 'In tube' samples	An item that has been sub-sampled by the QPS and submitted to the laboratory in a tube ready for analysis.
DAD/DADI	The DNA Analysis Database Interface (DADI) is used to maintain the data stored within the DNA Analysis Database (DAD) and to provide results management functions.
Paperless	Not involving a traditional casefile. Work is performed almost entirely in AUSLAB.
STRmix™	Statistical program used during case management to assess certain types of DNA profiles.

3 CASE FILE OVERVIEW

3.1 When is a case file required?

- Since the 1st of September 2009, low priority Volume Crime cases have been treated as 'paperless' and therefore do not have case files. See also 26874 (Procedure for Paperless Case Management and Review). In April 2010, paperless case management and review was expanded to also include all cases of both high and low priority (Volume and Major Crime) except for non-in-tube Sexual Assault cases (Yellow Team cases) or cases involving excessive numbers of crime scene/reference samples or complex profiles.

Not Current

- The decision as to whether a case should be paperless or have a case file created is at the discretion of the case manager. A case that has been initially managed paperlessly may be converted to a paper file if further exhibits are received at a later date.
- Case files are either created at the time of examination (for non-in-tube Sexual Assault cases) or at the time of case management (for complex cases).
- Each case file has a unique case number (Occurrence/QPRIME number, CRISP number or SSF/COR/CA number). Occurrence numbers and CRISP numbers are generated by QPS. SSF/COR/CA numbers are generated in AUSLAB and usually indicate a coronial matter.
- Information relating to a case, such as offence type, is recorded in AUSLAB. See 17116 (Procedure for the Receipt of DNA Exhibits) and 16004 (AUSLAB Users Manual – DNA Analysis).
- If a case contains items or documentation citing more than one case number, enquiries can be made to the QPS Sample Management Unit (SMU) to establish whether the cases are linked and can be reported together. Details of these checks must be included in the UR notes.

3.2 How to create a Case File

- Check AUSLAB to see if a case file already exists. If a file does exist, a new one does not need to be prepared and the file should be located.
- If a file does not exist and it has been determined that one is required, it will need to be prepared:
    - Place a barcode for the first received receipt (if multiple receipts are registered) on the case file folder in the box in the top right hand corner labelled 'case barcode'. This first receipt barcode should also be the barcode that the CS screen is registered under in AUSLAB. See Appendix 1 for details on the CS screen.
    - Write the case number at the top of the folder in the 'Case Number' field.
    - Write the initials of the examining scientist in the 'Examining Scientist' field. Multiple people can be added to this field for any subsequent examinations. If the case is a QPS 'in tube' case, this field should have 'N/A' entered in it.
    - Write the initials of the case managing scientist in the 'Case Managing Scientist' field. Multiple people can be added to this field for any subsequent case management.
    - If applicable, write the initials of the reporting scientist in the 'Reporting Scientist' field. If no statement is to be issued, this field should have 'N/A' entered in it.
    - Write the complainant's and suspect's/defendant's names (if known) on the lines next to the 'NAMES' fields (one name per line). Surnames should be written in capitals and given names in lower case. Write '(Comp/Def't)' or '(Sus)' after each name as appropriate. If the complainant is a company, the company name can be written on the case file, but for reporting purposes the complainant in these cases is 'Regina'.
    - Turn the folder to the side and fill out the details along the edge as indicated: case number; case type - found on the CS screen for the case in AUSLAB, e.g. assault (N/S); names - divide the line in half with a diagonal line and write the surname of the complainant on the left side and the surname of the suspect(s)/defendant(s) (one on top of the other if necessary) on the right side.
    - Place the receipt barcode on the Case File Particulars page 17038 in the box in the top left hand side of the page labelled 'Case File Barcode'. If no barcodes are available, print a new barcode from AUSLAB.
    - On the Case File Particulars page write the case number in the 'Case #' field.
    - Place the Case File Particulars page and receipt page(s) inside the case file and track the file in AUSLAB to the appropriate storage location. Since 26th September 2011, the QP127 (if provided) will be scanned into AUSLAB by Property Point staff and the original handed back to the QPS Officer with the exception of SAIKs where

Not Current

the QP127 will be scanned into AUSLAB and attached to the GMO notes, tracked and transferred to DNA Analysis.

3.3 Additional elements of a Case File

Upon completion, a case file may also contain:

- Examination notes
- Diagrams, photographs and/or photocopies
- Statistical calculations
- Profile results table
- Copies of results (Genotyper or GeneMapper ID-X printouts)
- Interpretations of results
- Copy of statement or intelligence report
- Records of any internal or external communication relating to the case, e.g. UR notes or emails.
- STRmix™ output files

3.4 Handwritten results and corrections within the Case File

- Any calculations, interpretations or changes to notes or results must be initialled and dated by the person performing the action.
- No pencil is to be used in the case file (unless used in diagrams or pictorial representations).

3.5 Case file storage and movement

- No exhibits are to be stored in the case file. This includes external proficiency samples. Original QPS property tags or reference sample envelopes are also NOT to be stored in the case file.
- Case file movement is to be recorded in AUSLAB. If the scientist responsible for the management of a case changes, this must be recorded on the front of the case file folder.
- Active case files are stored with the case analyst or in a designated storage location for the work area.
- Upon completion, scientists should transfer cases to either FBCFF1 (Case File Finish) or FBPR1. Administration assistance slips are available to attach to the front of the case file to direct the storage of the file or to outline any further administrative tasks that need to be performed prior to storage.
    - FBCFF1 is the location from which administrative staff will track case files (sequentially) into the compactus or another designated storage location. No further administrative tasks will be carried out on these cases.
    - FBPR1 is the location from which administrative staff will collect cases from in order to perform further administrative tasks such as page numbering and administrative reviews (left hand side only).
- Case files are kept indefinitely.

4 CASE MANAGEMENT OVERVIEW

- The purpose of case management is to collate and report any DNA results that have been obtained and to prepare the case file for a statement (if required) or for peer review. To achieve this, the case managing scientist may be required to:
    - Assess DNA results to determine whether reworking is required to improve results
    - Assess reworked and initial results to determine which is the best profile
    - Enter final EXR/EXH results into AUSLAB

Not Current

- Compile case file and finalise AUSLAB pages

- Statements and intelligence reports are to be prepared according to 17119 (Procedure for the Release of Results).
- All results are to be communicated as outlined in 23968 (Result Communications Procedure).

5 WORKFLOW

- Blue, Red, Yellow and high priority Volume team cases are allocated to a case scientist and/or reporting scientist as a result of notification from SSLU (by insertion on the CSRC list) or via the case management work lists for each coloured stream (YELCM, REDCM, BLUECM, VOLCM). Allocation to a particular scientist usually only happens if a statement is required. These cases will otherwise be routinely case managed by the Intelligence and Reporting teams through accessing the work lists in Auslab. Low priority volume cases are managed via the VOLLOW work list and are case managed by the Intelligence team. Samples auto populate the various CM lists once a 9PLEX or PLEX21 result has been obtained. Review of all results is managed through four Auslab worklists: MCREV: all major crime (high priority) paperless non-mixture samples; MCMIX: all major crime paperless mixture samples; VCREV: all low priority volume paperless non-mixture samples; and VCMIX: all low priority volume paperless mixture samples.
- 3 day turnaround time (TAT) cases are specifically allocated to a case scientist and/or reporting scientist as they arrive into the department.
  - The Management Team will be notified of the arrival of a 3 day TAT case by email and appropriate UR notes will be entered.
  - A Supervising Scientist will allocate to an appropriate case manager. This does not mean that the case managing scientist will necessarily become the reporting scientist should a statement be required.
  - Various tools may be employed to assist in meeting timeframes and to cover absence such as noting the case details on a central whiteboard and scheduling Groupwise appointments or tasks.
  - Reworks on priority 1 samples are to be ordered and case managed by the original allocated scientist

- The case management and review work lists are not to be utilised for 3 day TAT cases. The results for these samples will populate GREECM when they become available so they can be monitored by the Senior Scientists. They must be managed as soon as results become available and reviewed as soon as results are interpreted. To ensure there is no delay in QPS being informed of 3 day TAT results as soon as they are available, a workflow has been created for samples that are expected to be completed on a Friday. See 17119 (Procedure for the Release of Results).

6 ASSESSMENT OF RESULTS

For samples that are amplified through ProfilerPlus® or PowerPlex®21:

- When results become available for a sample, an assessment needs to be made as to whether reworks are required or whether sufficient information has already been obtained. This can be performed as each result becomes available. Not all results need to be available at the same time for these assessments to take place.
- To check whether results are available for a particular sample, enter into that barcode in AUSLAB and navigate to the 9PLEX or PLEX21 page. Press SF7 to view the results history screen. If a DNA profile is present in the 9PLEX or PLEX21 column, the initial 9PLEX or PLEX21 has been completed. If there are test codes present in subsequent columns and

Not Current

no profiles are seen in these columns, the sample may have been sent for reworks and processing is not yet complete.

- GeneMapper *ID-X* results are imported into AUSLAB prior to quality checking. Before using any results from GeneMapper *ID-X* ensure the audit entry for your sample shows that the batch has been completed.
- If there has been an issue noted during processing, Analytical staff will enter a specimen note referring the case manager to a particular batch audit entry. The case manager MUST look into the highlighted issue and enter a specimen note for that sample stating that they understand the issue and have deemed the sample ok to report.
- If there is a statement request for a low priority (priority 3) volume crime case, and one or more samples have been reported as 'No DNA detected' in the EXH, testing does not recommence. This result will be reported in the statement as 'DNA was not detected in this sample during the initial steps of DNA analysis and as a result no further testing was conducted' (wording is at the discretion of the reporting scientist).
- If a volume crime case or sample has its priority changed from low (3) to high (2), and the sample has been previously reported as 'No DNA detected' in the EXH, testing does not recommence. The sample will remain as 'No DNA detected'.
- If there are samples that have been reported as 'No DNA detected', and written communication is received from QPS that testing is to recommence, these samples will be processed but will not be reworked unless the case priority is changed from low to high.
- All DNA profile .jpeg images (for all runs) and STRmix™ output file .jpeg images are uploaded into Auslab by Operational Officers. All images must be checked by the scientist reviewing the sample.

For samples that have not been amplified:

- Validation studies have shown that samples with low template DNA (~100pg) that are amplified with PowerPlex®21 exhibit significant stochastic effects such as large allelic imbalance and allele drop-out. These effects can complicate the interpretation of both single source and mixed DNA profiles and therefore the following strategies have been employed.
- Samples with an undetermined quantitation value will be reported in their associated EXH as 'no DNA detected', regardless of priority.
- Any sample with a quantitation value of <0.01 ng/µL will not be amplified or sent for a Microcon as this will not yield enough template DNA to allow for reliable DNA profile interpretation. This result will be communicated using the 'DNA insufficient for further processing' EXH line. Occasionally a sample with a quantitation value <0.01 ng/µL may require processing – this will be at the case manager's discretion and in consultation with their line manager.
- Samples with an initial quantitation value between 0.01ng/µL and 0.0176ng/µL will automatically be sent for a Microcon to 20µL and be re-quantitated.

  - If the new quantitation value is between 0.0176ng/µL and 0.0244ng/µL the sample will be processed at half volume (7.5µL) and added to the appropriate case management list for interpretation. Once the result has been interpreted, the sample will be added to the 1CGF2 work list by the case manager. Currently these results are not reported back in an EXH.
  - If the new quantitation value is above 0.0244ng/µL, the sample will be amplified at half volume ad the results will be interpreted and reported back in an EXH.
  - If the new quantitation value is between 0.01ng/µL and 0.0176ng/µL, the sample will populate the appropriate case management list for assessment

Not Current

by a case manager to determine whether a full volume amp is necessary (taking into account the circumstances of the case and other results obtained within the case). When ordering a full volume amp, the case manager will need to add 'full vol amp' to the processing comments and complete the amplification volumes in the Shift 7 page. Samples amped at full volume will have a different Genemapper *ID-X* batch ID.

- See also Appendix 10 (Case Management workflow diagram 1)

6.1 Assessing results for Reworks

- It is QPS policy to rework Volume Crime samples (via any means available) for high priority cases only and all Major Crime samples. Low priority Volume Crime cases are only to be reworked via re-amplification, re-running (previously known as re-Genescanning – for 9PLEX samples only) or re-reading in GeneMapper *ID-X* until 12 alleles are obtained (NCIDD uploading threshold). No NucleoSpin cleanups or Microcon concentrations are to be ordered on low priority samples (unless discussion with your line manager has taken place).
- For ProfilerPlus®: If allelic imbalance occurs (<70% in a Genotyper profile or <50% in a GeneMapper *ID-X* profile), the alleles can be reported if the case managing scientist is confident that both alleles at the locus are true alleles. The profile should be examined carefully for evidence of a mixture; if there is no evidence of a mixture both alleles can be reported. The case managing scientist wanting to accept the alleles as true should record this on the EPG. By validating the 9PLEX page for such a sample, the reviewing scientist is agreeing that they approve of this interpretation. For paperless cases this is recorded in the specimen notes for the sample.
- For PowerPlex®21: Allelic imbalance (AI) will increase as the amount of template DNA decreases. The validation data shows that a template range between 0.132ng and 0.5ng gives an AI threshold of 45% (this figure can be lower). This information should be used when determining the number of contributors to a DNA profile.
- At plate reading stage, the reader will not need to make any change to a 'homozygous' peak designation. Following plate reading, PowerPlex®21 casework plates will be run through a macro to call a single peak at a locus (for example) '15', rather than '15,-' or '15,NR', regardless of peak height. This will allow the allele designation to be uploaded to Auslab as '15', ensuring that the GeneMapper *ID-X* results file will be appropriate for STRmix™ deconvolution. After the sample has been run through STRmix™, the case manager will then change the allele designation to either '15,15' or '15,NR' on the results history PLEX21 page (based on the STRmix™ deconvolution). The amended profile will then need to be re-saved.
- For all reworks, the 'comments' field on the 9PELX/PLEX21 page or the 'processing comment' should reflect the kit used for processing. For example if a microcon is ordered on a 9PLEX sample, the processing comment may be 'm'con to full P+'. 'P+' should be used for ProfilerPlus® samples, and 'PP21' for PowerPlex®21 samples.
- If a partial profile or NSD profile is obtained for a sample, an assessment should be made as to whether reworking that sample will be beneficial or if there are other profiles within the case that satisfy reporting requirements. If it is determined that a better profile is required, the following should be considered when determining the best rework strategy:
  - **The type of sample:** e.g. blood versus cells. Due to the generally high number of nucleated white cells in whole blood, a DNA profile is usually obtained from such samples. On the other hand, shed skin cells contain few or no nuclei and therefore it is

Not Current

more difficult to obtain a profile of DNA that has been deposited on an item through casual contact.

- **The quantitation value:** displayed in the *'FBQUAN'* or *'QUANT'* field in AUSLAB. The quantitation value is an estimate and should be assessed in conjunction with other factors. A partial or NSD profile from a sample with a high quantitation value may indicate inhibition. It should be noted that while quantitation values can be used as an indicator for the presence of inhibitory compounds in an extracted sample, lack of inhibition in a quantitation amplification does not necessarily mean there will be no inhibition in an STR amplification. This is because 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, 2µL of extracted sample is added to a quantitation 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 20µL may be added to the reaction for a 9PLEX sample, 15µL for a full volume amplification or 7.5µL for a half volume amplification for a PLEX21 sample (which would increase the relative concentration of inhibitory substances in the amplification reaction).

  There may be additional quantitation information available for a sample (depending on whether it was processed pre/post AUSLAB batch functionality):

  - PSVOL: this is the theoretical volume (in µL) of DNA extract to be added to the amplification reaction in order to achieve a total DNA template of 1.2ng for 9PLEX samples or 0.5ng for PLEX21 samples. Validation studies show that template DNA above this value can produce over-amplified DNA profiles which would likely be unsuitable for interpretation. It is therefore recommended that the input template DNA is not increased above 0.5ng.
  - CTB: this is the CT (cycle threshold) of the DNA extract which is the theoretical PCR cycle where fluorescence of a quantitation reaction increases over a pre-set value (i.e. threshold). This theoretical value is calculated by the software. The CT is compared against the standard curve of samples of a known concentration in order to calculate the quantitation value. A sample that provides a lower CT value (e.g. 25.34) contains more initial template DNA than a sample that gives a higher CT value (e.g. 27.22). Each cycle in a PCR amplification theoretically corresponds to a two-fold increase in product, therefore a difference in 1 CT equates to a two-fold difference in initial template amount. The CTB is expected to be between 15 and 40.
  - IPCCT: this is the CT (cycle threshold) of the Internal PCR Control. The IPCCT is expected to be between 20 and 30 for samples containing no inhibition. If the IPCCT is >40, it is reported as 'undetermined'.

>20 IPCCT <30, >15 CTB < 40	OK (pass)
IPCCT >30, CTB >40	FAIL (full inhibition, automatically has NucleoSpin clean up ordered by Analytical staff)
>20 IPCCT <30, CTB >40	OK (little DNA)
IPCCT >30, >15 CTB <40	OK (Partial inhibition, consider ordering a NucleoSpin clean up if poor results are obtained)

- **Initial amplification volume:** samples may be amplified at a variety of volumes up to a maximum of 20µL for 9PLEX samples, and 15µL for PLEX21 samples. However the default amplification volume for PLEX21 samples is 7.5µL (half volume). Due to normal variation of peak heights between runs, amplifying a sample at the same volume as a previous run may obtain a result with more reportable information.

Not Current

- **The number of alleles obtained**: 12 alleles are required to upload a profile to NCIDD. Samples below this stringency, but above 6 alleles, may be loaded to NCIDD under special circumstances and searched against the database (refer to 23890 – Uploading and Actioning Samples on NCIDD).
- **Examination notes**: Certain substances are known to be inhibitory to the PCR process. This includes a variety of commonly encountered substances, such as dyes used in clothing (particularly denim dyes) and some biological material (in particular, the red coloured haem in blood). Semen samples have also been observed to return an NSD profile after initial extraction with no indication of inhibition. Performing a NucleoSpin clean up may result in improved or full profiles for these samples.
- **Offence Details (if available)**: The information from the QP127, item packaging or from case conferences may assist in determining the evidential value of a particular item.
- **Results already obtained**: If multiple samples have been submitted for an item and one or more full 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 must be considered carefully and in the context of the case. If it is a possibility that there may be a different profile present, such as in the case of multiple offenders, then reworks should be considered.

- If a variant and/or off ladder allele has been observed on a GeneMapper *ID-X* profile the case manager must order a re-amplification to confirm that variant and/or off ladder allele. The case manager must also independently perform the calculation for allele designation. Refer to 17137 (Procedure for STR fragment analysis using GeneMapper *ID-X* software) Case manager must also agree with the calculation performed by the plate reading scientist (enter a specimen note stating this). In the absence of an extract, a re-run is acceptable.

6.2 Explanations of Reworking Methods

6.2.1.1 Concentration of DNA using Microcon columns (commonly referred to as 'Microconning')

- A Microcon filter column may be used to reduce the volume of a sample in order to increase the concentration of DNA. This is achieved by centrifuging the sample through a size exclusion membrane that allows smaller molecules such as salt and water through, but not DNA. Some inhibitors may also be concentrated alongside the DNA.
- Samples may be concentrated to half, full or 30µL for ProfilerPlus®, for PowerPlex®21 samples may be concentrated to half or 20µL.
- For ProfilerPlus® concentrating to half reduces the volume of the sample by approximately half; concentrating to full reduces the sample volume to ~10-15µL; concentrating to 30µL reduces the volume to ~30µL.
- For PowerPlex®21 concentrating to half reduces the volume of the sample by approximately half; concentrating to 20µL reduces the volume to ~20µL (after a microcon, all PowerPlex®21 samples will then be sent for quantitation).
- For ProfilerPlus® only: If 26µL or greater of sample remains after concentration, a quantitation will be performed. If less than 26µL is present, the sample will not be quantitated and the entire remaining volume of sample (or 20µL, if >20µL but <26 µL is present) will be used in the amplification reaction.
- The final volume of sample obtained after a Microcon concentration may be displayed in the results history screen in the column under the MICFCW test code. 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 that the sample was run on.

Not Current

- Due to some variation in volumes after reworking it may be possible to further rework a sample that has been Microcon concentrated. If the final volume of sample remaining after concentration is 50µL or greater a further Microcon may be requested.
- For further information see 19544 Concentration of DNA Extract using Microcon Centrifugal Filter Devices.

Microcon concentration should be considered if a sample has a low quantitation value and shows no indication of inhibition.
For PowerPlex®21: A Microcon can be used to increase DNA concentration, with the aim of achieving template DNA greater than 0.132ng (or a concentration of 0.0176 ng/µl for half volume and 0.0088ng/µL for full volume)

6.2.1.2 Clean up of DNA using NucleoSpin columns (commonly referred to as 'NucleoSpinning')

- A NucleoSpin column binds the DNA in a sample to a silica membrane which is then washed in an attempt to remove inhibitors and purify the DNA.
- As the final volume for a sample that has been cleaned up via NucleoSpin is approximately 100µL (less after quantitation and amplification are performed), there is sufficient volume to then concentrate the sample if required.
- It is also possible to re-NucleoSpin a sample if evidence of inhibition remains.
- For further information see 20967 (NucleoSpin Extraction of DNA).

NucleoSpin clean up should be considered if a sample shows signs of inhibition or if the examination notes suggest the sample could contain substances known to inhibit the PCR process, for example denim dye or seminal fluid.

6.2.2 Use of a different Amplification volume

- Too little or too much DNA in an amplification reaction can result in a partial profile. It is recommended that between 1 and 2.5ng of DNA (for 9PLEX samples) and no more than 0.5ng (for PLEX21 samples) is added to a reaction. Be mindful that (for PowerPlex®21 samples) a mixed DNA profile with a ratio of 5:1 and a template of 0.5ng, the 'minor' DNA contributor will have a template of around 0.083ng. Therefore the entire profile may not be suitable for interpretation given STRmix™ will interpret the profile as a whole, depending on the ratio and template. Samples can be re-amplified at different volumes with the maximum volume of sample added to an amplification reaction being 20µL for 9PLEX samples and 15µL for PLEX21 samples.
- Initial amplification volumes are calculated in relation to the quantitation value, with the goal of adding 1.2ng of DNA into the amplification reaction for a 9PLEX sample, and 0.5ng for a PLEX21 sample.

For a 9PLEX sample:

$$\frac{\text{Amount of DNA (ng)}}{\text{Sample concentration (ng/µL)}} = \text{Volume required for the amplification (µL)}$$

Example: $\frac{1.2\text{ng}}{0.1\text{ng/µL}} = 12\text{µL}$

(NOTE: Prior to CW#1484 the amplification volume was calculated using 2ng)

Not Current

When ordering a re-amplification, TV1 is always 20 minus SV1 (so that SV1 and TV1 add up to 20).

For a PLEX21 sample:

$$\frac{\text{Amount of DNA (ng)}}{\text{Sample concentration (ng/µL)}} = \text{Volume required for the amplification (µL)}$$

Example: $\frac{0.5\text{ng}}{0.1\text{ng/µL}} = 5\text{µL}$

When ordering a re-amplification, TV1 is always 7.5 for half volume and 15 for full volume minus SV1 (so that SV1 and TV1 add up to 7.5 or 15). Due to Auslab constraints, amplification volumes need to be entered into the specimen notes, rather than into the 'results history' page. This applies to PowerPlex®21 samples only.

Re-amplification should be considered if a profile shows allelic imbalance, is partial and has not been amplified at the maximum volume or if it is suspected there is excess DNA in the sample which could be causing inhibition. Increasing or decreasing the re-amplification volume, even by only a small amount can have a significant effect on a PLEX21 profile. Increasing or decreasing the re-amplification volume for a 9PLEX profile has less of an effect. According to validation data, PowerPlex®21 works within a narrower window.

6.2.3 Diluted re-amplification

- Samples can be diluted up to 1 in 20 for a 9PLEX sample and 1 in 15 for a PLEX21 sample through a re-amplification request. If the sample is still showing signs of excess at this dilution, it may be necessary to dilute the sample further.
- The aim of diluting is to obtain a concentration of DNA of 1.2ng/µL for a 9PLEX sample, so that 1µL from this solution can be used in the amplification reaction (thus adding 1.2ng of DNA). The aim for a PLEX21 sample is a concentration of 0.5ng/uL, so that 1µL from this solution can be used in the amplification reaction (thus adding 0.5ng of DNA). The equation below determines the values of SV2 if a dilution is required. For a 9PLEX sample TV2 is always 20 minus SV2 (so that SV2 and TV2 add up to 20). For a PLEX21 sample TV2 is always 7.5 minus SV2 (so that SV2 and TV2 add up to 7.5).

$$C_1V_1 = C_2V_2$$

C_1 is the concentration of the DNA extract as determined by the Quantitation 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/µL as mentioned above for a 9PLEX sample, and 0.5ng/µL for a PLEX21 sample, 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

Therefore the equation may be re-written as:

$$V_1 = C_2V_2 / C_1$$

OR

Not Current

SV2 = (1.2 x 20) / Quantitation (for 9PLEX)

SV2 = (0.5 X 7.5) / Quantitation (for PLEX21)

Dilutions may be needed if a sample is showing signs of excessive amounts of DNA or preferential amplification. It may be useful to dilute a sample with a high quantitation value and signs of inhibition in order to dilute the inhibitor.

6.2.4 Pooling of samples

- Multiple samples submitted from the same exhibit can be pooled after extraction. This is usually done in combination with Microcon concentration of the DNA. Take note of the maximum volumes that can be added to Microcon and NucleoSpin columns if planning to use this method (≤ 500µL).

Pooling of samples should be considered if multiple samples have been submitted from the same area and have yielded partial or NSD profiles.

6.2.5 Re-running

- Re-running involves running a PCR product through the 3130*xl* capillary electrophoresis instrument again. Due to normal variation of peak heights between runs, this may obtain a result with more alleles above reporting threshold but may also increase the height of peaks that have drop-out associated with them therefore artificially representing them as homozygous peaks. Re-running should only be considered if there are peak shadows, spikes, blobs or bad baseline interfering with the interpretation of the profile. Re-running should not be done with PowerPlex®21 samples in order to increase peak heights above the 'Limit of Reporting'. Although not recommended, if the sample is critical a re-run may be ordered in consultation with a HP5, and appropriate specimen notes should be added to explain why the re-run has been ordered. Re-running can also be useful for investigations into suspected 'capillary carry-over'.

6.2.6 GeneMapper *ID-X* Re-reading

- For PowerPlex®21 the GeneMapper *ID-X* software threshold for casework samples is 40RFUs for peaks to be designated as alleles. There is no homozygote threshold for PowerPlex®21 as these peaks are assessed by STRmix™. The thresholds for ProfilerPlus® are 50RFUs for heterozygous peaks and 200RFUs for homozygous peaks. Samples which were originally analysed using the 3130*xl* and read using Genotyper software can have the re-read test code ordered for GeneMapper *ID-X* analysis at the lower validated thresholds. This can only be performed on samples that were analysed using the 3130*xl* and not the 3100 as these thresholds are not validated for data from the 3100. Any Genotyper batches since 10.03.2008 will be 3130*xl* batches. The lower thresholds will label most peaks that were between 75 - 150 RFU (or designated as NR) in Genotyper.

Re-reading should be considered when older cases are reactivated and partial profiles were obtained for samples run on the 3130xl.

6.2.7 Spin-baskets

- A spin-basket contains the original sample substrate that was submitted to the Analytical section and extracted. This sample may still contain information and can be re-extracted.

Re-extracting a spin-basket should be considered for samples of great importance where all other rework techniques have been unsuccessful or when there is a possible issue with the quality of the first extract.

Not Current

6.2.8 Re-sampling

- If an item obtained an NSD profile and all rework options have been exhausted, re-sampling of the item (if a whole item was received) may be considered. Alternatively, examining other items that were not initially examined should be considered.

6.2.9 Re-quanting Differential Lysis swabs

- With the implementation of the Maxwell instruments for the DNAIQ extraction of semen swabs, the epithelial fraction of certain samples are held in the Analytical section and not processed post-extraction. This procedure applies to Priority 2 female SAIK swabs only. All other epithelial fractions from Differential Lysis Extraction samples (e.g. fabric, condoms, Priority 1 SAIK swabs) proceed through the post-extraction steps.
- The samples not proceeding to DNA profile stage will have a processing comment added by the Evidence Recovery Team: 'ext&hold'.
- If the Case Manager requires an epithelial fraction to be profiled, they will need to order a re-quant test code and check the DNA Priority.

6.3 Requesting Reworks

6.3.1 Reworks on AUSLAB batch functionality samples

- All reworks for current samples are carried out through the SF7 Results History screen of the sample.
- Specific tests codes are available for each rework. Refer to 24486 (Explanations of Analytical Test Codes and Batch Types) for the reworks available in AUSLAB and the test codes to be used.

  To request a rework:

  - View the 9PLEX page of the sample
  - Press SF7 to view the results history screen
  - Press SF8 and enter the 'reason for addon' when prompted, e.g. partial profile
  - Enter the 'addon test code' if known or press F1 to view the orderable look up table and select the desired rework
  - Enter 'y' when prompted 'Proceed with addon?'
  - The Results History screen now displays the rework test code in the adjoining column
  - The rework will then be processed through the Analytical Section.
- If the rework requested is a re-amplification or diluted re-amplification, the required volume must be specified:
  - Page down to view the SV1, SV2, TV1 and TV2 fields
  - Enter into each field by pressing F2
  - Prompt appears 'Are you sure y/n' – press 'y'
  - Enter the desired volume and press enter
  - This step must be repeated for all volumes
  - SVI and TV1 must add up to 20µL (for 9PLEX) and 7.5µL (for PLEX21)
  - SV2 and TV2 are used when a dilution is required. For a standard amplification reaction, that is, not a dilution, these fields must be '0'.
  - To enter the volumes required for a dilution see 24012 Miscellaneous Analytical Section Tasks. PLEX21 samples must have their volumes entered into the specimen notes, rather than the SV1, SV2 etc fields.
- If the rework is for a **re-run**, the amplification batch and sample position must be specified. This information is obtained from the Audit Trail (if the sample has been previously amplified multiple times, be careful to choose the correct batch). Enter this information when prompted after you enter in the rework code (an F1 lookup table is available) or it can

Not Current

be added on the 9PLEX(2) page in the re-run processing comments field. The information entered needs to be checked by a second case managing scientist and a specimen note entered indicating that the information is correct. Re-runs should not be ordered on PLEX21 samples.

- Amplification products are not kept indefinitely. The availability of a PCR product should be checked prior to ordering a re-run. For more recent batches, the Analytical Section enters audit notes against the amplification batch when the PCR product has been discarded.
- If the rework is for a **GeneMapper *ID-X* re-read**, the original Genotyper ID and folder number must be specified in the processing comments. Enter this information when prompted after you enter in the rework code (an F1 lookup table is available) or it can be added on the 9PLEX(2) page in the Microcon processing comment field.
- When requesting a **Microcon** rework, the volume to which it is to be concentrated must be entered into the processing comments, that is, to half, to 30µL or to full for ProfilerPlus® and half or 20µL for PowerPlex®21. Enter this information when prompted after you enter in the rework code (an F1 lookup table is available) or it can be added on the 9PLEX(2) page in the Microcon processing comment field.
- To request a **Microcon straight after a NucleoSpin**, request a NucleoSpin test code only and then enter a processing comment stating Microcon to half/30/full for ProfilerPlus® or half/20 for PowerPlex®21 after NucleoSpin cleanup.
- Once a rework is ordered, an interim EXH must be entered for high priority cases. If the interim EXH that has been selected contains no interpretation, such as 'interim result – sample undergoing rework', the result can be validated by the person who entered it. If an interpretation is included in the selected interim EXH, such as 'Interim result - Mixed profile obtained - rework reqd', the result must be validated by someone other than the person who entered it (and must be competent to do so).

Extra barcodes required for processing of a sample

- There is a limit to the number of test codes available for reworks on a single barcode. For ProfilerPlus® or PowerPlex®21 case work samples, there are 3 x re-amplification test codes (AMP1CW, AMP2CW, AMP3CW), 2 x NucleoSpin test codes (NCLCW, NCLCW2), 2 x Microcon test codes (MICFCW, MICCW2), 2 x re-run test codes (RRCW, RRCW2), 1 x re-quant test code (REQC) and 1 x re-read (GMCW) test code.

- If a sample requires further reworking but the available test codes have been used, an extra barcode needs to be created for the sample. **Re-extracting from a spin basket** also requires an additional barcode as there can only ever be one extract in existence for each barcode.
- Between 29 October 2007 (when the first automated DNA IQ casework batch was created) and 19 March 2008 (when routine Off Deck Lysis procedures began) the extraction process required some samples to be **sub-sampled in Analytical** prior to extraction. If this was the case for a particular sample, a specimen note will indicate that the sample was too large and was sub-sampled by Analytical scientists. If satisfactory results were not obtained from the extraction of the portion sub-sampled by Analytical scientists, the remainder of the sample can be requested to be processed under another barcode.
- See Appendix 2 for registering an extra barcode for additional reworks.
- Another process that requires the use of an extra barcode is when several samples are **pooled** together. Refer to Appendices 3 and 4 for pooling pre-batch functionality samples and 17142 (Examination of Items) for pooling post-batch functionality samples.
- Samples that require a **dilution greater than 1 in 20** (for 9PLEX) or **1 in 15** (for PLEX21) or have exhausted the available re-amplification test codes will also require an additional

Not Current

barcode to be requested. See Appendix 5 for instruction on requesting a dilution of a sample.

- Cases that have been received and processed using ProfilerPlus® will have any new receipts of casework samples profiled and interpreted using the ProfilerPlus® system. New evidence samples received for a case which has been profiled using ProfilerPlus® will be profiled using PowerPlex®21. Only the 9 common loci between kits will be used for comparison purposes. For cases where a statement is required, a paragraph explaining the comparison of ProfilerPlus® casework samples and PowerPlex®21 reference samples must be entered in the preambles section. See also 17119 (Procedure for the Release of Results).

6.3.2 Reworks on Pre-AUSLAB batch functionality samples

- If a sample has been completed in DNAMaster/DAD and subsequent reworks are required they are carried out through AUSLAB.

To request a rework:

  - View the 9PLEXX page of the sample
  - Enter the registration screen for the sample by pressing SF10 and copy the registration (F7, F4, SF5)
  - Scan in a new barcode
  - Change the specimen field to 'TRANS'
  - Enter the appropriate DNA priority for the sample
  - The sample Info 1 field must contain the DNA# of the sample
  - Order a 9PLEX or PLEX21 test code depending on the request from QPS
  - When prompted to enter a processing comment identify the type of rework required, e.g. Microcon to full
  - Save the registration screen be pressing F7, F4, F4
  - The DNA# must then be entered into the 'connected barcode' field of the 9PLEX page
  - Once reworks are finalised, the 'Accepted Barcode' field needs to be filled out. If the original DNAmaster profile is the best profile, enter the DNA# into this field. If the AUSLAB profile is the best profile, add the barcode to this field.

Note: During registration, 'TRANS' must be entered into the specimen field before adding the 9PLEX test code

- If a sample to be reworked has never been registered in AUSLAB (e.g. an old F# sample) see Appendix 6 for instruction on requesting a rework.

6.3.3 COfiler

Prior to samples routinely being processed using PowerPlex®21, additional work using the COfiler kit could be ordered if required. Previously, samples processed using the ProfilerPlus® kit could also be amplified with the COfiler kit which amplifies an additional 4 loci.

- This was requested in the registration screen (SF10) of a sample by ordering the test code 'COFIL' for crime scene samples or 'COFILR' for reference samples.
- The COfiler page will has its own results history screen which can be accessed using SF7.
- After a COFIL test code had been requested, the required amplification volumes were automatically populated based on the selected ProfilerPlus® amplification volumes.
- Any ProfilerPlus® sample can be processed using the PowerPlex®21 kit to amplify additional loci, as the COfiler kit is no longer used.

Not Current

6.3.4 Reworking evidence reference samples

- After its initial run, any evidence 9FTAR reference samples with analysis/profile issues are reworked by the plate reader by entering the comment CPUNCH or BPUNCH PP, (comment will trigger next step and it will auto order the appropriate rework) The CPUNCH comment triggers an EFTA code to be ordered and the BPUNCH comment triggers an EBLD to be ordered. This means the FTA card is punched and extracted.
- Any evidence PLEX21 samples which have issues after the initial run will be reworked by a change in PCR cycle number; the initial run being 26 PCR cycles. The plate reader comment will trigger the subsequent rework (FTARUN=27 cycles, FTAOSD=25 cycles, FTARPT=26 cycles). Samples which have an initial run resulting in an NSD or partial profile will be reworked using 27 PCR cycles, excess (XS) samples with 25 PCR cycles, and samples requiring a repeat to confirm an issue (variants, ULPs, OLAs) will be reworked with 26 PCR cycles. After this 2nd run, if the sample still has issues it goes to CPUNCH or BPUNCH (full manual extraction).
- If the reworked sample still has issues (applies to ProfilerPlus® and PowerPlex®21 samples), the plate reader enters the comment EVDRW and inserts the sample onto the EVDCM work list which the Intelligence Team monitors and actions on a weekly basis.
- It may be necessary for the case manager to order reworks on evidence reference samples if it has not yet been actioned from the EVDCM work list.
- The reworks that are available to order on ProfilerPlus® reference samples are: 3 x re-amplifications (AMP1RE, AMP2RE, AMP3RE); 1 x re-run (RRREF); 1 x Microcon (MCREF); 1 x NucleoSpin (NCLRF); 1 x re-quantitation (REQR); and 1 x GM-*IDX* re-read (GMREF).
- The reworks that re available to order on PowerPlex®21 reference samples are: 3 x re-amplifications (R21AM1, R21AM2, R21AM3), 2 x re-run (21RRRF, 21RRF2), 1 x microcon (MCONR), 1 x re-quantitation (21REQR), 1 x nucleospin (NSPNR).
- It is important that the correct rework test code is ordered for reference samples via the SF7 results history screen. **Reference sample reworks must not be ordered with case work test codes**.
- Once a sample has been processed under an EFTA/EBLD, an extract exists. If the above reworking techniques have not yielded a full profile, a further extraction can be ordered but must be under a new barcode. There can only be one extract in existence for each barcode.
- If, after several attempts, a full profile is still not available, a request may be made to QPS for another evidence reference sample to be collected and delivered to DNA Analysis. Discussion should take place with your line manager before ordering extra barcodes on evidence reference samples.

6.4 Samples with Undetermined Quantitation Values

- This applies to samples that have an undetermined quantitation value for 9PLEX samples, and less than the Quant LOD (0.0021ng/uL) for PLEX21 samples.
- A designated Analytical Section staff member will perform the following case management steps: See also 19977 (Automated Quantification of Extracted DNA using the Quantifiler Human DNA Quantification Kit).
    - For 9PLEX: Access the VSL list and check that each sample has an IPC <30, the Quant is Undetermined, the Team is Volume & the priority is 3.
    - For PLEX21: Access the VSL list and check that each sample has an IPC <30, the Quant is less than the Quant LOD (0.0021ng/uL)
    - On the 9PLEX/PLEX21 page press SF7 to access the results history screen. Save the profile (which will be blank) by pressing F7 Select Preferred then SF6 Save

Not Current

Preferred Profile. This will transfer the quantitation information to the 9PLEX/PLEX21 page.

- Add your name to case scientist field, "finished" to the DNA profile result field, and today's date to the completed date field on the 9PLEX/PLEX21
- On the 9PLEX(2)/PLEX21(2) page, enter the Quant batch ID to complete the batch, and press F6 to validate the page
- On the EXH page enter the barcode into the Lab no field of the next blank EXH line and enter "NDNAD" (no DNA detected) into the result/status field. NOTE: if the sample is a sub-sample, the EXH will be entered into the parent barcode (see Client Reference barcode to find parent barcode).
- List insert the sample onto the VOLUND list (if the sample is a sub-sample, insert both the 9PLEX/PLEX21 and EXH barcodes onto the list).
- Use SF9 to access the results summary page. If the sample is the only sample in the case, or all other samples in the case are also undetermined or completed, then the case can be written off.
- Enter into the CS page and change the case status to "Sent to Peer Review"
- Remove the sample from the VSL list
- If there are more samples in the case, and the remaining samples have not yet been finalised then no further work is required by the Analytical Section case manager. The EXH for the undetermined quant sample will be reviewed from the VOLUND work list, and the remaining samples and case will be case managed and reported by FRIT.

- A competent Analytical Section staff member will review the samples from the VOLUND work list:
  - Access the VOLUND list and check that each sample has an IPC <30, the Quant is Undetermined, the Team is Volume & the priority is 3.
  - For 9PLEX and PLEX21 samples: check that the case managing scientist has entered their name, entered 'finished' into 'DNA profile result' field and the date into the relevant field.
  - Check that the Quant batch ID has been entered on the 9PLEX(2)/PLEX21(2) page
  - Enter your name into the reviewed by field and validate (F6) the 9PLEX/PLEX21 and 9PLEX(2)/PLEX21(2) pages
  - Review the information entered into the EXH page. If correct, enter "rev" or "r" into the corresponding peer review field and press F6 to validate the page
  - Use SF9 to access the results summary page. If the sample is the only sample in the case, or all other samples in the case are also undetermined or completed, then the case can be written off.
    - Enter into the CS page and change the case status to "Analysed Report not Required" (ARNR), the date completed field to today's date (t) and the exhibits field to "destroyed, subsample retained" (DESTSR)
    - Press F6 to validate the page
    - Navigate to the administrative review page and enter your name into both Reviewed by fields, today's date in both Date of review fields, "N/A" in all other fields except for "Yes" in the All results checked and validated field
    - Press F6 to validate the page and remove the sample from the VOLUND list (F5)
  - If there are more samples in the case, and the remaining samples have not yet been finalised then no further work is required by the Analytical Section case manager. The remaining samples and case will be case managed and reported by FRIT.

6.5 Cease Work

- For a sample that no longer requires any work to be carried out on it, a CWORK test code should be requested from the SF7 results history screen. The priority of the sample should be changed to 6 on the registration screen (SF10).

Not Current

- The sample is then allocated to the cease work batch allocation list. 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, no further processes will be undertaken.
- The cease work page needs to be completed with details of the person ordering the cease work and the reason that no further work is to be carried out on the sample.
- If work is to be re-started on a sample at a later date due to a priority upgrade or advice from QPS, order a re-work test code as normal and change the priority as appropriate. If the sample had not been extracted prior to the CWORK being ordered, a second barcode is required in the same way that re-extracts are ordered. An appropriate EXH line should also be entered for samples that have been re-started, for example, 'Testing restarted on advice from QPS' (refer to 23008 Explanations of EXR/EXH Results for further detail).
- See Appendix 7 for detail on finalising samples that are no longer required.

7 FINALISING RESULTS

- Once a result has been assessed and chosen as the final result for a sample, it should be saved in AUSLAB as the best profile, and the appropriate interpretation should be entered in the EXR/EXH page for validation and transfer across the forensic interface.

7.1 Saving a preferred profile in AUSLAB

- The results of a sample are displayed in the Results History screen which is accessed from the 9PLEX/PLEX21 page of a sample. This screen lists all of the results that have been obtained for a sample.

  To save a preferred profile

  - From the 9PLEX/PLEX21 page press SF7 to view the results history screen
  - To select the preferred profile, navigate 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/PLEX21 page.
  - To change the preferred profile, simply enter back into the results history page and repeat the above steps, selecting the new preferred profile.

Not Current

Diagram 1: Results History screen (SF7)

- For 9PLEX samples: changes are able to be made to the saved preferred profile, e.g. if the scientist thinks that a called peak is stutter instead of a true peak. Any changes must be made on the Results History screen (SF7) and the preferred profile re-saved. These changes need to be made before the 9PLEX page is reviewed. An audit entry should also be inserted stating why the change was made. 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 noted on the profile print out for the sample. For paperless case, a specimen note should be entered detailing the changes made. The original Genotyper or GeneMapper *ID-X* files are not to be altered.
- If a change is required for a 9PLEX sample due to an error during plate reading, the following needs to occur:
    - Only a person deemed competent to train in plate reading is to update GeneMapper ID-X. This person will change and re-export the project.
    - The case manager is to email the original plate reader and CC the GeneMapper ID-X Co-ordinator, outlining the issue.
    - The profile should be amended in AUSLAB by the case manager.
- The case manager then places the corrected EPG within the casefile or converts and uploads the corrected EPG to AUSLAB (for paperless cases).
- For PLEX21 profiles, the plate reader is responsible for removing blobs, spikes, artefacts and post-stutter. After this has been done, profiles are run through a macro to remove stutter.

- If a change is required to a PLEX21 sample (ie if the plate reader has left a labelled artefact on the profile) at case management stage, the following will need to occur:
    - The GeneMapper *ID-X* results file will need to be altered and re-exported.
    - Only a person deemed competent to train in plate reading is to update GeneMapper ID-X. This person will change and re-export the project.
    - The case manager is to email the GeneMapper *ID-X* Co-ordinator, outlining the issue.
    - The profile should be amended in AUSLAB by the case manager
    -
- The case manager then places the corrected EPG within the casefile or converts and uploads the corrected EPG to AUSLAB (for paperless cases).
- The *'Completed Date'* field (for both 9PLEX and PLEX21) and the *'DNA Profile Result'* field automatically populate when a profile is saved as the preferred profile to the 9PLEX/PLEX21 page. If the profile section of the 9PLEX/PLEX21 page remains blank, such as for samples with connected barcodes, these fields need to be manually entered with the date (this information can be obtained from the audit trail).
- If the preferred profile has been reassessed and then subsequently changed (due to further reworking) the information entered into the *'Reviewed by'* field on the 9PLEX/PLEX21 page must be deleted and re-reviewed by another competent case manager.

7.2 Case Management of Paternity samples

For paternity cases, an EXH will have to be registered under a new barcode so that results can be communicated back to QPS via Auslab. A follow-up phone call should be made to DRMU to explain the new barcode and EXH. The format for the results to be entered into the new EXH is: **child barcode** in Lab No. field, **profile result** in Result/Status field, **alleged father/mother** in Linked No. field, **name** in Warm Link Name (of alleged father/mother).

- If a Guthrie card is used and an EXH is registered on that barcode, a subsample barcode will usually be registered for the sample submission. The initial line in the EXH will be: **Guthrie card barcode** in Lab No. field, **profile result** in Result/Status field.
- If the putative father sample is an intelligence sample, the relevant EXH would be 'Intel report required for further Interpretation'.
- Liaise with DRMU if required to determine the appropriate EXH line to use to best suit their method of reporting.

7.3 Using Coronial samples as Reference Samples in EXHs

- A subsample for the bone/muscle is to be reported back matching itself, and therefore appear as a reference sample match in AUSLAB.
- This allows the coronial sample to become the reference sample for that continuation of the case.
- Barcode details and person details (Date of Birth, name and type of exhibit) are to be provided to QPS DRMU before the information in the EXH is sent.

7.4 Printing cumulative tables

- Cumulative results tables may be prepared in the initial stages of case management to assist with printing profiles as they list all samples from a case in one Excel table, including which Genotyper and/or GeneMapper *ID-X* runs they have been analysed on.
- A cumulative table may be prepared at the conclusion of case management to represent final results if the case manager feels that it will assist in interpretation and review. A

Not Current

cumulative table is required if a 95A Evidentiary Certificate is to be issued. See also 17119 (Procedure for the Release of Results).

- The table formatting can be changed to suit the preferences of a particular scientist however profile results should not be edited in the cumulative table. All changes to results should be made through AUSLAB with appropriate audit entries or through the DADI by a Corrections User.

7.4.1 AUSLAB Batch Functionality Cumulative Tables

To create a Cumulative table:

- Enter into the 9PLEX page for a sample in the case
- Press F9 to display the Cumulative Results for the case. Any lab numbers without a profile recorded against them have not had their preferred profile saved or have not had their batches completed and will not have a profile exported
- 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, e.g. H:\06068881.txt
- If you do not save the file with the extension .txt you can add this later by navigating to the file in your H drive and renaming it with the .txt extension
- Open the macro 'QIS 19952 Cumulative Result Macro' located in I:\Macros and enable macros when prompted. This macro is suitable for 9PLEX cases only.
- Click on '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

- The Cumulative Results function will only display samples for one particular UR number. All associated evidence samples, COR samples and samples from other associated cases will not automatically pull into the Cumulative Results table. A sample from each UR number needs to be exported separately.

Diagram 2: Cumulative Results screen in AUSLAB (F9)

To combine cumulative results from different UR numbers in one table:

- Export separate Cumulative Results files for each UR number that needs to be displayed together in a final table.
- Import the first file into the macro 'QIS 19952R4 Cumulative Result Macro'
- Click the 'Append Data' button and enter your initials again
- Navigate to find the next saved Cumulative Results file and double-click on it
- Continue to append each file.

- 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 in AUSLAB prior to export or entered into the Excel spreadsheet, or manually entered into the spreadsheet. Currently the 'Cumulative Results' macro is only suitable for 9PLEX cases. Cumulative tables for PLEX21 cases will need to be created manually.

7.4.1.1 Pre-AUSLAB Batch Functionality (DNAmaster/DAD) Results Tables

- Prior to AUSLAB Batch Functionality, all results obtained 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 DNA Analysis Database Interface (DADI). Refer to 25583 (Use of DNA Analysis Database Interface).

7.5 Printing Genotyper and GeneMapper *ID-X* profiles

- Genotyper profiles are located in J:\User3100\Results Finalised\PRE-LIMS and I:\User3100\AAARESULTS FINALISED\POST-LIMS
- As of the 16th February 2009, results have been analysed using GeneMapper *ID-X*. GeneMapper *ID-X* profiles are located in P:\Profile PDFs and only accessible from computers with GeneMapper *ID-X* installed (contains all DNA profile results from 16th February 2009 until June 2012). As of July 2012, all DNA profile results are located in O:\Profile PDFs (accessible from all network PCs). A brief sample description must be written on each profile.
- All runs must be printed for each sample. The preferred profile for each individual sample barcode must be stamped with 'Reported Profile' and the interpretation of the profile written on the bottom of the page, and signed and dated by the person making the interpretation.
- EPGs that have been converted to JPG must be uploaded to AUSLAB for samples that are to be loaded to NCIDD. This is required even if the case is being managed with a traditional paper file.
- For details on how to upload JPGs to AUSLAB refer to 26874 (Procedure for Paperless Case Management and Review).

7.6 Requesting a mixture page in AUSLAB

- For 9PLEX samples: If a mixture is present in a profile and it is possible to separate the mixture into major and minor contributors, or if the mixture can be conditioned against a known profile, a mixture page should be registered and completed in AUSLAB.

To request a mixture interpretation page:

- Enter into the 9PLEX page of the sample
- Press SF10 to enter into the sample registration screen
- Enter in the test code required, i.e. MIXT for major/minor or MIXC for conditioning

Not Current

- 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 at the time of the interpretation

- To print the mixture interpretation page for inclusion in the case file press SF11, then F7 and direct to a printer.
- For PLEX21 samples: If a mixture is present in a profile which is assessed by the case manager as suitable for STRmix™ deconvolution and subsequent NCIDD upload, a Manual NCIDD Upload form PowerPlex®21 31512 should be completed. The EXH reviewer will then deliver the paperwork to the Intelligence team for upload to NCIDD. Following upload, the paperwork will be scanned into Auslab. For information on mixture interpretation guidelines using STRmix™ see also 31523 (Interpretation and Statistical Analysis of DNA profiles Using the STRmix™ Expert System).
- For 9PLEX samples: if a 'minor' component in a mixture is assessed as suitable for comparison purposes, a 'zoom' of the profile .jpeg image must be uploaded into Auslab by the case manager.
- For PLEX21 samples: a 'zoom' of the profile .jpeg image may need to be uploaded into Auslab in order to assist the case manager/reviewer in determining number of contributors to a DNA profile. This assessment and upload should be done by the case manager.

7.7 Entering Final EXR/EXHs

- Final EXR/EXHs should be entered in accordance with 17119 (Procedure for the Release of Results) and in consultation with 23008 (Explanations of EXR/EXH Results) and see also 31523 (The Interpretation and Statistical Analysis of DNA Profiles using the STRmix™ Expert System).
- EXR and EXH pages vary slightly in their appearance however the information entered is the same (for 9PLEX samples). EXH pages for PLEX21 samples are the same as for 9PLEX pages, however due to interpretational changes in DNA profiles processed through PowerPlex®21 most of the EXH lines used will be different.

Forensic Register Exhibit Report
Item Desc: 1 x SAIK
Location : Taken from complainant
Screening: SEMEN
Rationale:

Team : Yellow
Collected By: SOC Off.
Forensic Rel: V
Operation :

	Lab No.	Result / Status	Linked No.	Warm Link Name	Peer Review
1		Micro positive for sperm. Submitted-Results pending			Reviewed 03-Nov-08
2		Mixed DNA profile conditioned on			Reviewed 26-Mar-09
3		Mixed profile. Remain profile after cond. - insuff NCIDD	ukm1		Reviewed 26-Mar-09
4					

Diagram 3: Final results in an EXH page

Not Current

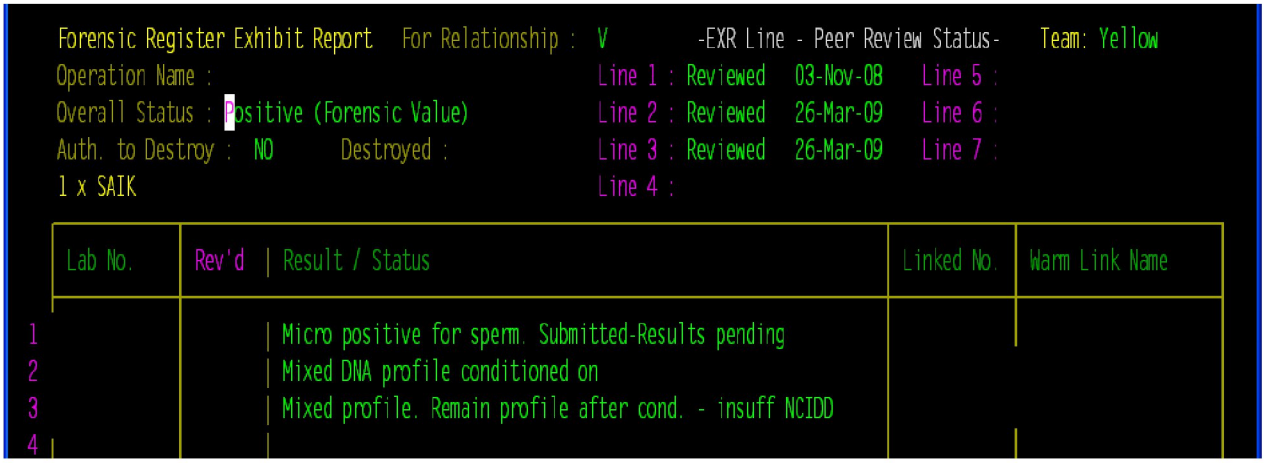


Diagram 4: Final results in an EXR page

- 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) 'UKM1' (for a male profile), 'UKF1' (for a female profile) or 'UKP1' (if gender is undetermined) is entered into the Linked No. field. Each subsequent unknown is given a consecutive denomination, e.g. UKM2, UKM3 etc. This applies to single source samples profiled through PowerPlex®21. It also applies to single source ProfilerPlus® samples, Major/Minor mixtures and 'Remaining' profiles. See also 31523 (Interpretation and Statistical Analysis of DNA profiles Using the STRmix™ Expert System)
- Use of unknowns in mixture EXHs (PowerPlex®21) – Profiles deconvoluted and uploaded to NCIDD from STRmix™ need to have a new barcode assigned to the actual profile being uploaded. These profiles act as sub-samples and need to be registered in AUSLAB.
    - Copy registration of relevant EXH and register new barcode (Shift F10, F7, F4, Shift F5), add associated EXH barcode to Client Reference (so it appears as External ID in Shift F9), add MISC to Specimen Type, add details to Sample Info Field (eg. UKM1, or reference sample barcode), request FBIOLW test code and enter through the fields. Save registration. Validate the FBIOLW page in AUSLAB. See also 17119 (Procedure for the Release of Results)
- NOTE: If a sample cannot be explained by one of the EXH results available, an intelligence letter should be sent to QPS to outline the interpretation. See also 24015 (Procedure for Intelligence Reports and Interstate/Interpol Requests).

7.8 Finalising Results for samples with Extra Barcodes

- Where an extra barcode has been used for reworking there are some additional steps that need to be undertaken to ensure a clear link between the two barcodes and to explain why the final result may be reported under a barcode which is different to the one that a presumptive result was reported under.

7.8.1 Finalising 9PLEX/PLEX21 pages with extra barcodes

- Every 9PLEX/PLEX21 page should have a profile saved as preferred unless the sample has no 9PLEX/PLEX21 result, such as those pooled after extraction and those diluted by Analytical after quantitation. Samples that had processing ceased and those with no DNA detected will also have no information saved into the 9PLEX/PLEX21 page.
- The *'Connected Barcode(s)'* field should contain all barcodes that have been used in the processing of the sample and/or all barcodes that a sample has been pooled with.

Not Current

- The *'Accepted barcode'* field should contain the barcode under which the final preferred result was obtained.

7.8.2 Finalising EXR/EXH pages for samples with extra barcodes

- If the barcode of the final preferred profile is the same as the original barcode used to report the presumptive results, the final result can be reported via EXR/EXH under that barcode.
- If the barcode of the final preferred profile is different to the original barcode used to report the presumptive results (but refers to the same sample), an EXR/EXH line explaining why must be entered. The final result is then reported under the barcode that it was processed under.

Example 1 (for 9PLEX/PLEX21 samples):

A sample with barcode 111111111 was submitted to Analytical. The sample was diluted in Analytical due to an excessive quantitation value. This diluted sample was assigned the barcode 222222222, and continued through the amplification process. The profile for 222222222 was assessed to be male, full and unique within the case (with no reference profiles). The final EXH below is for a 9PLEX sample. The EXH would be different for a PLEX21 sample ie 'NCIDD upload single source DNA profile' would be the 'Result/Status' field.

Lab No.	Result/Status	Linked No.	Warm Link Name
111111111	Submitted – results pending		
111111111	Sample processed and final results under	222222222	
222222222	9 loci DNA profile. Uploaded to NCIDD	UK M1	

Example 2 (for 9PLEX/PLEX21 samples):

Wet and dry swabs of the handle of a knife were taken and submitted separately to the Analytical section. Exhibit barcode (knife) – 111111111; Wet swab – 222222222; Dry swab – 333333333. The presumptive EXR/EXH was entered under the barcode for the wet swab. Both the wet and dry swabs yielded partial profiles with sub-threshold peaks, and it was decided to pool the samples. Samples were pooled under barcode 444444444 and processed further. A partial profile (13 alleles) matching that of the suspect (John Smith), barcode: 555555555, was obtained. The EXH would be different for a PLEX21 sample ie. 'SS DNA profile < 9 loci LR 1 million - 1 billion' would be the 'Result/Status' field.

Lab No.	Result/Status	Linked No.	Warm Link Name
222222222	Submitted - results pending		
222222222	Sample pooled and processed under	444444444	
444444444	Partial DNA profile	555555555	SMITH, J.

7.8.3 Creating new EXH barcode for PLEX21 profiles post-deconvolution (PLEX21)

- If an exhibit has been sub-sampled, and a mixture is obtained from a sub-sample that can be deconvoluted leading to a profile that can be uploaded to NCIDD, a new EXH should be registered to hold this information
- The 'Sample processed and final results under' EXH should be used in the parent EXH
- An email should be sent to QPS DRMU explaining the new EXH

Not Current

7.9 Finalising Results in AUSLAB for Pre-AUSLAB Batch Functionality samples

Samples that were initially processed under the DNAmaster system, but have since undergone additional processing through AUSLAB, need to be finalised in the following way:

- Samples processed prior to AUSLAB Batch Functionality were assigned an additional identifier by the Analytical section known as a DNA#. This number was used to identify samples during processing in Analytical.
- Samples extracted through DNAMaster and further worked in AUSLAB 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(s)'* field on the 9PLEX/PLEX21 page for the sample with the DNA#.
- Any samples processed in AUSLAB prior to Batch Functionality will have a 9PLEXX page registered. The 9PLEXX page does not display 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.

7.10 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. These profiles must have at least 12 alleles for NCIDD matching.
- Profiles of less than 12 alleles may be loaded to NCIDD in special circumstances. Please consult with the Senior Scientist in the Intelligence Team prior to uploading. Any matches generated will be reported through an EXR/EXH. In certain circumstances, a profile with less than 12 alleles (including sub-threshold information) can be loaded to NCIDD, and any matches will be reported back to QPS via and Intelligence report written by the case scientist.
- Mixed DNA profiles can be interpreted for Intelligence purposes and uploaded to NCIDD by the Intelligence team. For 9PLEX samples within high priority cases only:
    - Add EXH 'Mixture Interp reqd – Intel profile loaded to NCIDD'
    - Complete mixture page with major/minor alleles for upload (non-loadable alleles to be entered into 'minor' component
    - Reporting team review EXH line, 9PLEX page and mixture page.
    - Comment field on mixture page to read 'major – intel load'
    - List insert to NCIDD and BVAA work lists

    The Intelligence team will then monitor the BVAA work list, upload the profile to NCIDD with the suffix '-Intel', and write and issue the Intelligence report via QPS email communication. The original report will be stored within the Intelligence area in Block 6.
- Profiles that match known deceased persons or complainants in sexual assault cases are not to be uploaded to NCIDD. Refer to 23890 (Uploading and Actioning Samples on NCIDD) for QHFSS policy on which case work samples can be uploaded to NCIDD.
- Once a sample to be uploaded has been selected, the case manager must list insert it onto the NCIDD worklist (through Shift-F12 NCIDD). The reviewer should check in the audit trail that this has been done.
- If the DNA profile to be uploaded to NCIDD is from a mixture which has only been partially deconvoluted through STRmix™, and another single source profile appearing to match the

Not Current

partially deconvoluted profile is not yet completed (however looks as though it will be completed within 1-2 days), do not upload the partial deconvoluted profile. A partially deconvoluted profile would be considered an Intelligence upload, where a regular NCIDD upload is preferential. Wait for the single source to be completed for upload purposes. List insert the samples involved to your personal communications list in Auslab so that you can case manage them as results become available. See also 31523 (Interpretation and Statistical Analysis of DNA profiles Using the STRmix™ Expert System).

- For PLEX21 mixed DNA profiles, refer to 31512 (Manual NCIDD Upload form PowerPlex 21). This should be used for mixed DNA profiles that have been deconvoluted in STRmix™ and have a contribution that is required to be uploaded to NCIDD. This form should be signed and dated by the case manager and reviewer, then delivered to the Intelligence Team where the profile will be uploaded. The form will be scanned under the EXH.

7.10.1 Printing an NCIDD upload form from DADI

- Pre-AUSLAB batch functionality samples that are selected for upload cannot be list inserted on the NCIDD work list and an upload form must be printed and delivered to the Intelligence Team.
- To obtain an upload form for a sample on DNAmaster/DAD, open DADI and search for the sample. Click on the Print Upload Form button. Refer to 25583 (Use of DNA Analysis Database Interface (DADI).
- A barcode may be printed from AUSLAB and attached to the form in the appropriate location for these samples to allow for easier scanning into AUSLAB.

8 CASES THAT ARE NO LONGER REQUIRED

- Information may be received that indicates that a case is no longer required. This may be in the form of an email from the QPS, an 'N' appearing in the Forensic Relationship field for a case/sample in AUSLAB, or insertion on the FBNLR work list by SSLU.
- Refer to Appendix 7 for instruction on how to finalise cases that are no longer required.
- For cases dated prior to September 2009: for items no longer required, SSLU will add NWQPS into the EXH, case manager will finalise case.
- For cases dated September 2009 onwards: SSLU will add the relevant samples to FBNLR list, case manager will add appropriate EXH (NWQPS or NWQPSR) and will finalise case.
- If the EXH 'NWQPSR' (No further work required as per QPS – results available) is reported back for a sample, and QPS decide that results are required, SMU will advise SSLU via email. This will then be communicated by SSLU via the CSRC Auslab work list so that case can be reactivated and the relevant sample(s) reported. The priority will remain as low (3) unless otherwise advised by QPS.

9 FILE COMPILATION

9.1 Suggested order of pages (from top to bottom)

- Case file particulars page
- Copy of final statement (if written)
- Most recent printout of UR notes, emails and other communications*
- DNA results table (if deemed necessary)
- Reference samples – receipt page then profile

Not Current

- QP127 (if available) and receipt page
- Examination notes:
    - Description of item
    - Diagrams
    - Photos/photocopies/AUSLAB images*
    - Profiles
    - Mixture interpretation sheets if applicable
    - Statistical calculations if applicable
- Subsequent QP127 (if available), receipt page and examination notes etc…

  * these items are not required to be printed if the case is not going to court

9.2 Page numbering

- Only cases that are going to court (Statements of Witness or Evidentiary Certificates) need to be page numbered.
    - The Case File Particulars page is always Page 1 (except upon reactivation when the additional Case File Particulars page will be numbered page 1 and the original Case File Particulars page will be renumbered as the next consecutive number in the case file).
    - Case Files are numbered from the back of the case file to the front.
    - Number and initial each page, including the reverse of the page if both sides have been used.
    - Ensure the Case number is recorded on each page.
    - Write the total number of pages on the front of the case file and initial and date as indicated.
    - Assistance is available from the Administrative Team for page numbering.
- For those cases that aren't going to court, the total number of pages simply needs to be noted on the front of the case file, that is, each individual page does not need to be numbered.

9.3 Statement compilation

- Refer to 17119 (Procedure for the Release of Results) for the correct format for statements or reports issued by DNA Analysis.

9.4 AUSLAB finalisation

- EXR/EXH page – ensure each sample has the appropriate interpretation entered
- 9PLEX/PLEX21 page – ensure each sample has a saved preferred profile.
- FBEXAM – ensure this page is validated. This page will not validate if required fields do not have entries, e.g. Examination Trolley. Enter N/A or refer to the examination notes for details.
- CS – change the status to "Sent to Peer" and validate.
- Forensic Receipt page – ensure this page is validated
- Return Destruction and Report Release Details – Validate these pages.
- Tech Review Page (FBTR) – order an FBTR from the registration page if required
- FBCALC – order an FBCALC (for 9PLEX samples only) from the registration page if Kinship has been used. Complete and validate.

Not Current

9.5 Preparing a case file for peer review

- Prior to submitting a case file for final review or prior to a statement being issued, the following is required:
    - Ensure that all items/exhibits have been examined or prioritised appropriately.
    - Ensure that appropriate reworks have been performed.
    - Establish whether further testing needs to be performed
    - Ensure that all samples are finalised and a preferred profile saved on the 9PLEX/PLEX21 page.
    - Enter the final results in to the EXR/EXH.
    - All profiles have been printed and included in the case file. Each profile should have a brief description of the sample written on it and the best profile for each sample should be stamped with 'Reported Profile'. An interpretation of the profile must also be written on the EPG and signed and dated by the person making that interpretation.
    - Ensure that appropriate profiles have been selected for upload to NCIDD. Only one example of each profile is to be loaded to the database.
    - Ensure that the reference sample receipt is printed for each evidence sample. To print the reference sample receipt page press SF11, then F7 and direct to a printer. Ensure that all evidence samples associated with the case are present in the final table (if one exists).
    - STRmix™ printouts for all paper cases.
    - For 9PLEX cases: if a statement has been requested, ensure that profiles requiring a genotype frequency have had the statistical calculation performed through the Kinship program and that the results are printed and included in the file.
    - For PLEX21 cases: if a statement has been requested, ensure that profiles requiring a STRmix™ interpretation have had the statistical calculation performed through the STRmix™ program and that the results are printed and included in the file.
    - For 9PLEX cases: ensure that any mixed profiles have been interpreted using the MIXT or MIXC pages in AUSLAB or the determination of genotypes (if required). A copy of the worksheet or a print-out of the page from AUSLAB should be included in the file.
    - For PLEX21 cases: ensure that any relevant profiles have been interpreted using the STRmix™ program.
    - For 9PLEX cases: if applicable, ensure that any complex mixtures are interpreted with appropriate 'Popstats' hypotheses and/or calculations.

Not Current

10 REACTIVATED CASES

On occasion, some cases require further work after they have been finalised and reviewed.

- 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.
- A UR note should be entered detailing the reason for the re-activation, e.g. Reactivated for further examination of exhibits, or Reactivated for statement purposes. This is helpful for Property Point when deciding whether or not exhibits can be returned to QPS.
- An assessment of previously reported and uploaded profiles should be undertaken. In July 2007, it was decided (in conjunction with QPS) that all crime scene profiles (except Known Deceased and complainants in sexual assault cases) could be uploaded. Prior to this any crime scene sample that matched a complainant profile for **any** case type was **not** uploaded to NCIDD. Since the introduction of GeneMapper *ID-X* software and lower thresholds, it may also be advantageous to rework samples in an attempt to obtain more information from a profile than may have previously been reported as insufficient for interpretation (if time restrictions permit).

- A new case file particulars page is required to easily distinguish between the original section of the file that has been reviewed and the newly added pages.
- Any additional Administrative and Technical Review needs to be requested on a new barcode.
    - Technical reviews are only required on cases with a statement / addendum statement.
- If the case was processed using ProfilerPlus®, any samples on future receipts for that case will also be processed with ProfilerPlus®.

10.1 Case managing samples from the 1EVD list

- Evidence samples are added to the 1EVD list by Operational Officers through list insertion from the case CS screen. When a reference sample is complete it will be case managed from the 1EVD list (see Appendix 9).
- Case status should be changed to 'reactivated', Evidence sample should then be compared to all relevant profiles with EXRs/EXHs/mixture pages updated accordingly.
- Case manager to delete original case manager and review name, add their name as the case scientist, then manually list insert case or EXH to appropriate review list for review.
- UR note to be added for 9PLEX/PLEX21 cases to say 'comparison complete-awaiting review', change status to 'sent to peer', manually delete sample from 1EVD list.
- Cases that have been received and processed using ProfilerPlus® will have any new receipts of casework samples profiled using the ProfilerPlus® system. New evidence samples received for a case which has been profiled using ProfilerPlus® will be profiled using PowerPlex®21. Only the 9 common loci between kits will be used for comparison purposes. The EXR/EXH lines used for update purposes will need to be selected appropriate to the kit used for initial processing (ProfilerPlus® / PowerPlex®21). See also 23008 (Explanations of EXR/EXH Results).
- Any interstate person samples submitted for analysis by the DNA Management Section (QPS) that have been obtained from people located interstate are to be treated as Evidence samples (as per advice from the Queensland Police Service).

11 CASE FILE MANAGEMENT OFF SITE

- 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 should be recorded when prompted documenting why the case file is to be borrowed. The person taking the file off site is solely responsible for maintaining chain of custody and confidentiality at all times.
- If the case file is requested by court officials a photocopy of the file is to be offered. The case file is the original copy and this must be retained by QHFSS DNA Analysis.
- 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 (e.g. Freedom of Information Requests). Where this is the case the Team Leader must be notified in advance and 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 the anticipated return date. When the original case file is returned the copy should be destroyed.

12 COURT APPEARANCES

- Notices to attend and give evidence should be recorded in AUSLAB.
- Any court appearances should be recorded in AUSLAB. A CCD code should be requested and the pages filled out appropriately.

Not Current

13 REFERENCES

Inman, K & Rudin, N. (2001) *Good Forensic Practice - Obligations of the Analyst*, in Principles and Practice of Criminalistics. Boca Raton:CRC Press.

14 ASSOCIATED DOCUMENTS

1	16004	AUSLAB Users Manual – DNA Analysis
2	17038	Case File Particulars
3	17116	Procedure for the Receipt of DNA Exhibits
4	17119	Procedure for the Release of Results
5	17137	Procedure for STR fragment analysis using GeneMapper *ID-X* software
6	17142	Examination of Items
7	19544	Concentration of DNA Extract using Microcon Centrifugal Filter Devices
8	19977	Automated Quantification of Extracted DNA using the Quantifiler Human DNA Quantification Kit
9	20967	NucleoSpin Extraction of DNA
10	23008	Explanations of EXR/EXH Results
11	23890	Uploading and Actioning Samples on NCIDD
12	23968	Result Communications Procedure
13	24012	Miscellaneous Analytical Section Tasks
14	24015	Procedure for Intelligence Reports and Interstate/Interpol Requests
15	24486	Explanations of Additional Test Codes and Batch Types
16	25583	Use of DNA Analysis Database Interface (DADI)
17	26874	Procedure for Paperless Case Management and Review
18	31512	Manual NCIDD Upload form PowerPlex 21
19	31523	Interpretation and Statistical Analysis of DNA profiles Using the STRmix™ Expert System

Not Current

15 AMENDMENT HISTORY

Version	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

11	Apr 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 Apr 2008	J Connell	Transferred section on preparing case file for presumptive EXR/EXH validation to Examination of Items SOP
13	12 Feb 2009	K Lee	Major rewrite; 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.
14	28 Oct 2009	K Lee	Updated with reference to GeneMapper *ID-X* software; changed "Pre/Post LIMS" references to "Pre/Post AUSLAB Batch Functionality"; removed unnecessary flow charts; updated hyperlinks and associated documents; introduced paperless case management; re-arranged for better flow and grammatical correctness; Introduced more definitions; included instruction on locating profiles for printing.
15	27 Jan 2012	K Pippia	Introduced new worklists; added section on reworking evidence samples; added VOLUND process; addressed changes in processes since last update; removed references to re-Genescanning and introduced references to re-reads; updated hyperlinks; addressed comments raised against last revision; updated FBNLR process
16	12 Nov 2012	Alicia Quartermain, Emma Caunt, Justin Howes	Updated all processes to include implementation of PowerPlex®21 and STRmix™

Not Current

16 APPENDICES:

1 The Case Management Screen

2 Requesting reworks on an extra barcode for AUSLAB batch functionality samples

3 Pooling Pre-AUSLAB Batch Functionality samples which are registered in AUSLAB

4 Pooling Pre-AUSLAB Batch Functionality samples which are not registered in AUSLAB)

5 Requesting a Diluted re-amplification

6 Requesting reworks for Pre-AUSLAB Batch Functionality samples which are not registered in AUSLAB

7 Finalising cases that are no longer required

8 Workflow for Case Management

9 Workflow for 1EVD AUSLAB worklist

16.1 Appendix 1: The Case Management Screen

AUSLAB test code: CS

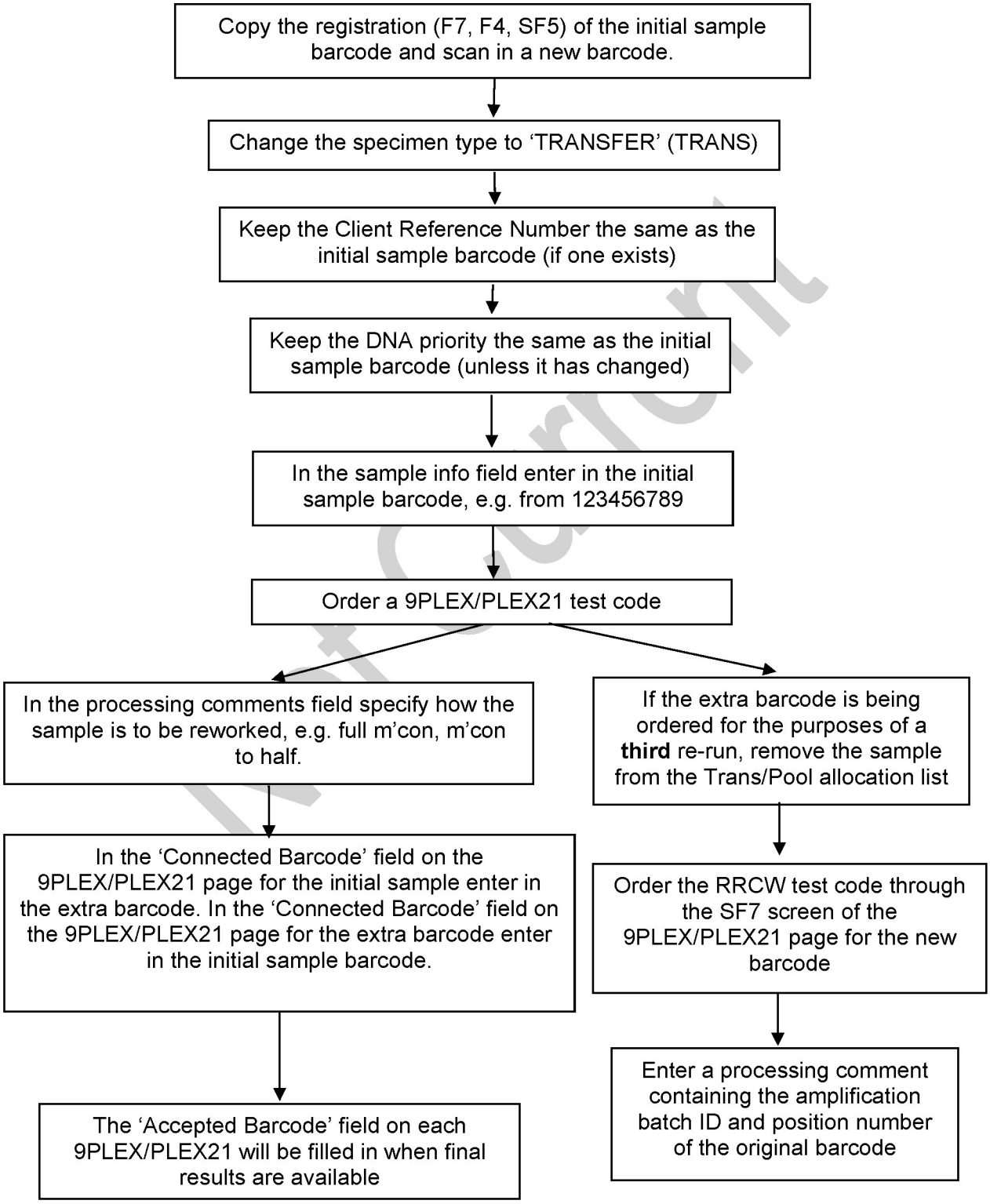
Purpose: The Case Management Screen is requested on the first laboratory number registered for the case. There should be only one Case Management screen for each case. The Case Management screen provides general details on the case.

- **Status** –The case status 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
  - 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 the review process.
  - REPORT ISSUED – case has been reviewed and statement has been sent. Entered by the reviewer following tech/admin review.
  - ANALYSED - REPORT NOT REQUIRED – case has been reviewed and no statement has been requested. Entered by the reviewer following tech/admin review.
  - NO TESTING REQUIRED – case has been written off, no work was required.
  - REACTIVATED – case has been reopened for more work or statement preparation.
  - 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 name, DOB, Class)** – Names, dates of birth and classes of people involved in the case, e.g. complainants, suspects, defendants, deceased, elimination.
- **Case Scientist** – Scientist who has been allocated the case, generally the reporter.
- **Primary Case Scientist** – Scientist who has performed the examinations. This field remains blank for in-tube cases.
- **Case Type** – e.g. Armed Robbery, Assault, Murder, Property, Proficiency Testing, Paternity, Sexual Assault, Coronial/DVI. This is supplied by QPS.
- **Crime Class Code** – information provided by QPS, 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.
- **Biol/Police Priority** – Used to assist in case prioritisation.
- **Date Completed** – date case review is completed.
- **Exhibits** – indicates status of exhibits.

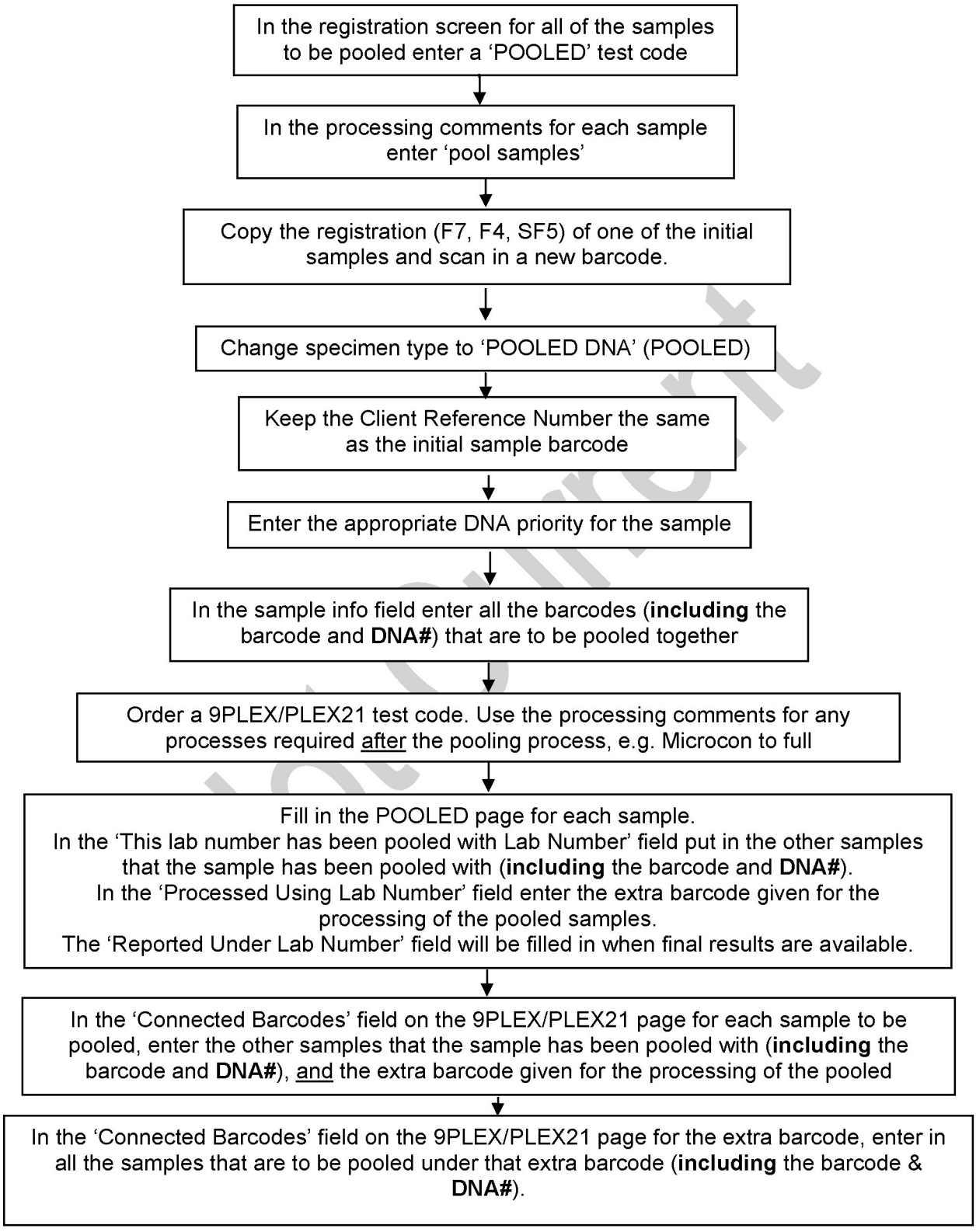
Not Current

16.2 Appendix 2: Requesting reworks on an extra barcode for AUSLAB Batch Functionality samples

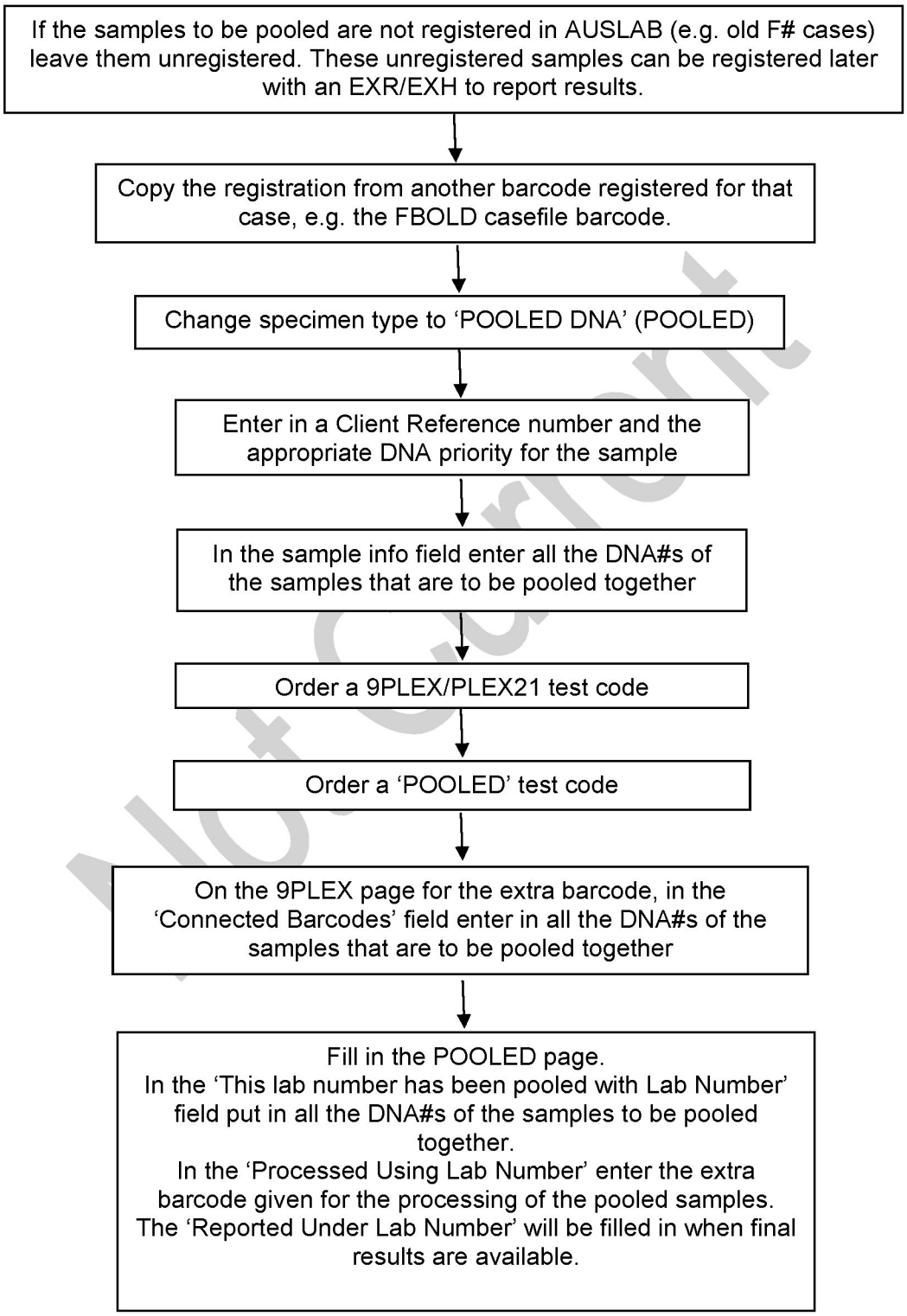
Follow this flowchart for samples that have been wholly processed in AUSLAB but where the number of rework test codes has been exhausted.



16.3 Appendix 3: Pooling Pre-AUSLAB batch functionality samples which are registered in AUSLAB



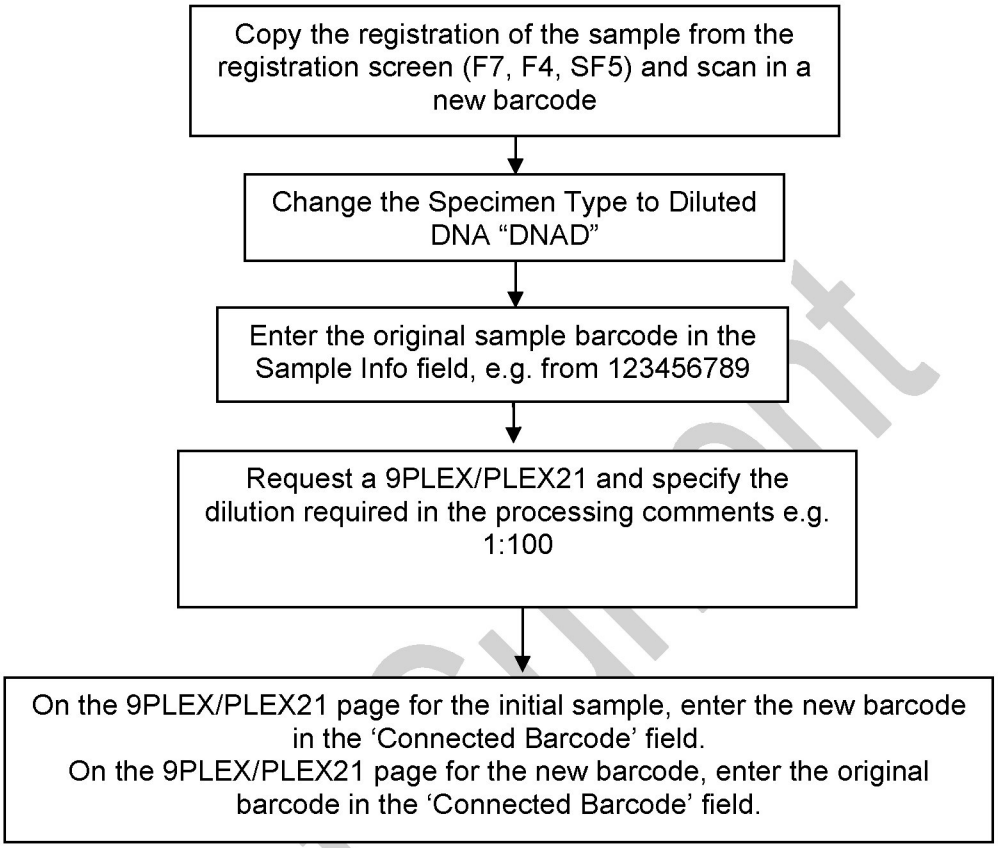
16.4 Appendix 4: Pooling Pre-AUSLAB batch functionality samples which are not registered in AUSLAB



Not Current

16.5 Appendix 5: Requesting a diluted re-amplification

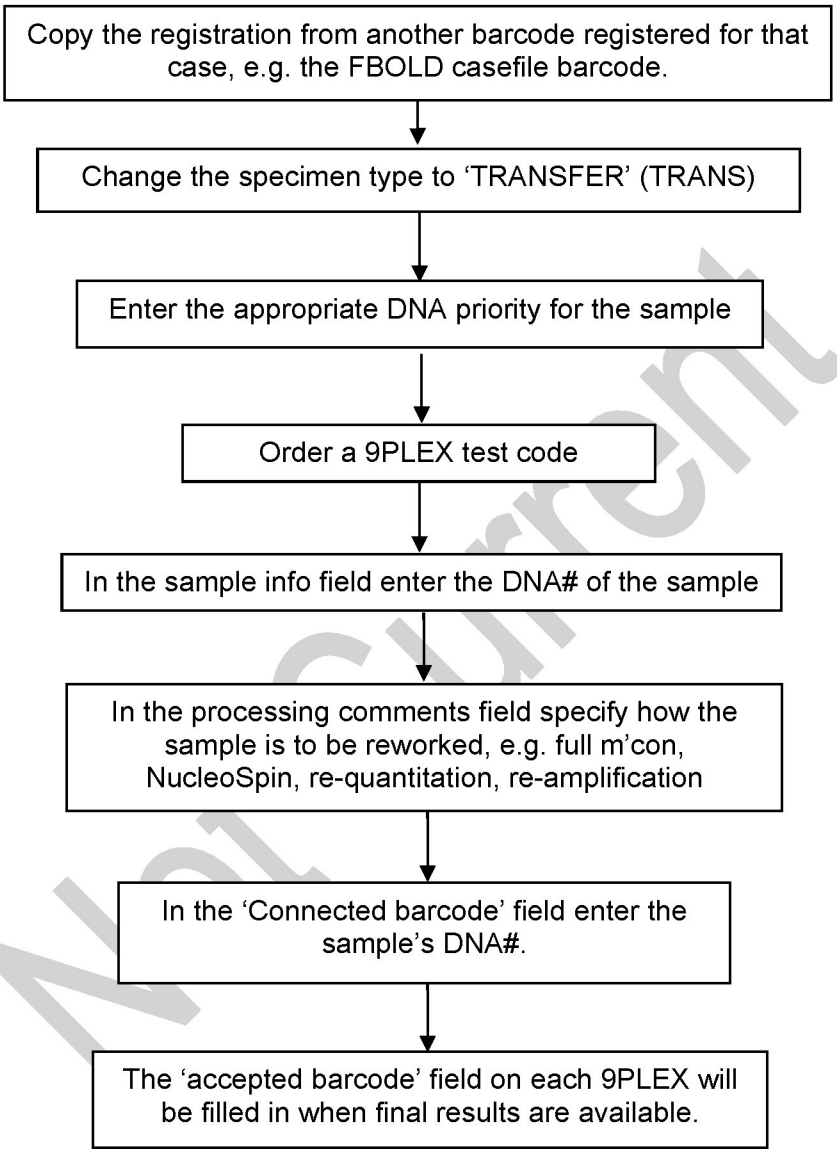
Use the following flow chart when requesting dilutions exceeding 1 in 20 or when all re-amplification test codes have been exhausted:



Not Current

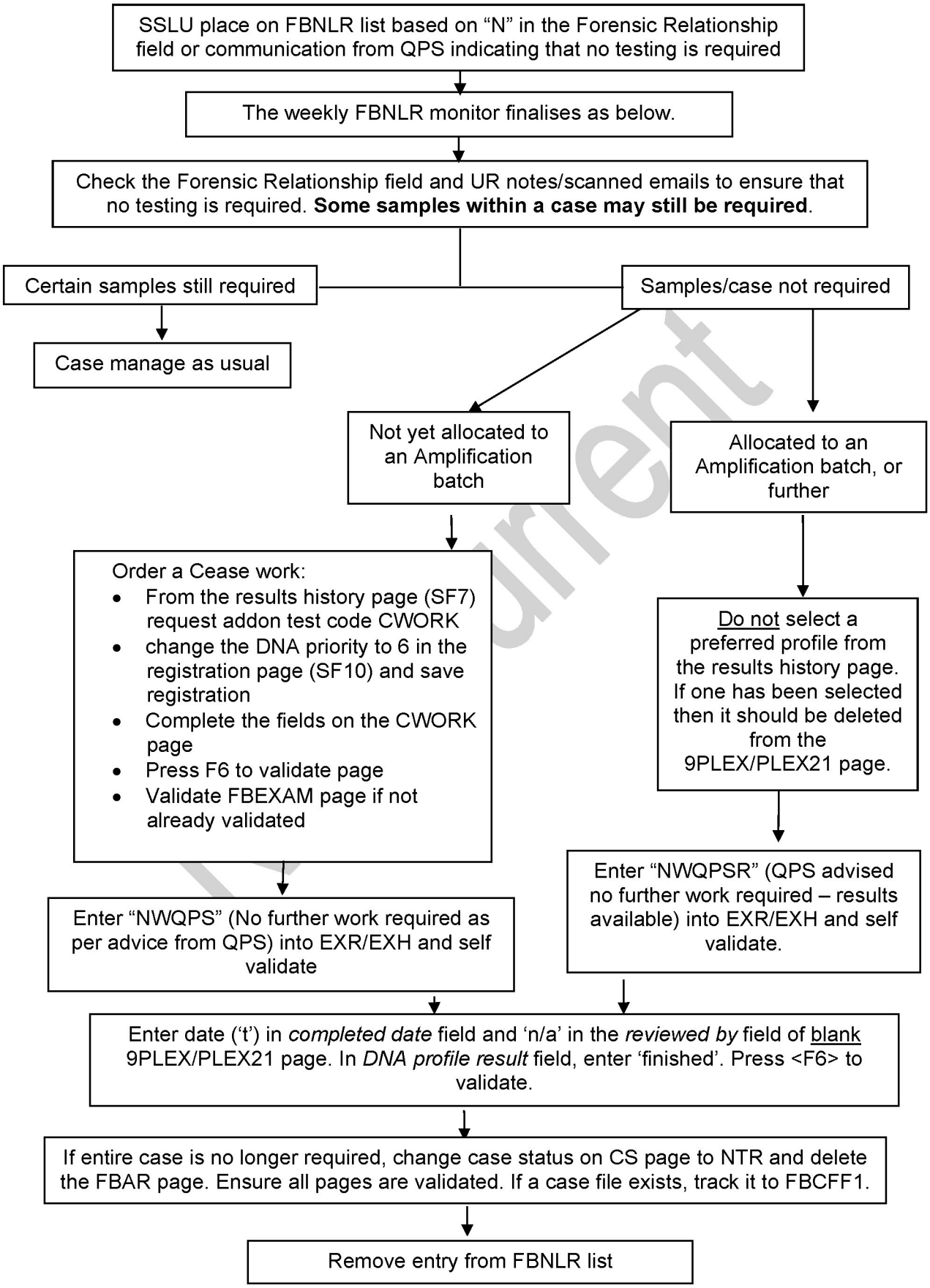
16.6 Appendix 6: Requesting reworks for Pre-AUSLAB Batch Functionality samples which are not registered in AUSLAB

Use the following flow chart when requesting reworks on samples completed in DNAMaster/DAD and not registered in AUSLAB.

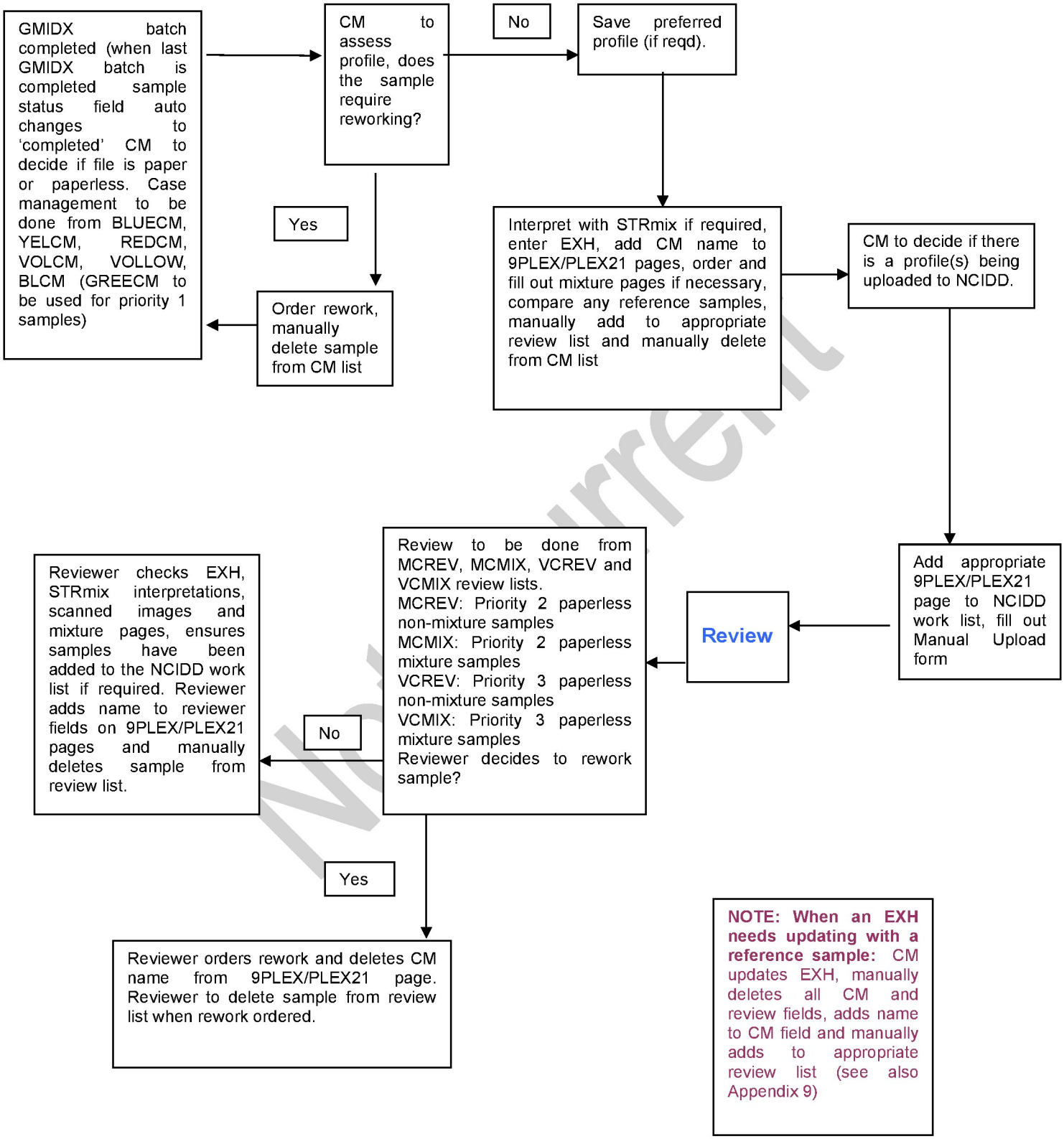


Not Current

16.7 Appendix 7: Finalising cases that are no longer required

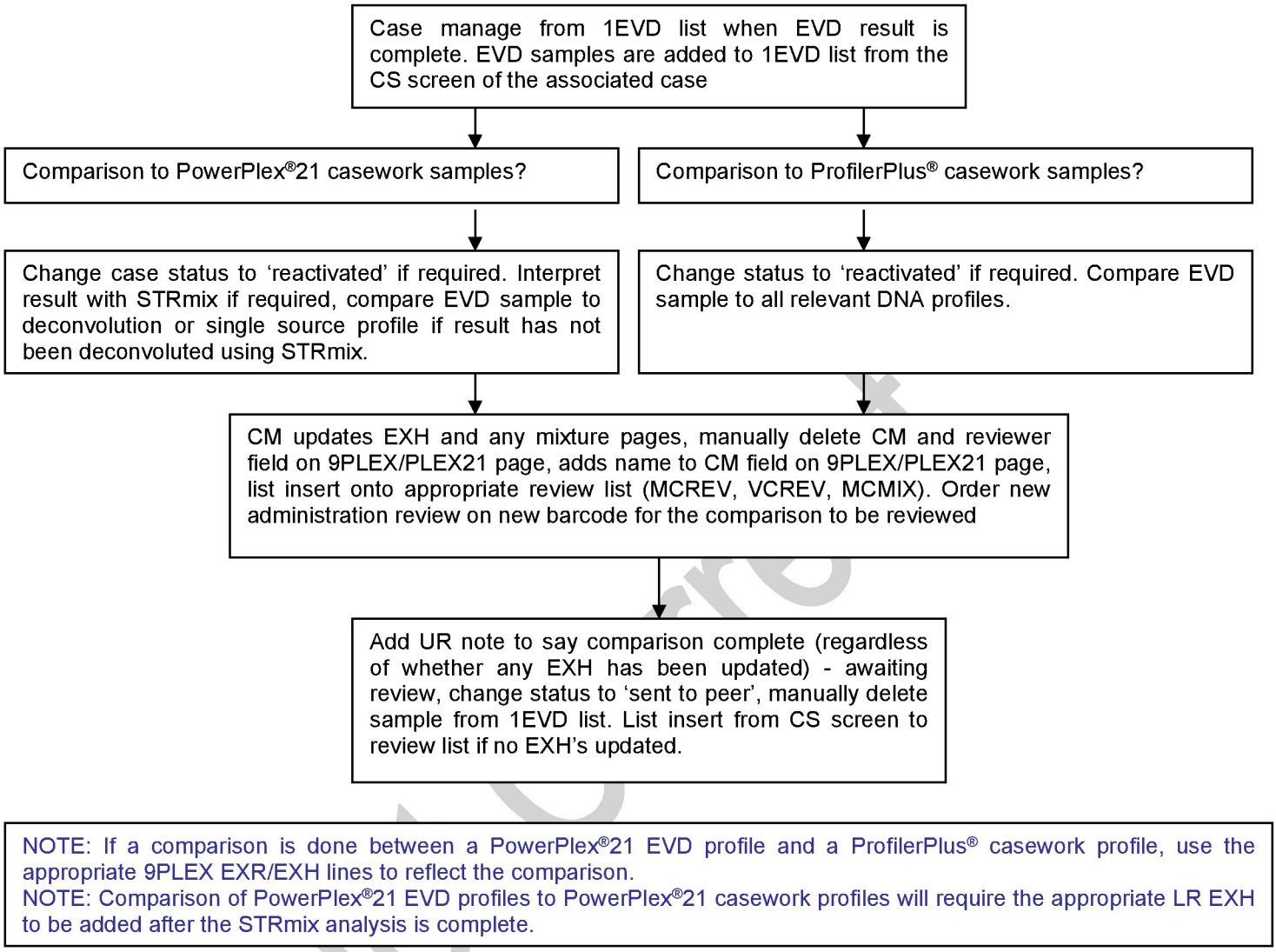


16.8 Appendix 8: Workflow for Case Management (see also Appendix 10, Workflows 1-6)

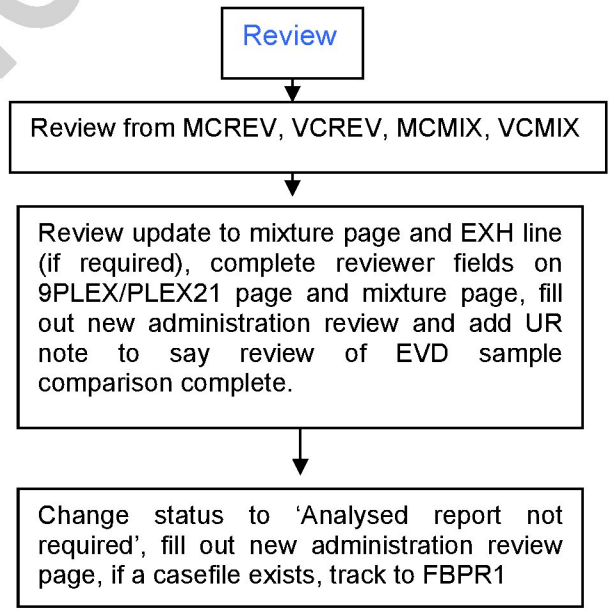


Not current

16.9 Appendix 9: Workflow for 1EVD Auslab worklist

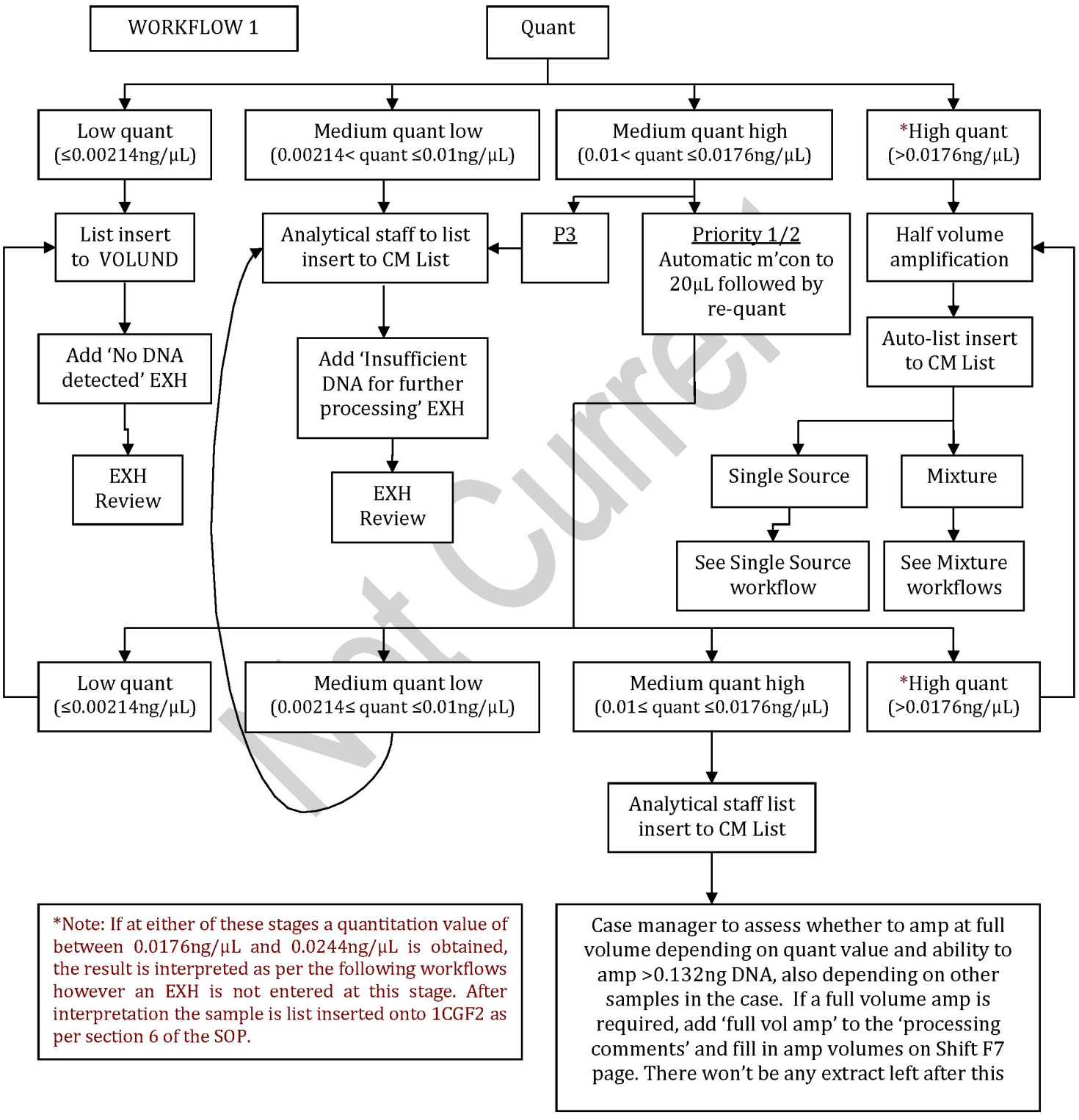


NOTE: If a comparison is done between a PowerPlex®21 EVD profile and a ProfilerPlus® casework profile, use the appropriate 9PLEX EXR/EXH lines to reflect the comparison.
NOTE: Comparison of PowerPlex®21 EVD profiles to PowerPlex®21 casework profiles will require the appropriate LR EXH to be added after the STRmix analysis is complete.



16.10 Appendix 10: Workflows (1-6) for Case Management with STRmix™

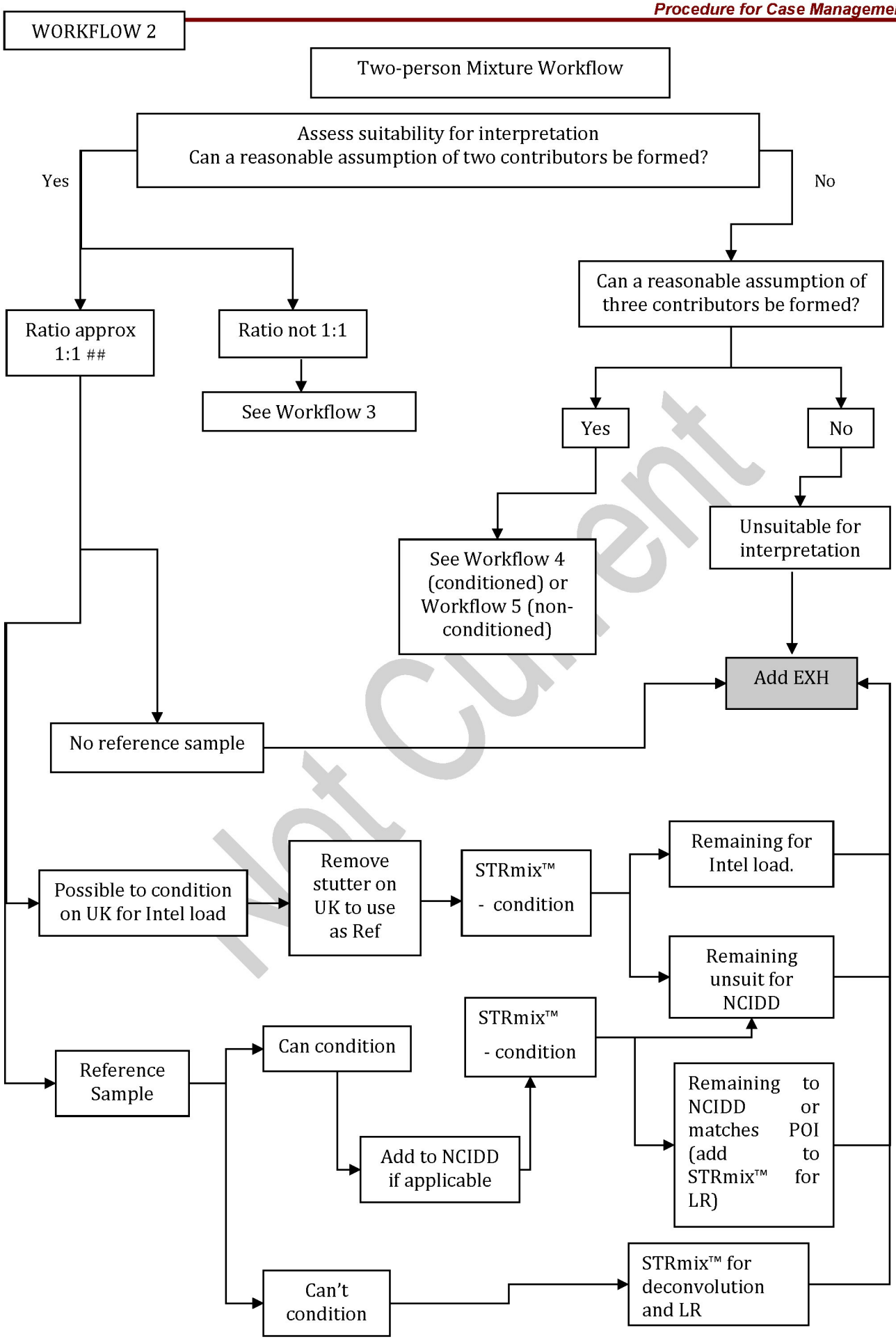
Note: The below process will be used for both P2 and P3 samples, with the exception that P3 samples will not have an automatic Microcon. P1 samples will follow the same process but will be case managed by the allocated case manager regardless of the quant result. They will not be case managed through the CM lists.



*Note: If at either of these stages a quantitation value of between 0.0176ng/µL and 0.0244ng/µL is obtained, the result is interpreted as per the following workflows however an EXH is not entered at this stage. After interpretation the sample is list inserted onto 1CGF2 as per section 6 of the SOP.

Case manager to assess whether to amp at full volume depending on quant value and ability to amp >0.132ng DNA, also depending on other samples in the case. If a full volume amp is required, add 'full vol amp' to the 'processing comments' and fill in amp volumes on Shift F7 page. There won't be any extract left after this

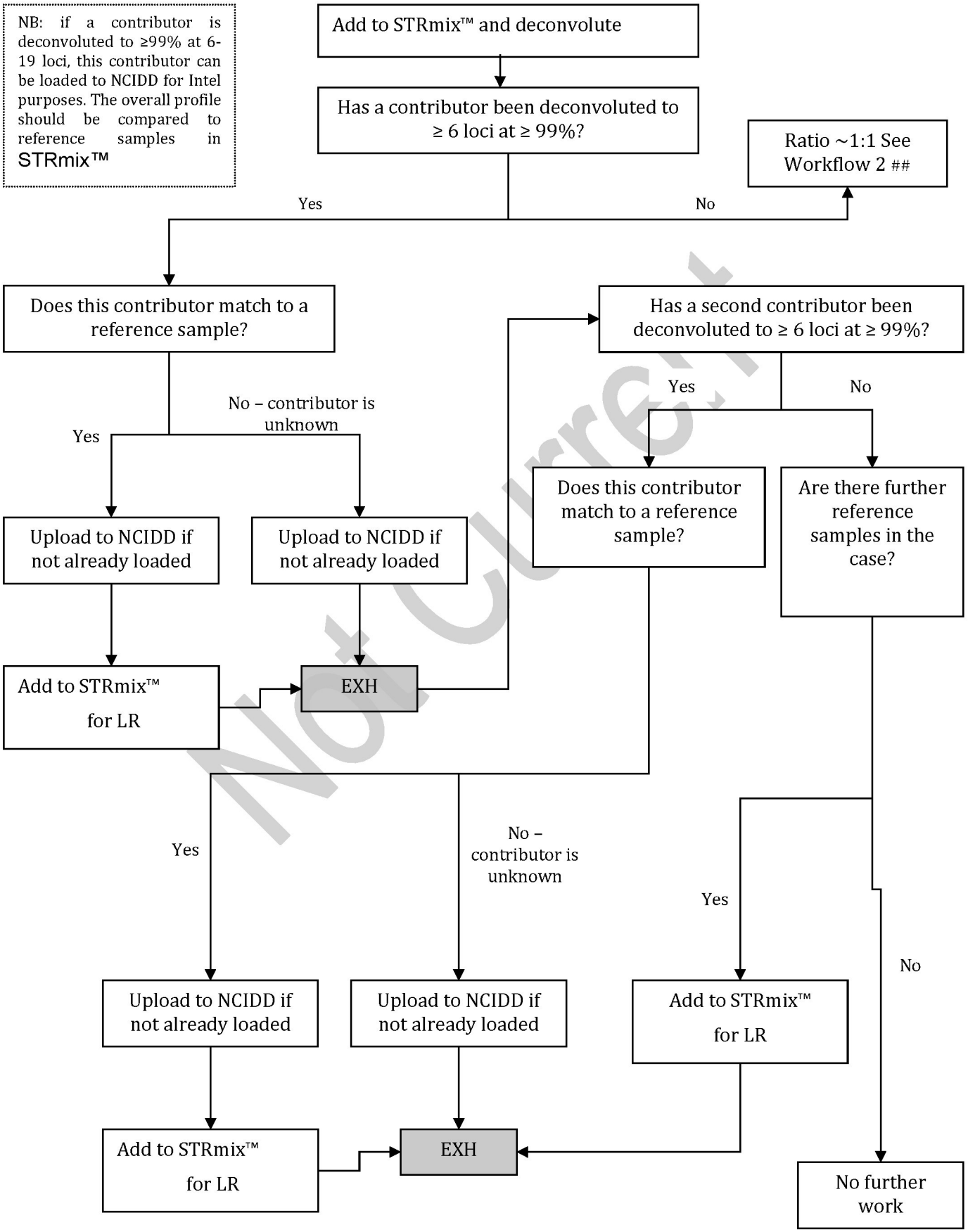
Not Current


WORKFLOW 2
Two-person Mixture Workflow
Assess suitability for interpretation
Can a reasonable assumption of two contributors be formed?
Yes
No
Ratio approx 1:1 ##
Ratio not 1:1
See Workflow 3
Can a reasonable assumption of three contributors be formed?
Yes
No
See Workflow 4 (conditioned) or Workflow 5 (non-conditioned)
Unsuitable for interpretation
Add EXH
No reference sample
Possible to condition on UK for Intel load
Remove stutter on UK to use as Ref
STRmix™ - condition
Remaining for Intel load.
Remaining unsuit for NCIDD
Reference Sample
Can condition
STRmix™ - condition
Add to NCIDD if applicable
Remaining to NCIDD or matches POI (add to STRmix™ for LR)
Can't condition
STRmix™ for deconvolution and LR

Not Current

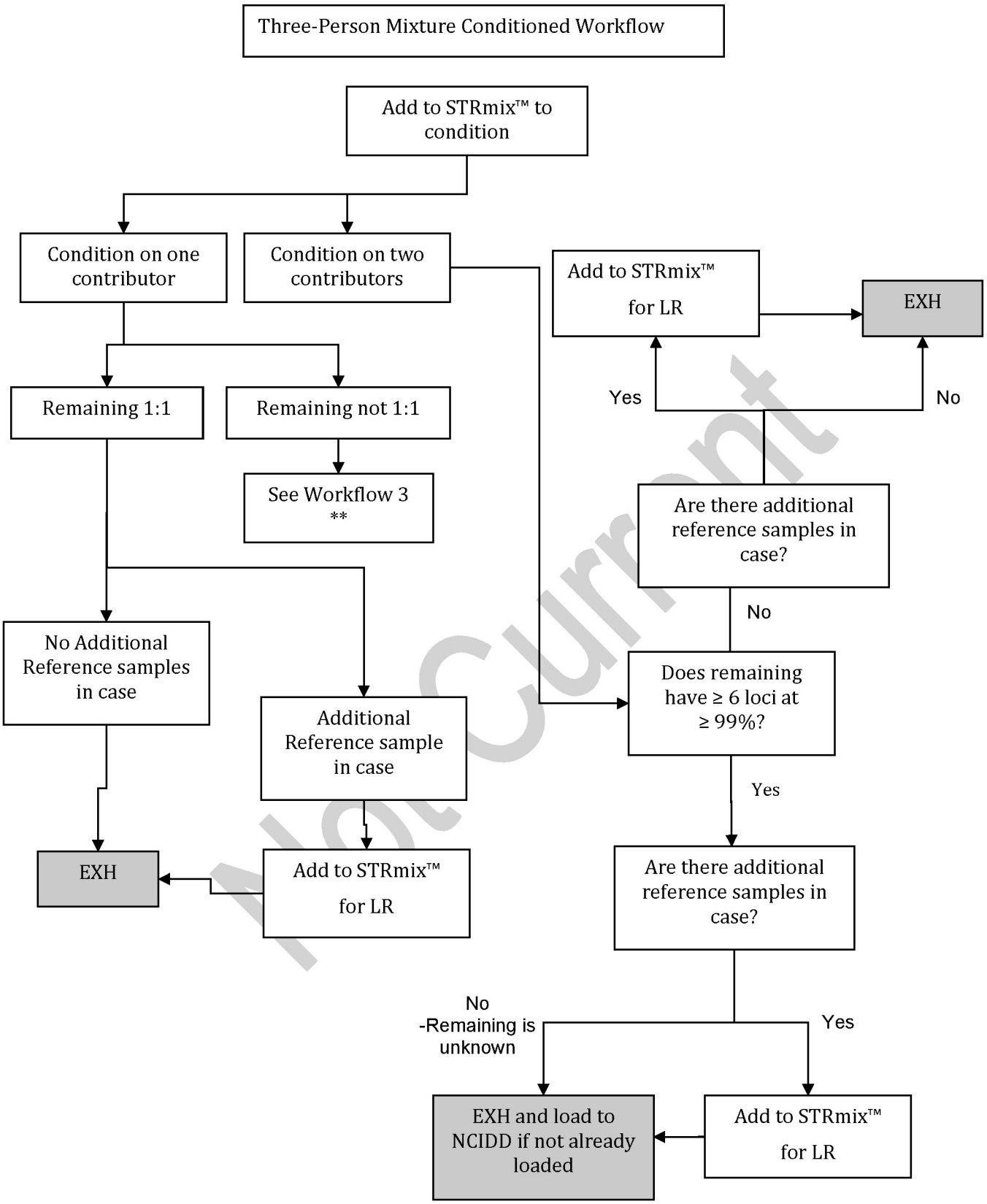
WORKFLOW 3

Non 1:1, Two-person Mixture Workflow

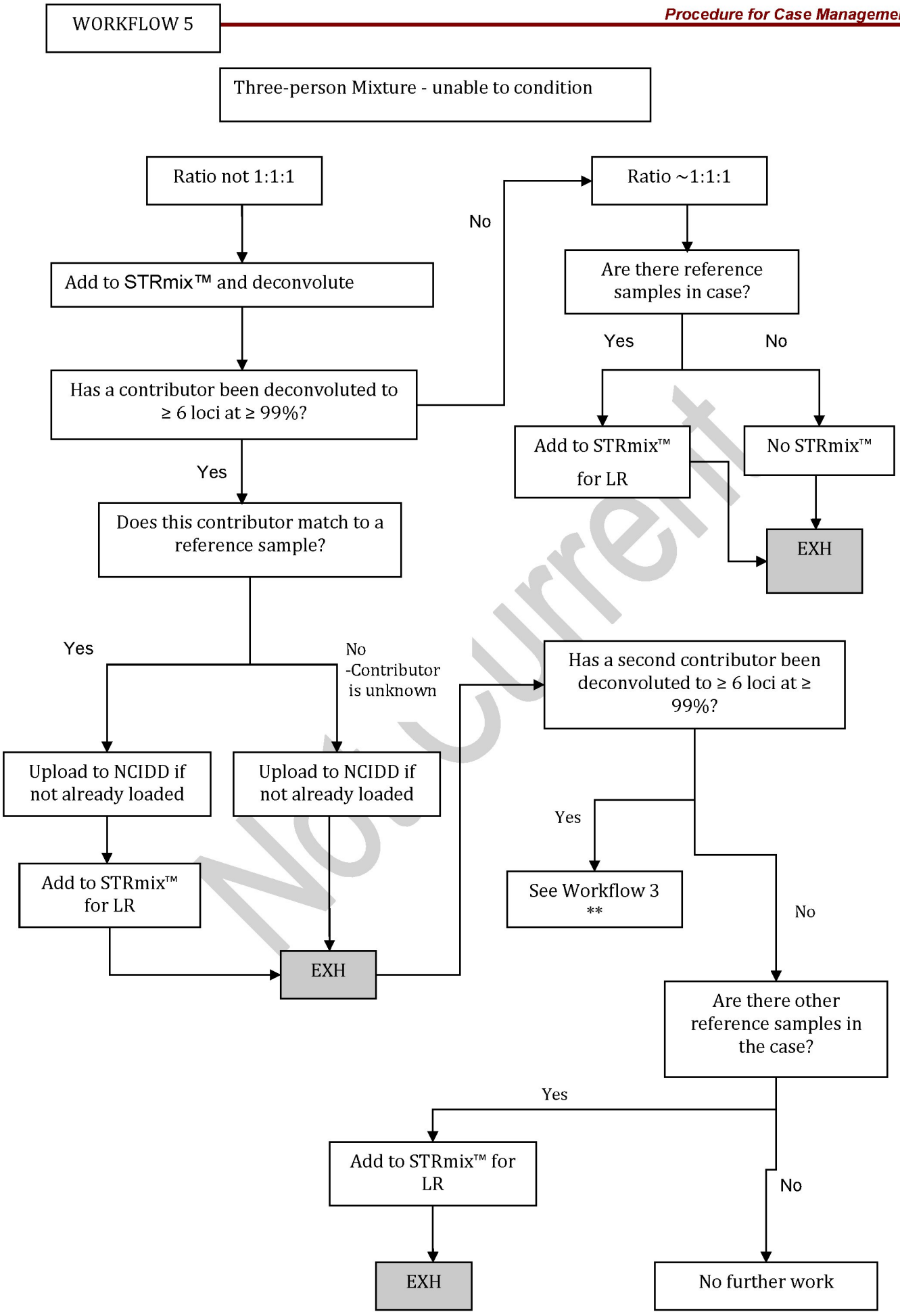


Not Current

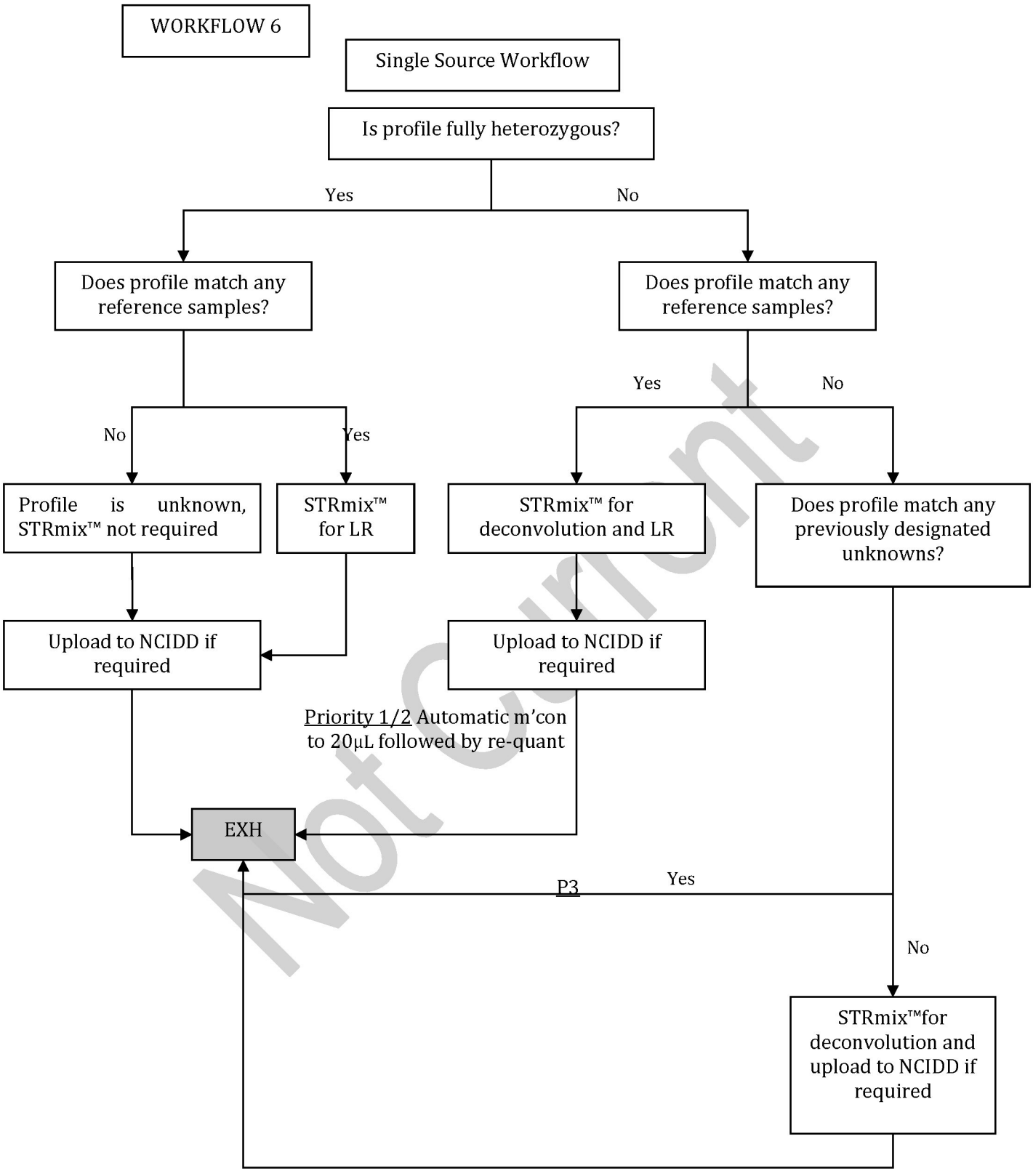
Queensland Government


Three-Person Mixture Conditioned Workflow
Add to STRmix™ to condition
Condition on one contributor
Condition on two contributors
Remaining 1:1
Remaining not 1:1
See Workflow 3 **
No Additional Reference samples in case
Additional Reference sample in case
EXH
Add to STRmix™ for LR
Add to STRmix™ for LR
EXH
Yes
No
Are there additional reference samples in case?
No
Does remaining have ≥ 6 loci at ≥ 99%?
Yes
Are there additional reference samples in case?
No -Remaining is unknown
Yes
EXH and load to NCIDD if not already loaded
Add to STRmix™ for LR

Not Current


WORKFLOW 5
Three-person Mixture - unable to condition
Ratio not 1:1:1
Add to STRmix™ and deconvolute
Has a contributor been deconvoluted to ≥ 6 loci at ≥ 99%?
No
Ratio ~1:1:1
Are there reference samples in case?
Yes
No
Add to STRmix™ for LR
No STRmix™
EXH
Yes
Does this contributor match to a reference sample?
Yes
No -Contributor is unknown
Upload to NCIDD if not already loaded
Upload to NCIDD if not already loaded
Add to STRmix™ for LR
EXH
Has a second contributor been deconvoluted to ≥ 6 loci at ≥ 99%?
Yes
See Workflow 3 **
No
Are there other reference samples in the case?
Yes
Add to STRmix™ for LR
EXH
No
No further work

No Current


WORKFLOW 6
Single Source Workflow
Is profile fully heterozygous?
Yes
No
Does profile match any reference samples?
Does profile match any reference samples?
No
Yes
Yes
No
Profile is unknown, STRmix™ not required
STRmix™ for LR
STRmix™ for deconvolution and LR
Does profile match any previously designated unknowns?
Upload to NCIDD if required
Upload to NCIDD if required
Priority 1/2 Automatic m'con to 20µL followed by re-quant
EXH
P3
Yes
No
STRmix™for deconvolution and upload to NCIDD if required

Not Current

Department of Health

Queensland Government

MEMORANDUM

To: Helen Gregg, A/Executive Director, Forensic and Scientific Services

Copies to: Professor Keith McNeil, Deputy Director-General and Chief Medical Officer, Prevention Division and Chief Clinical Information

From: Shaun Drummond, Acting Director-General

Enquiries to: David Harmer, Senior Director, Social Policy and Legislation Branch. [redacted]

Subject: Urgent amendment to Standard Operating Procedure required

File Ref: C-ECTF-22/12758

It has been brought to my attention that the following wording is currently used in witness statements where DNA was in the range 0.001ng/uL (LOD) - 0.0088ng/uL:

'insufficient DNA for analysis' or 'insufficient DNA for further processing'

This wording may convey the impression that further processing or analysis is not possible. To avoid this impression and ensure witness statements make clear that further analysis may be possible in some cases, please immediately amend the Standard Operating Procedure and other guidance for staff to require that the following alternative text is used in witness statements:

Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling.

The sample may have insufficient DNA to result in a DNA profile suitable for interpretation. It is possible that further testing may result in an interpretable DNA profile in some cases.

If there is a requirement to clarify witness statements already submitted that use the descriptions '*insufficient DNA for analysis' or 'insufficient DNA for further processing',* use the above wording in any clarifying statement.

Please share this memorandum with Forensic DNA Analysis Unit staff.

Should you require further information, the Department of Health's contact is Mr David Harmer, Senior Director, Social Policy and Legislation Branch on telephone [redacted]

Shaun Drummond
Acting Director-General
05/08/2022

APPENDIX

Procedural and technical overview of DNA profiling at Forensic DNA Analysis, Forensic and 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), 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 Queensland Health 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.

DNA profiles are initially assessed to determine the number of contributors. This value will be the minimum number of people that are required to reasonably explain the observed profile, however, it is noted that there is always the possibility that the profile is a result of a different number of contributors.

As such, 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 are 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.

<u>DNA Profiles Assumed To Originate From One Person (Single Source)</u>

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 16 May 2022 and contained in the pages numbered 1 to 7 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 16 May 2022

APPENDIX

Procedural and technical overview of DNA profiling at Forensic DNA Analysis, Forensic and Scientific Services, Health Support Queensland

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.

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.

<u>DNA Profiles Assumed To Originate From One Person (Single Source)</u>

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 of semen stains on a whole item, such as clothing or bedding can 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 28 April 2021 and contained in the pages numbered 1 to 7 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 28 April 2021

Document Management: 34006 - V4.0 - Procedure for the Release of Results Using the Forensic Register

Version Status: Active

Add | Edit | Delete | View Document | Print Comments | History

General | Reviews and Approvals | Notifications | **Comments** | Controlled Copies | Version History | Associations | Records | Workflow

Comments By	Comment Date	Response By	Response Date	Comment Noted
☑ Justin HOWES	08/08/2022			Pending
☐ Adrian PIPPIA	22/07/2022			Not Required

Comments

8/08/2022 8:38:05 AM Justin HOWES:

Where results were obtained in the quant range (0.001ng/uL (LOD) - 0.0088ng/uL) and were reported as 'insufficient DNA for analysis' or 'insufficient DNA for further processing', as of 08 August 2022 any statement in draft or to be written with such samples are to be described in the body of the statement as:
Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling.
The sample may have insufficient DNA to result in a DNA profile suitable for interpretation.
It is possible that further testing may result in an interpretable DNA profile in some cases.

This is as per A/DG direction in memo dated 05/08/2022. Further as per A/EDFSS advice, if asked by the client via conference or evidence, that we will now use these words. Reports are not required to be reissued, but if requested by the client to reissue, these words would be used.

Response

Created on 8/08/2022 8:38 AM by Justin HOWES

Quality Information System (v2.10.7482 26/06/2020 Release Notes) Copyright © 2020, Health Support Queensland, Queensland Health - All Rights Reserved -

\\10.50.33.251\x\zz_Toolbox_Export_Temp\eDiscoveryToolbox\Case1982\1015\871_1025044342843\WIT.0016.0110.0001_R_71d7b.xls

Implementation Date	Details	Project Leader
16/02/2009	Started using **GeneMapper to analyse results**.	CW/TEN
16/02/2009	**Implemented new thresholds**. Reference: 50 RFU het, 150 RFU hom, AI 70%. Casework: 50 RFU het, 200 RFU hom, AI 50%.	CW/TEN

Area Affected

All

All

Date Raised	Item added by	Define Issue	Has it been seen before? (if Yes - Where?)
1/01/2021	John Smith	Apparent artefact at D18S51. Artefact shifts between labelling as a 17.1 or 17.2 variant allele. No stutter is observed for this artefact. Only observed in samples from peri-anal, rectal or penile areas	Yes (in Case XXXXXXXxXX)

Who can made the decision on what needs to happen?	Teams Affected	Assessment of Issue
John Smith	Reporting	Adds contributor to otherwise single source assumed known contributor, height of artefact not consistent with another contribution dropping out. No expenditure of money, time or resources required.

Actions	Details of communications that have occurred (to who, when and how)
Removed artefact from FR GeneMapper table.	
Annotated epgs and re-loaded to Forensic Register	
Notations added to case in Forensic Register.	
Added to odd profile register	All reporters via Microsoft Teams on 02/02/2021

Other notes for consideration

EXEMPLAR ONLY