KR-01

[redacted]

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**

[redacted]

HealthSupport Queensland

Minutes

Forensic DNA Analysis Management Team Meeting

Date: 1 February 2018
Time: 9:30am to 10:05am
Venue: FSS CR611

Chair: Justin Howes

Secretariat: Paula Brisotto

Attendees: Cathie Allen (CJA), Justin Howes (JAH), Kerry-Anne Lancaster (KAL), Kylie Rika (KDR), Luke Ryan (LBR), Paula Brisotto (PMB), Sharon Johnstone (SMJ), Wendy Harmer (WAH).

Apologies: Kirsten Scott (KDS), Allan McNevin (ARM), Amanda Reeves (AJR)

1.	**Welcome and apologies**	
Item no	**Item**	**Action**
1.1	**Confirmation of previous minutes** (7 December 2017)	KDR
1.2	**Conflicts of Interest –** Nil. Agenda sent out prior to meeting, if any conflicts exist, these are to be discussed with chair prior to meeting.	N/A
1.3	**Please note:** It is the responsibility of the Senior Scientist to communicate Management Team meeting details, unless otherwise discussed.	All

2.	**Guest Speakers / Presentations**	
Item no	**Item**	**Action**
2.1	Nil	

3.	**Business arising from previous meeting (see Action Register below)**	
Item no	**Item**	**Action**
3.1		
3.2		
3.3		

4.	**Workplace Health & Safety Issues**	
Item no	**Item**	**Action**
4.1		
4.2		
4.3		
4.4		

5.	**Project Updates**	
Item no	**Item**	**Action**
5.1	**Project #146 –** *GlobalFiler Validation* – currently assessing what is required to complete the validation 01/02/2018 – nil update	Ongoing
5.2	**Proposal #170:** *Reassessment of in-house stutter thresholds and stutter file used in STRmix*: this report won't be needed if v2.0.6 not being validated for 3500. There is more work being done on stutter for v2.5 so another report will be forthcoming. **Post-meeting follow-up by KDR 01/02/2018:** Thresholds to be tested against known mixtures.	Will require a report at the same time as report for STRmix v2.5.
5.3	**Project #175 C –** *Validation of STARlet C – for CE*: Experimental design signed. Lab work commenced 01/02/2018 – nil update	Script development commenced – onsite in 2018
5.4	**Project #181 –** *Sensitivity of Sperm microscopy*: 01/02/2018 – awaiting fresh control sample.	To be commenced.
5.5	**Project #182 -** *PP21 WEN CW 3500xL Validation*: project to pull together information from 177 and 186 for implementation. Report is in draft and requires addition of mixtures. 05/02/2018: linked to #186 and #177	Mixtures need to be added to report.
5.6	**Project #183 –** *Implementation of NIFA (Bonaparte)*: Update 07/12/2017 – KML was scheduled to do audit on NIFA however given this has not been implemented, the audit has been postponed. 01/02/2018 – nil update	Nil update
5.7	**Project #184 –** *Evaluation of the efficacy of microcons*: 01/02/2018 – Options paper drafted for Priority 2 samples – to be provided to QPS for decision. 05/02/2018: Priority 3 samples commenced in PP21, and process for P3 follows validated and implemented processes as per SOPs.	Options paper drafted for QPS consideration.
5.8	**Project #185 –** *Validation of Quantstudio 5*: Installation 2nd week of February.	Labwork to be commenced
5.9	**Project #186 -** *Assessment of 3500xL Analysis of Casework Powerplex21 samples*: some feedback received. Further labwork required. 05/02/2018: linked to #182 and #177	Ongoing - further labwork underway
5.10	**Project #187 -** *Verification of STRmix v2.0.6 for use with the 3500*: is likely to be closed as a new project will be opened for v2.5 05/02/2018: nil update	To be closed with a note against project
5.11	**Project #188 –** *Verification of retained supernatant batches on Maxwell*: 01/02/2018 – lab work to be commenced. Samples have been collected.	Lab work to be commenced.
5.12	**Project #189 –** *Continuation of Y-filer plus – remainder of validation plus implementation*: 01/02/2018: see Item 2.1	See item 2.1 above
5.13	**Project #190 -** *MPS as Investigative Tool RSS18-004*: 01/02/2018 – Liaison with QPS next step.	Waiting on Approval of Deed of Agreement
5.14	**Project #191** – Effect of HCl on DNA persistence and profiling. 01/02/2018: proof of concept in draft.	Lab work commenced results being analysed.
5.15	**Project #192 -** *QIAsymphony Bone Extraction:* 01/02/2018 To commence mid-Feb – when resources available in ER team to crush and prepare bone.	Lab work to be started mid Feb.

	Projects on Hold	
5.16	Project #172 – Phadebas testing from suspension in ERT: *Pending outcome of project on how suspensions are made. (12.05.2016)*	Nil update
5.17	Project#176 – Investigation into ICMP protocol:	Nil update

6.	Workflow impacts	
Item no	Item	Action
6.1	3130xL – auto sampler issues meant 3130xL down for 1.5 days. (LBR)	
6.2	Items received: SAIKs continue to be high in 2018. QPS stats show an increase in items received compared to previous years – generally 20,000 to 22,000 items received, however in 2017 25,000 items received.	
6.3		
6.4		

7.	Matters for decision	
Item no	Item	Action
7.1	Nil	

8.	Matters for noting	
Item no	Item	Action
8.1	HR Reminder - if a member of staff comes in late (planned or otherwise) could an email please be sent to the generic admin account, advising whether they are utilising leave for their absence (lateness). If using leave, what type and how much? This will ensure that should an AVAC entry be required that it is included in the daily AVAC, rather than having to generate an extra AVAC. Thank you	All – please pass this information on to your teams.
8.2	CJA attended Emergency Planning Committee (EPC) meeting – Comm Games update: a number of exercises being carried out in Feb 18 – not involving FSS at present. EPC carrying out a desktop exercise in February. Emergency evacuations test planned for July. A fire was detected in block 10(?). Due to a faulty light switch. Please ensure any faults or suspected faults are checked and reported.	For noting
8.3	PMB: Comm Games committee update – most areas business as usual. For FDNA, looking at increasing stock levels and SAIK levels prior to the Games. Verification of 2nd Symphony. Validation of 35ooxL and Bone extractions of the Symphony. Possibly Desktop exercise with QPS for large DVI. CJA - FSS mortuary will be the designated mortuary for any Comm Games incidents.	For noting.

Next Meeting

Date: **15 February 2018**

Time: 11:15am

Venue: **FSS CR611**

ACTION REGISTER

Minutes Reference	Item Number	Subject	Action	Action Officer	Status
28.09.2017	8.1	NIFA training (SMJ)	\\Bs-qhss-fs1\data1\ForBiol\DNA Analysis Team Meetings\DNA Analysis Management Team\2017\Jul_to_Dec 2017\Summary of NIFA Training Sept 2017_SMJ.doc JAH to produce status update for higher level briefing/ reporting. 01/02/2018 - ongoing	JAH	Ongoing
28.09.2017	8.5	Secondary Employment: If request made through Greg Shaw previously, another request needs to be made to Paul Csoban.	Line Managers to follow up with their staff members.	All	Closed
07/12/2017	2.1		Thomas Nurthen - Y Filer Plus project (including presentation regarding Australasian Y STR teleconference) (TEN & KDR) attachment Proposal discussed – in addition teleconference was discussed. TEN/KDR to update document with teleconference info and also gap analysis for what experiments need to be done to complete each option (# of samples). Email of 13.12.2017 01/02/2018 – a lot of information coming through from all jurisdictions. TEN/KDR progressing through information. Two members from Y group to collate information from all users to form some recommendations. Summary due by end of March. Gap analysis progressing. Education/training ideas being gathered.	KDR/TEN to update document	
07/12/2017	4.2		Risk Man – implemented on 20/11/2017. Incident in OO team which required ambulance attendance. KDS attempted to log incident in Risk Man however the options in Risk Man for classification of the incident where very insufficient and the incident could not be accurately recorded. KDS sent screen shots of incomplete submission to HSQ Safety Performance. Job logged to add additional classifications into Risk Man. Job is still outstanding. 01/02/2018 – nil update	All staff to log in and ensure that their line manager is correct (Line Manager is your immediate supervisor).	

07/12/2017	4.3	Reporting – two staff have had RSI issues associated with mouse use. Two new mouse have been purchased for these two staff and it seems to relieve the RSI.	KDR and reporting to investigate FR enhancements to reduce the number of clicks and RSI. 01/02/2018 – some FR enhancements have helped. Paul Bellchamber has done an assessment and provided a report. FRIT seniors and Team Leader to meet and discuss recommendations.	KDR / Reporting Teams	Ongoing
07/12/2017	4.4	OHS audit conducted this week. Finding – "Green Man" exit signs are missing from some light/signs. These are to be located/replaced.	01/02/2018 – OHS have provided signs.	KDS	Closed

HealthSupport Queensland

Minutes

Forensic DNA Analysis Management Team Meeting

Date: 7 December 2017
Time: 9:30am to 11:15am
Venue: FSS CR611

Chair: Luke Ryan (LBR)

Secretariat: Luke Ryan (LBR)

Attendees: Cathie Allen (CJA), Kirsten Scott (KDS), Kylie Rika (KDR), Megan Mathieson (MLM), Paula Brisotto (PMB), Sharon Johnstone (SMJ), Wendy Harmer (WAH).

Apologies: Justin Howes (JAH), Amanda Reeves (AJR), Allan McNevin (ARM)

1.	**Welcome and apologies**	
Item no	**Item**	**Action**
1.1	**Confirmation of previous minutes** (28 September 2017)	KDS
1.2	**Conflicts of Interest** – Nil. Agenda sent out prior to meeting, if any conflicts exist, these are to be discussed with chair prior to meeting.	N/A
1.3	**Please note:** It is the responsibility of the Senior Scientist to communicate Management Team meeting details, unless otherwise discussed.	All

2.	**Guest Speakers / Presentations**	
Item no	**Item**	**Action**
2.1	Thomas Nurthen - Y Filer Plus project (including presentation regarding Australasian Y STR teleconference) (TEN & KDR) attachment Proposal discussed – in addition teleconference was discussed. TEN/KDR to update document with teleconference info and also gap analysis for what experiments need to be done to complete each option (# of samples). Email of 13.12.2017	KDR/TEN to update document

3.	**Business arising from previous meeting (see Action Register below)**	
Item no	**Item**	**Action**
3.1		
3.2		
3.3		

4.	Workplace Health & Safety Issues	
Item no	**Item**	**Action**
4.1	Hep B titre checks for existing staff – update: titre checks can be arranged, however booster shots will not be provided by FSS-Infection control. (PMB). Also titre checks can be requested by exception following a WHS incident where Hep B might be an issue.	All to note
4.2	Risk Man – implemented on 20/11/2017. Incident in OO team which required ambulance attendance. KDS attempted to log incident in Risk Man however the options in Risk Man for classification of the incident where very insufficient and the incident could not be accurately recorded. KDS sent screen shots of incompleted submission to HSQ Safety Performance. Job logged to add additional classifications into Risk Man. Job is still outstanding.	All staff to log in and ensure that their line manager is correct (Line Manager is your immediate supervisor).
4.3	Reporting – two staff have had RSI issues associated with mouse use. Two new mouse have been purchased for these two staff and it seems to relieve the RSI.	KDR and reporting to investigate FR enhancements to reduce the number of clicks and RSI.
4.4	OHS audit conducted this week. Finding – "Green Man" exit signs are missing from some light/signs. These are to be located/replaced.	KDS

5.	Project Updates	
Item no	**Item**	**Action**
5.1	**Project #146** – *GlobalFiler Validation* – currently assessing what is required to complete the validation	Ongoing
5.2	**Proposal #170:** *Reassessment of in-house stutter thresholds and stutter file used in STRmix*: this report won't be needed if v2.0.6 not being validated for 3500. There is more work being done on stutter for v2.5 so another report will be forthcoming.	Report for v2.5 will finalise this project.
5.3	**Project #175 C** – *Validation of STARlet C – for CE*: Experimental design signed. Lab work commenced	Script development commenced – onsite in 2018
5.4	**Project #177** – *3500 CW WEN samples*: this is now under 186.	To be closed with note against project
5.5	**Project #181** – *Sensitivity of Sperm microscopy*:	ARM - Project to recommence – additional in Part 2 do experimental design to be conducted.
5.6	**Project #182 -** *PP21 WEN CW 3500xL Validation*: project to pull together information from 177 and 186 for implementation. Report is in draft and requires addition of mixtures.	Mixtures need to be added to report.
5.7	**Project #183** – *Implementation of NIFA (Bonaparte)*: Update 07/12/2017 – KML was scheduled to do audit on NIFA however given this has not been implemented, the audit has been postponed.	Nil
5.8	**Project #184** – *Evaluation of the efficacy of microcons*: report currently being drafted	Draft report to Mgt Team feedback required by Dec 20.
5.9	**Project #185** – *Validation of Quantstudio 5*: Installation 2nd week of February.	Nil update
5.10	**Project #186 -** *Assessment of 3500xL Analysis of Casework Powerplex21 samples*: some feedback received. Further labwork required.	Ongoing - further labwork underway
5.11	**Project #187 -** *Verification of STRmix v2.0.6 for use with the 3500*: is likely	To be closed with a note

	to be closed as a new project will be opened for v2.5	against project
5.12	**Project #188 –** *Verification of retained supernatant batches on Maxwell*: Experimental design waiting on outstanding feedback	Approved – to be commenced
5.13	**Project #189 –** *Continuation of Y-filer plus – remainder of validation plus implementation*:	See item 2.1 above
5.14	**Project #190 -** *MPS as Investigative Tool RSS18-004*:	Waiting on Approval of Deed of Agreement
5.15	**Project #191 –** Effect of HCl on DNA persistence and profiling.	Lab work commenced results being analysed.
5.16	**Project #192 -** *QIAsymphony Bone Extraction:* Experimental design waiting on outstanding feedback.	Approved – to be commenced.
	Projects on Hold	
5.17	Project #172 – Phadebas testing from suspension in ERT: *Pending outcome of project on how suspensions are made. (12.05.2016)*	Nil update
5.18	Project#176 – Investigation into ICMP protocol:	Nil update

6.	**Workflow impacts**	
Item no	**Item**	**Action**
6.1		
6.2		
6.3		
6.4		

7.	**Matters for decision**	
Item no	**Item**	**Action**
7.1		
7.2		
7.3		
7.4		

8.	**Matters for noting**	
Item no	**Item**	**Action**
8.1	Insect identification (WAH). Termites located onsite – routine inspections and pest control have not located any termite damage. Cockroaches have been located, a new pest control company have been employed and they will use new pest control chemicals to control. Lice have been located as well and these can be controlled using domestic spray and cleaning.	
8.2		
8.3		
8.4		
8.5		
8.6		
8.7		
8.8		

Next Meeting

Date: 2018

Time:

Venue: **FSS CR611**

ACTION REGISTER

Minutes Reference	Item Number	Subject	Action	Action Officer	Status
28.09.2017	8.1	NIFA training (SMJ)	\\Bs-qhss-fs1\data1\ForBiol\DNA Analysis Team Meetings\DNA Analysis Management Team\2017\Jul_to_Dec 2017\Summary of NIFA Training Sept 2017_SMJ.doc JAH to produce status update for higher level briefing/ reporting. Nil update 07/12/2017	JAH	
28.09.2017	8.5	Secondary Employment: If request made through Greg Shaw previously, another request needs to be made to Paul Csoban.	Line Managers to follow up with their staff members.	All	

KR-03

Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

November 2017

Justin Howes and Cathie Allen

Project Proposal #184 Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

Published by the State of Queensland (Queensland Health), November 2017

For more information contact: Forensic DNA Analysis, Forensic and Scientific Services, Department of Health, GPO Box 48, Brisbane QLD 4001.

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: Justin Howes
Title: Team Leader – Forensic Reporting and Intelligence Team
Phone: [redacted]
[redacted]

Version history

Version	Date	Changed by	Description
1.0	30/11/2017	Justin Howes	Document Created.

Document sign off

This document has been **approved** by:

Name	Position	Signature	Date
Cathie Allen	Managing Scientist		

The following officers have **endorsed** this document

Name	Position	Signature	Date
Justin Howes	Team Leader FRIT		

Name	Position	Signature	Date
Paula Brisotto	Team Leader ER & Q		

Name	Position	Signature	Date
Luke Ryan	Senior Scientist Analytical		

Name	Position	Signature	Date
Allan McNevin	Senior Scientist ER		

Name	Position	Signature	Date
Kirsten Scott	Senior Scientist Q & P		

Name	Position	Signature	Date
Sharon Johnstone	Senior Scientist Intel		

Name	Position	Signature	Date
Amanda Reeves	Senior Scientist Reporting 1		

Name	Position	Signature	Date
Kylie Rika	Senior Scientist Reporting 2		

Contents

1. Abstract

All samples that underwent a Microcon® process were evaluated and categorised into whether there was meaningful information obtained or not. This evaluation focussed primarily on samples processed in 2016 that underwent an 'auto-microcon' process. Arguably minimal value in proceeding with this automatic processing step was found. Given this, further workflow streamlining processes could be implemented that would provide significant processing efficiencies, and cost and time savings such that these efforts could be better placed in processing higher DNA-yielding samples.

2. Introduction

Microcon® Centrifugal Filter Devices desalt and concentrate macromolecular solutions such as DNA-containing solutions. They employ Amicon's low binding, anisotropic, hydrophilic regenerated cellulose membrane [1].

The use of Microcon® filters to concentrate extract has been a standard post-extraction process within Forensic DNA Analysis to reduce the volume of extract from approximately 100uL to ≤20µL for amplification with AmpFℓSTR® Profiler Plus®, and to ≤35µL for amplification with PowerPlex® 21 system (PP21).

Since the implementation of PP21 amplification kit within Forensic DNA Analysis for casework samples in December 2012, extracts with low Quantification values were recommended to be concentrated. Templates of <0.132ng were found to exhibit marked stochastic effects after amplification [2]. Consequently, a workflow that directed extracts automatically to a concentration step based on Quantification value was implemented ('auto-microcon' process).

Anecdotally, the suitability to provide the Queensland Police Service (QPS) with DNA profile Intelligence from extracts that have been concentrated has been noted to be limited. Furthermore, extracts that are of low quant value that have been automatically concentrated have been observed to rarely yield DNA information for QPS.

NB. Project #163 – *Assessment of results obtained from 'automatic-microcon' samples* [3] was conducted to evaluate the results of samples that were processed with the 'auto-microcon' process. A recommendation of this project was to re-evaluate after the introduction of the Forensic Register in conjunction with the use of Quantifiler® Trio DNA Quantification Kit.

This recommendation was based on the perceived ease of retrieving data from the FR as opposed to AUSLAB, and with the thought that the FR would soon be implemented. For the purposes of this project, it is not considered essential to have the FR implemented if the data can be retrieved from AUSLAB. However, it is considered important that the data be spanning a sufficient period of processing, and be based on the same Quantification system namely the Quantifiler® Trio DNA Quantification Kit.

The purpose of this project is to evaluate the suitability for interpretation of DNA profiles that may be obtained after the post-extraction concentration step using the Microcon® centrifugal filter devices. This evaluation includes an assessment of those samples that underwent the 'auto-microcon' process. This evaluation is based on a data mine of extracts in the year 2016 that were concentrated with Microcon® centrifugal filter devices, and assesses the 'suitability' of PP21 profile outcomes as a function of quant values obtained from using the Quantifiler® Trio DNA Quantification Kit.

This evaluation looks at two data sets as a function of the Quantification value:

1. PP21 DNA profile outcomes from extracts that were processed through the 'auto-microcon' process;

2. PP21 DNA profile outcomes from all extracts that were concentrated with the Microcon® filter devices.

3. Resources

The following resources were required for this validation/project:

Forensic DNA Analysis staff and computer time to retrieve data from AUSLAB and to use Microsoft Excel.

4. Methods

4.1. Data retrieval from AUSLAB (LIMS)

Data was retrieved from AUSLAB using Extended Enquiries. Data was searched for samples that had a testcode of 'XPLEX' and 'MCONC1' ordered in the year 2016 in Forensic DNA Analysis. Samples with the XPLEX testcode were High Priority (P2) samples.

The data was output with the corresponding Quantification value and the reported DNA profile interpretation (Exhibit Report Line in the Exhibit Report

(EXH)) for that particular barcode. If the barcode was a sub-sample, the corresponding EXH line for the sub-sample was output.

For ease of data interrogation, the RAW data (I:\Change Management\Proposal#184 - Evaluation of the efficacy of Microcons\Data\RAW Data from AUSLAB) had a column added to describe whether the sample underwent the 'auto-microcon' process ('AUTO' = 0.001ng/μL<Quant <0.0088ng/μL) or not ('MANUAL' = Quant >0.0088ng/μL). Another column was added to describe whether there was a Quantification value returned in the data collation ('TRUE' = Quant value obtained), or not ('FALSE' = no Quant value obtained (ie. 0 ng/μL).

The data excluded samples that had not returned a DNA profile result, Quality samples (including environmental monitoring samples), have no quant value in the data export, or have quality issues noted.

4.2. Data interrogation

The data was interrogated by assessing the DNA profile outcome results reported as Exhibit Report lines as a function of the Quantification value.

The Exhibit lines were interrogated and grouped into two interpretation outcomes as follows:

1. 'Fail': DNA profile interpretation outcomes of 'Complex unsuitable for interpretation', 'No DNA profile', 'Partial unsuitable for interpretation', 'No DNA Detected';

2. 'Success': All other DNA profile outcomes.

5. Experimental Design

5.1. Experiment 1: Assessment of 'auto-microcon' results

Intent
Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 through the 'auto-microcon' workflow.

Data Analysis

The samples applicable to this experiment had Quantification values in the range 0.001ng/µL to 0.0088ng/µL, and a total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value. A percentage of samples that fell into these categories was determined.

The 'auto-microcon' data could be expressed as a function of Quantification value.

Of the DNA profile interpretation outcomes of 'success', the data was broken down further to determine the percentage of samples that were reworked prior to the DNA profile outcome of 'success'.

The percentage of samples that had an 'auto-microcon' process and led to an NCIDD upload was obtained. This data could be filtered further into the outcome from the NCIDD load, at the time of data collection.

5.2. Experiment 2: Assessment of all DNA profile results from extracts that have had a concentration step.

Intent

Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 and underwent a post-extraction concentration step using Microcon® centrifugal filter devices.

Data Analysis

The samples that were applicable to this experiment had Quantification values above 0.001ng/µL, and underwent the Microcon® process. This included the 'auto-microcon' samples, and those that had a Microcon® rework performed (termed 'manual'). This combination of data was termed 'combined data'.

A total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value.

The percentage of samples that fell into these categories ('manual' and 'combined') was determined. 'Manual' referred to the samples beyond the 'auto-microcon' range that were reworked with the Microcon® process, and 'combined' referred to all samples ('auto-microcon' and 'manual').

There was a point where the number of 'success' samples was approximately the same as the number of 'fail' samples when the Microcon® process was performed. This appeared to be approximately Quant = 0.02ng/uL. Therefore, the data was interrogated further at a Quantification value lower than this mark to determine what percentage of samples in certain ranges led to DNA profile interpretation outcomes of 'success'.

From this data, a sub-section of samples was interrogated further to evaluate the effect on DNA Intelligence that was obtained. A range of samples with Quantification range up to 0.015ng/uL was chosen and a total number of samples was determined. This Quantification value was chosen as it was the approximate value where all samples below this value that underwent a Microcon® process, led to an approximate, round figure of 85% 'failure'.

With this Quantification value chosen, the data was interrogated further. The percentage of samples in this range that were determined to be a 'success' and were reworked further was determined.

The percentage of samples that were in this Quantification range and led to an NCIDD upload was determined. This data could be filtered further into the outcome from the NCIDD load. This data could then be used to evaluate the potential for samples to not provide meaningful DNA Intelligence to QPS if the Microcon® process was re-defined in some way.

5.3. Experiment 3: Datamine of the difference in pre- and post-Microcon® Quantification values

Intent

Evaluate the difference between the values obtained from the Quantification process in samples that have had a Microcon® concentration step applied.

As this is purely a datamining experiment, only the samples that have yielded a result of 'success' was examined.

Data Analysis

The samples applicable to this experiment had Quantification values above 0.001ng/μL where the final result was 'success'.

The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/μL and 0.015ng/μL were examined.

This range was considered by the author to be able to provide a sufficient demonstration of the trend of the data.

6. Results and Discussion

6.1 Assessment of 'auto-microcon' results

For samples in the 'auto-microcon' Quantification range, the total number of samples that were processed this way (excluding certain samples as per Section 5.1) was N= 1449 samples.

The percentage of samples that resulted in a determination of 'fail' was 89.4% (Fig 1). As expected, the number of 'fails' increased when the Quantification decreased and approached the Limit of Detection of Quantification ie. 0.001ng/uL (Fig 2). This was considered to be due to there being less DNA detected in the extract, and therefore less DNA to concentrate.

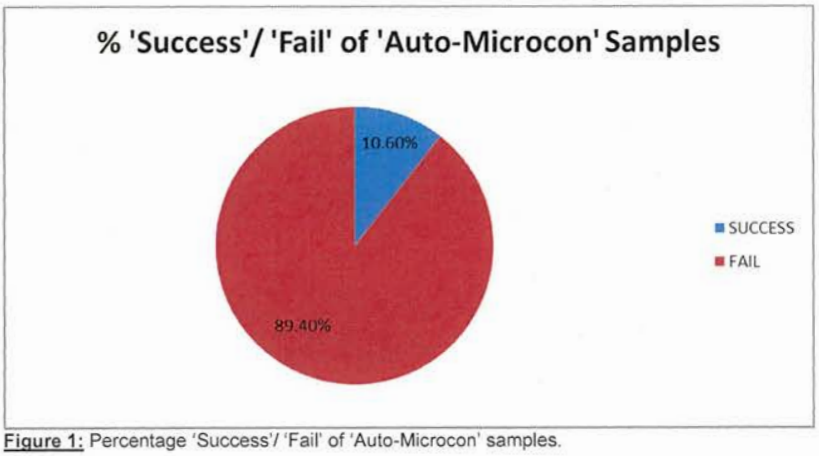

Figure 1: Percentage 'Success'/ 'Fail' of 'Auto-Microcon' samples.

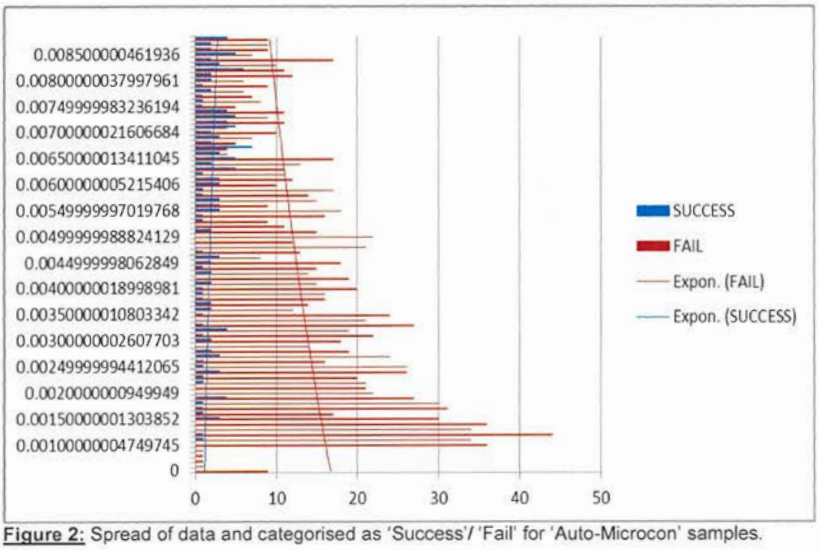

Figure 2: Spread of data and categorised as 'Success'/ 'Fail' for 'Auto-Microcon' samples.

In order to reach a DNA profile interpretation outcome of 'success', it was found that 74.7% of samples had an additional rework to the Microcon® process (Fig 3).

You are implying that "success" of automcon result is due to post mcon rework but the reworks are prob due to # of contrib. assessment No. contributors guidelines don't work for Auto-mic samples, but Rework section of report to be removed.

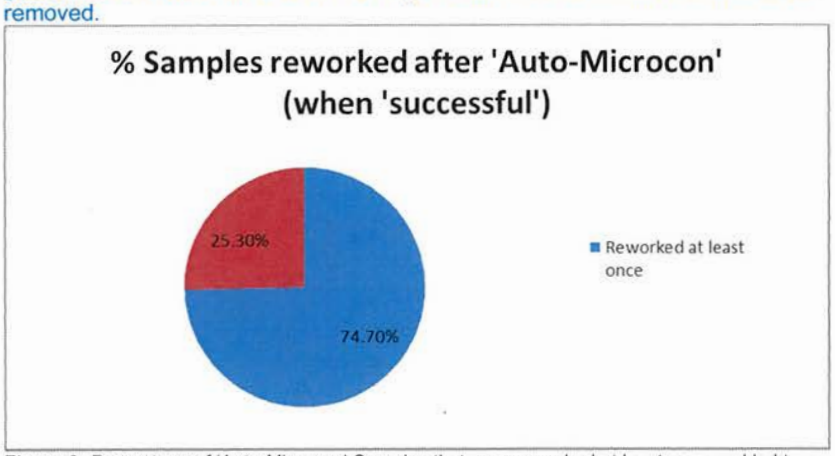

Figure 3: Percentage of 'Auto-Microcon' Samples that were reworked at least once and led to a 'successful' DNA profile outcome.

In putting the data behind Figures 2 and 3 together, if an 'auto-microcon' process was not conducted and was subsequently requested by the client for samples in this Quantification range, there would be approximately a 10% chance of obtaining a 'successful' DNA profile interpretation. Furthermore, in order to achieve that outcome, approximately 75%(this % may not be the case for vol crime under a model of "interp what you can with one amp". Highly likely that most of these reworks are to confirm No. of contrib. given the guidelines. See above.

of these 'successful' samples would have needed a further rework. This means, for these samples, there would be a turnaround time factor for the client to consider, and in a potential fee-for-service model with requesting clients, being prepared to have increased processing costs associated with these low-quant samples would be a client consideration.

If samples were not processed through the 'auto-microcon' process, what DNA Intelligence would the client miss out on? To evaluate this, the 'success' data was drilled down to the samples that had some NCIDD interaction and in particular, where they were the only samples in the case that were NCIDD-suitable for that particular profile (Fig 4). This represented 1.86% of all 'auto-microcon' samples. In looking at samples that provide *new* Intelligence, that is DNA information available for future linking, or has provided a cold-link, this equated to 1.45% of all 'auto-microcon' samples.True but only relevant for vol crime not major crime where LR's can be calculated. The definition of success here is only relevant for vol crime not major. Warm Links are captured here (LR profiles). All the data is based on Major crime samples.

This 1.45% of samples would be the pertinent value for the client to consider if the 'auto-microcon' process was not performed. In considering this, it would be important to evaluate the time and cost for processing, and the opportunity to concentrate efforts on other higher yielding samples. In saying this, with the ease of communication through the Forensic Register, these samples could process if the client has no other forensic Intelligence assisting the matter, or if the item is considered to be of critical priority.

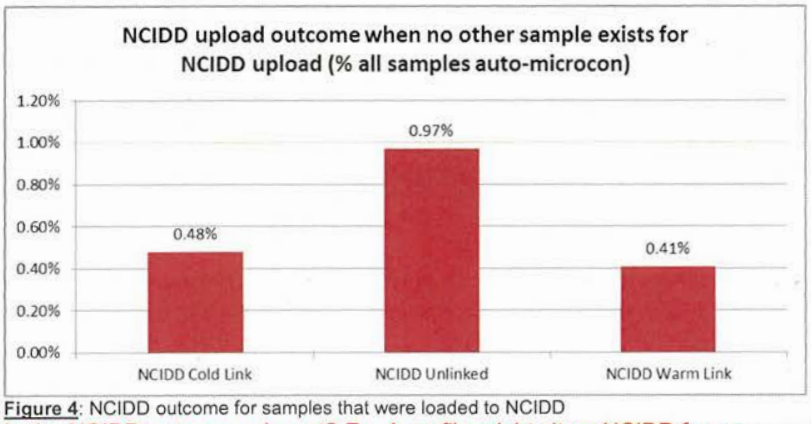

Figure 4: NCIDD outcome for samples that were loaded to NCIDD

Is the NCIDD outcome relevant? Eg. A profile might sit on NCIDD for years and not link

Ultimately, this data means that for approximately 90%(not sure how this is calculated? – this is the 89.4% value above) of samples that underwent an 'auto-microcon' process, there is arguably negligible DNA profile Intelligence for the client. If the 'auto-microcon' was not applied, there would be the following advantages, including but not limited to:

-the potential to make available at least 1449 processing positions for other samples including further available positions that would have been used for reworks,

-the lack of a need for the considerable efforts required to prepare and process Microcon® (and further rework) batches for this number of samples,

-consumable and labour savings in the end-to-end processing of these samples, and

-time and effort could be redirected in the laboratory workflow to other activities including service extensions like Y-STR profiling.

Only relevant if considering intel only samples. For major crime, we need to think about how many samples gave good LR's but no upload? Captured in warm link data.

6.2 Assessment of all DNA profile results from extracts that have had a concentration step.

All samples from 2016 that had a Microcon® process were determined. The total number of samples was N= 2201 samples, excluding certain samples as per Section 5.1.

The percentage of samples that resulted in a determination of 'fail' was 78.5% (see Fig 5). As expected, in looking at the spread of the 'combined' data, the number of 'successes' increased when the Quantification increased (Fig 6).

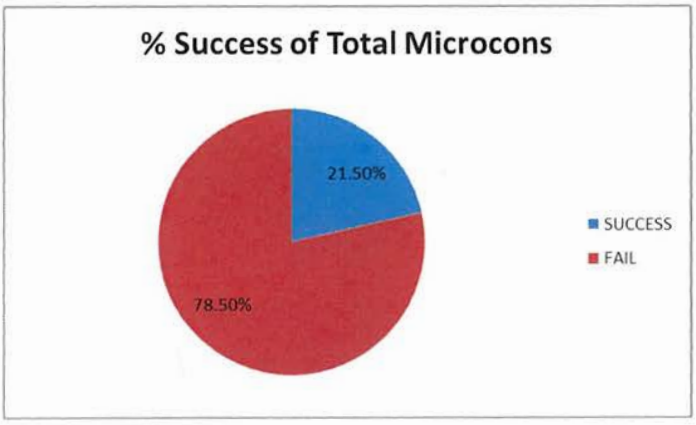

Figure 5: Percentage 'Success'/ 'Fail' of all Microcon® samples ('combined' data).

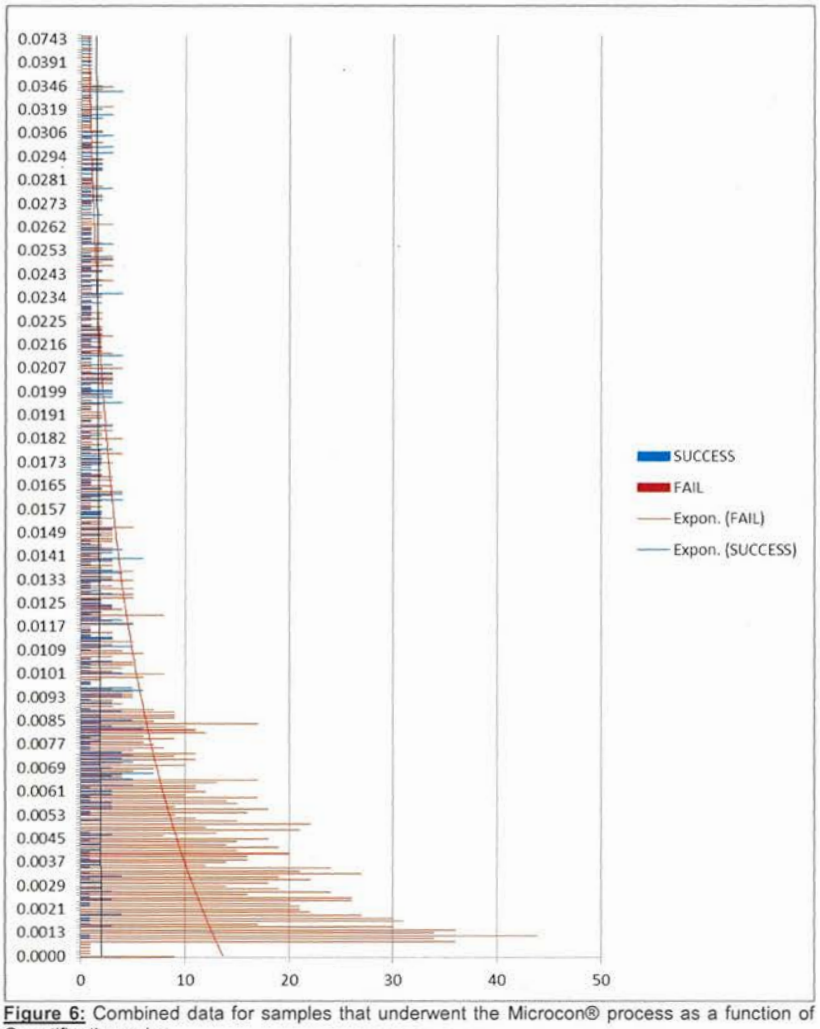

Figure 6: Combined data for samples that underwent the Microcon® process as a function of Quantification value.

As mentioned in Section 5.2, the Quantification value where there was roughly the same number of 'success' and 'fail' samples was approximately 0.02ng/uL. It must be noted that this is a rough estimate *at this* particular Quantification value, and it is based on limited samples that returned that Quantification value. It can be argued that taking a range of Quantification values to look at the overall success/fail percentages could provide the client with approximate likelihoods of obtaining meaningful DNA Intelligence.

A number of ranges were looked at to determine the percentage 'success' of samples with Quantification values in various ranges (Fig 7). The ranges were established up to the highest Quantification value of 0.02ng/uL. As expected, the percentage 'success' increased as the Quantification increased due to the higher amount of DNA in the extract available to be concentrated.

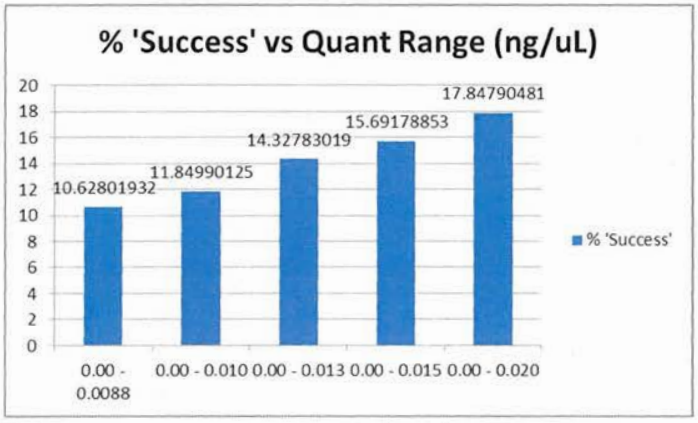

Figure 7: Percentage 'success' for samples that underwent a Microcon® process

In viewing the data in Fig 7, a limitation is that all samples that fell in the 'auto-microcon' range, had a Microcon® process performed, whereas there are samples that are in higher Quantification ranges that might not have required a Microcon® concentration rework step to yield useful DNA profiles. These samples were not evaluated.

A lower Quantification value to where the number of 'successes' roughly equalled the 'failures' was chosen to be the upper end of data ranges that were evaluated further. The value chosen was 0.015ng/uL. Table 1 and Figure 8 describe the risk to NCIDD upload for samples in these ranges if Microcon® concentration steps were not performed.

Table 1: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

	% No other samples to Upload in Quantification ranges (Q)		
	Q = 0.00ng/uL to 0.01ng/uL (total samples in range = 1519)	Q = 0.00ng/uL to 0.0133ng/uL (total samples in range = 1696)	Q = 0.00ng/uL to 0.015ng/uL (total samples in range = 1778)
NCIDD Cold link	0.92	0.88	1.01
NCIDD Unlinked	0.53	0.77	1.24
NCIDD Warm Link	0.46	0.83	0.90

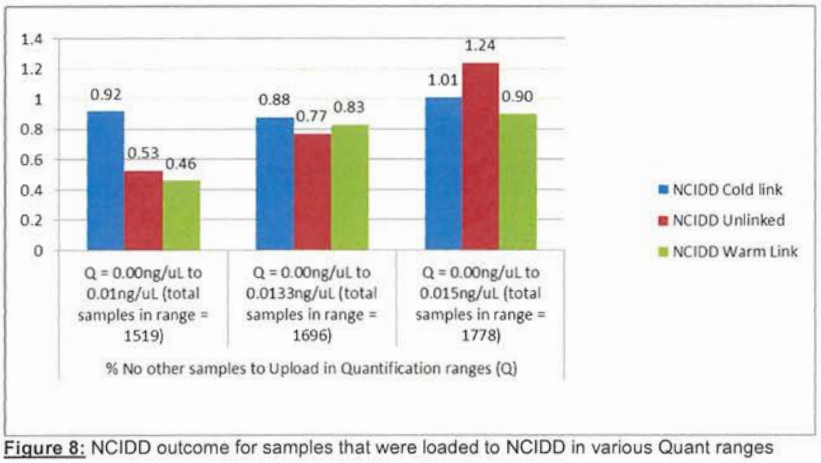

Figure 8: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

Approximately 1.45% of samples in the Quantification range up to 0.01ng/uL resulted in 'new' DNA Intelligence. This percentage is the same as that found in the 'auto-microcon' range. This percentage increased to 1.65% and 2.25% for the Quantification ranges up to 0.0133ng/uL and 0.015ng/uL respectively.
This is because most of the data was from the automcon range, the data added from 0.0088 – 0.01 would not change the outcome (the data shouldn't be combined)
For eg. 0.001-0.0088 – say there is 1000 samples in this set with 1.45% success Versus 0.0088-0.01 – say there is 10 samples in this set with 10% success. Because the first set is so huge, adding the second set will only slightly change the outcome
Being re-evaluated in v2.

The number of further reworks required to obtain 'success' outcomes decreased as the Quantification increased. This is not unexpected given higher DNA yields detected would not necessarily require as many reworks in order to yield DNA profiles.

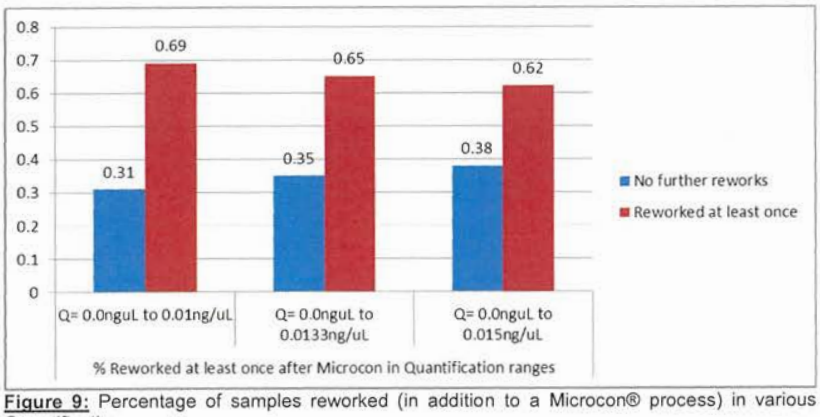

Figure 9: Percentage of samples reworked (in addition to a Microcon® process) in various Quantification ranges.

6.3 Datamine of the difference in pre- and post- Microcon® Quantification values

The samples applicable to this experiment had Quantification values above 0.001ng/μL where the final result was 'success'. The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/μL and 0.015ng/μL were examined.

As the Microcon® process concentrates the DNA extract from approximately 100uL to approximately 35uL, in theory it would be a reasonable expectation to obtain approximately two to three-fold increases in DNA Quantification after concentration. Figure 10 shows the plot of the differences found for samples that resulted in 'success'.

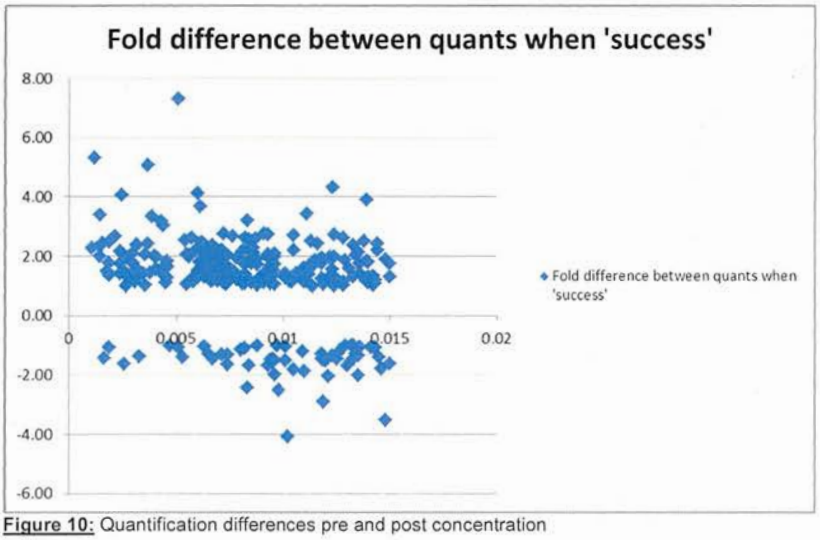

Figure 10: Quantification differences pre and post concentration

The findings are not unexpected as the scatter focusses mostly around two-fold increases in Quantification. It was also not unexpected to observe the variable results. Anecdotally, variability in success rates is found at profile management stage when assessing results of samples that have had this concentration step.

DNA can be lost in the process as seen in Fig 10 where the Quantification values decreased after concentration. Variability in results could be attributed to a number of things, including but not limited to the slight differences between operators and instrumentation, the differences in substrate type and level of degradation, and the variability in Quantification result.

7. Conclusion and Recommendations

The data analysis demonstrated that there was arguably minimal value in performing the 'auto-microcon' concentration step. This opinion was formed by analysing the data from 2016 where it was found that for all samples that underwent the 'auto-microcon' step, 89% did not yield meaningful results.

It was found that in considering all samples that underwent a Microcon® step at some stage in 2016, 78.5% did not yield meaningful results. As expected, when the Quantification value increased, the percentage of meaningful results increased. However, it was also demonstrated in the data analysis that the Quantification values did not always improve after Microcon®, but where they

did, the magnitude of change was roughly equivalent to the change in volume (from neat to concentrated sample).

Based on the data analysis, the following recommendations are offered:

1. Cease 'auto-microcon' processing with the following exceptions:
   a. Priority 1 samples (Critical Priority); and

   b. Coronial/DVI samples where profiles are mostly single-source and quite often incomplete profiles may be enough to provide Intelligence on possible identity.

   c. P2 samples (pending recommendation 4)

2. Cease processing all Priority 3 samples up to the Quantification value of 0.0133ng/uL (template of 200ng).
   Before choosing this value, we should assess data from 0.0088-0.0133 independently from data from 0.001-0.0088 to fully investigate the merits of choosing this value
   Have re-evaluated ranges.

3. For samples in the range described in Recommendation 2, automatically send result information via the Forensic Register to QPS at Quantification stage. This result information is recommended to be the exhibit result line of 'DNA Insufficient for Further Processing'. This recommendation is an extension to the current 'No DNA Detected' process, which looks at Priority 2 samples yielding Quantification results of less than the Limit of Detection.

4. Re-analyse Priority 2 samples in the range 0.0088ng/uL to 0.0133ng/uL after a six month period of processing to evaluate whether Recommendation 2 can be extended to Priority 2 samples – using non intel criteria to assess the results.
   Have re-evaluated ranges.

5. Communicate the change in process to QPS and ensure that QPS are aware that for samples in the ranges mentioned in Recommendations 1 and 2, that they could be requested for Microcon® concentration steps at any point in time. This request can be made via the Forensic Register after they have received the 'DNA insufficient…' result line.

   Overall, I think this idea is good. I guess my concern being that this data and analysis has been done on a certain set of samples and then trying to use this to extrapolate to future processes when we don't know what interp rules there will be for vol crime in PP21 etc.... ie comparing apples with oranges in a way.

~~7.~~8. References

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[1] QIS 19544v11 – Concentration of DNA Extracts Using Microcon Centrifugal Filter Devices

[2] PowerPlex® 21– Amplification of Extracted DNA Validation. Megan Mathieson, Thomas Nurthen, Cathie Allen. December 2012. Forensic DNA Analysis.

[3] Project #163 - Assessment of results obtained from 'automatic-microcon' samples. Josie Entwistle, Allison Lloyd, Kylie Rika, Thomas Nurthen, Cathie Allen. August 2015. Forensic DNA Analysis.

KR-03-1

Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

January 2018

Justin Howes and Cathie Allen

Project Proposal #184 Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

Published by the State of Queensland (Queensland Health), November 2017

For more information contact: Forensic DNA Analysis, Forensic and Scientific Services, Department of Health, GPO Box 48, Brisbane QLD 4001.

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:

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Version history

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Document sign off

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Name	Position	Signature	Date
Kylie Rika	Senior Scientist Reporting 2		

Contents

1. Abstract

All samples that underwent a Microcon® process were evaluated and categorised into whether there was meaningful information obtained or not. This evaluation primarily focussed on samples that underwent an 'auto-microcon' process in 2016. The results suggest there to be arguably minimal value in performing the 'auto-microcon' process due to the limited meaningful DNA Intelligence obtained from these samples. Given this, further streamlining of workflow processes could be implemented that would provide significant efficiencies such that these efforts could be better placed in processing higher DNA-yielding samples.

Given the short TAT for feedback, the Reporting 5's have combined their final feedback. Specific feedback can be found throughout the body of this document, but the combined general feedback is:

1. Can appreciate the value in streamlining processes, but concerned that data for P2 samples is being used to extrapolate for P3 results that we don't yet have interp/processing rules around.
2. Should we be extrapolating around results at all? No one ever really knows what result will be obtained from a particular sample – it has to be tested for the 'true' result to be revealed. It is a false economy to analyse result that give 'assumed known contributor' and retrospectively ascribe them nil value, as the samples are taken and submitted to see whether or not there is 'foreign' DNA present… having said this, the 'value' of each result changes according to the specific sample/case history. Not confident about removing a test that we know does have some value.
3. Note that there seems to be urgency around this proposal being implemented, which might not allow time for full consideration of all potential risks/impacts. For this reason, is it possible to just implement for P3 samples, and revisit in 3 months for viability of extension to P2 samples (see recommendations). Concerned that trying to use P2 results (with one set of interp outcomes and purpose) to forecast for P3 results (with another set of interp outcomes and purpose) is confusing, and combined with the haste, we may miss something. For example, P2 sample goes through auto-mic and gives a partial profile that doesn't match POI could provides important exclusionary intelligence for the case – have we considered the exclusionary benefits appropriately under this proposal?

2. Definitions

DNA Profile Intelligence: DNA profile information available for interpretation by Forensic DNA practitioners that is able to be provided to clients.

Fail: In this report, this is DNA profile information that was not suitable for comparing to reference DNA profiles. This word was used to filter the data into two possible outcomes (fail/success).

NCIDD: National Criminal Investigation DNA Database.

QPS: Queensland Police Service.

Success: In this report, this is DNA profile information that was obtained that was suitable for comparing to reference DNA profiles. This word was used to filter the data into two possible outcomes (fail/success).

3. Introduction

Microcon® Centrifugal Filter Devices desalt and concentrate macromolecular solutions such as DNA-containing solutions. They employ Amicon's low binding, anisotropic, hydrophilic regenerated cellulose membrane [1].

The use of Microcon® filters to concentrate extract has been a standard post-extraction process within Forensic DNA Analysis to reduce the volume of extract from approximately 100uL to ≤20µL for amplification with AmpFℓSTR® Profiler Plus®, and to ≤35µL for amplification with PowerPlex® 21 system (PP21).

Since the implementation of PP21 amplification kit within Forensic DNA Analysis for casework samples in December 2012, extracts with low Quantification values were recommended to be concentrated. Templates of <0.132ng were found to exhibit marked stochastic effects after amplification [2]. Consequently, a workflow that directed extracts automatically to a concentration step based on Quantification value was implemented ('auto-microcon' process).

Anecdotally, the suitability to provide QPS with DNA profile Intelligence from extracts that have been concentrated has been noted to be limited. Furthermore, extracts that are of low quant value that have been automatically concentrated have been observed to rarely yield DNA information for QPS.

NB. Project #163 – *Assessment of results obtained from 'automatic-microcon' samples* [3] was conducted to evaluate the results of samples that were processed with the 'auto-microcon' process. A recommendation of this project was to re-evaluate after the introduction of the Forensic Register in conjunction with the use of Quantifiler® Trio DNA Quantification Kit.

This recommendation was based on the perceived ease of retrieving data from the FR as opposed to AUSLAB, and with the thought that the FR would soon be implemented. For the purposes of this project, it is not considered essential to have the FR implemented if the data can be retrieved from AUSLAB. However, it is considered important that the data be spanning a sufficient period of

processing, and be based on the same Quantification system namely the Quantifiler® Trio DNA Quantification Kit.

The purpose of this project is to evaluate the suitability for interpretation of DNA profiles that may be obtained after the post-extraction concentration step using the Microcon® centrifugal filter devices. This evaluation includes an assessment of those samples that underwent the 'auto-microcon' process. This evaluation is based on a data mine of extracts in the year 2016 that were concentrated with Microcon® centrifugal filter devices, and assesses the 'suitability' of PP21 profile outcomes as a function of quant values obtained from using the Quantifiler® Trio DNA Quantification Kit.

This evaluation looks at two data sets as a function of the Quantification value:

1. PP21 DNA profile outcomes from extracts that were processed through the 'auto-microcon' process;

2. PP21 DNA profile outcomes from all extracts that were concentrated with the Microcon® filter devices.

~~3.~~4. Resources

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The following resources were required for this validation/project:

Forensic DNA Analysis staff and computer time to retrieve data from AUSLAB and to use Microsoft Excel.

~~4.~~5. Methods

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~~4.1.~~5.1. Data retrieval from AUSLAB (LIMS)

Data was retrieved from AUSLAB using Extended Enquiries. Data was searched for samples that had a testcode of 'XPLEX' and 'MCONC1' ordered in the year 2016 in Forensic DNA Analysis. These were High Priority (P2) samples.

The data was output with the corresponding Quantification value and the reported DNA profile interpretation (Exhibit Report Line in the Exhibit Report (EXH)) for that particular barcode. If the barcode was a sub-sample, the corresponding EXH line for the sub-sample was output.

For ease of data interrogation, the RAW data (I:\Change Management\Proposal#184 - Evaluation of the efficacy of Microcons\Data\RAW Data from AUSLAB) had a column added to describe whether the sample underwent the 'auto-microcon' process ('AUTO' = 0.001ng/µL<Quant <0.0088ng/µL) or not ('MANUAL' = Quant >0.0088ng/µL). Another column was added to describe whether there was a Quantification value returned in the data collation ('TRUE' = Quant value obtained), or not ('FALSE' = no Quant value obtained (ie. 0 ng/µL).

The data excluded samples that had not returned a DNA profile result, Quality samples (including environmental monitoring samples), have no quant value in the data export, or have quality issues noted.

5.2. Data interrogation

The data was interrogated by assessing the DNA profile outcome results reported as Exhibit Report lines as a function of the Quantification value.

The Exhibit lines were interrogated and grouped into two interpretation outcomes as follows:

1. 'Fail': DNA profile interpretation outcomes of 'Complex unsuitable for interpretation', 'No DNA profile', 'Partial unsuitable for interpretation', 'No DNA Detected';

2. 'Success': All other DNA profile outcomes including single source DNA profiles matching assumed known contributors or different reference DNA profiles, mixtures that were suitable for comparison to reference DNA profiles, DNA profiles that were suitable for loading to NCIDD.

NB. These descriptions were used to filter the data. A 'fail' does not mean there was a Quality failure in the process; a 'success' does not necessarily mean a DNA match.

~~5.~~6. Experimental Design

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~~5.1.~~6.1. Experiment 1: Assessment of 'auto-microcon' results

Intent

Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 through the 'auto-microcon' workflow.

Data Analysis
The samples applicable to this experiment had Quantification values in the range 0.001ng/µL to 0.0088ng/µL, and a total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value. A percentage of samples that fell into these categories was determined.

The 'auto-microcon' data could be expressed as a function of Quantification value.

The percentage of samples that had an 'auto-microcon' process and led to an NCIDD upload was obtained. This data could be filtered further into the outcome from the NCIDD load, at the time of data collection.

Data on the DNA profile outcomes for various suspected biological types was obtained. Furthermore, data on the profile outcomes for various substrate types was obtained.

6.2. Experiment 2: Assessment of all DNA profile results from extracts that have had a concentration step.

Intent
Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 and underwent a post-extraction concentration step using Microcon® centrifugal filter devices.

Data Analysis

The samples that were applicable to this experiment had Quantification values above 0.001ng/µL, and underwent the Microcon® process. This included the 'auto-microcon' samples, and those that had a Microcon® rework performed (termed 'manual'). This combination of data was termed 'combined data'.

A total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags

were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value.

The percentage of samples that fell into these categories ('manual' and 'combined') was determined. 'Manual' referred to the samples beyond the 'auto-microcon' range that were reworked with the Microcon® process, and 'combined' referred to all samples ('auto-microcon' and 'manual').

There was a point where the number of 'success' samples was approximately the same as the number of 'fail' samples when the Microcon® process was performed. This appeared to be approximately Quant = 0.02ng/uL. Therefore, the data was interrogated further at a Quantification value lower than this mark to determine what percentage of samples in certain ranges led to DNA profile interpretation outcomes of 'success'.

From this data, a sub-section of samples was interrogated further to evaluate the effect on DNA Intelligence that was obtained. A range of samples with Quantification range up to 0.015ng/uL was chosen and a total number of samples was determined. This Quantification value was chosen as it was the approximate value where all samples below this value that underwent a Microcon® process, led to an approximate, round figure of 85% 'failure'.

The percentage of samples that were in this Quantification range and led to an NCIDD upload was determined. This data could be filtered further into the outcome from the NCIDD load. This data could then be used to evaluate the potential for samples to not provide meaningful DNA Intelligence to QPS if the Microcon® process was re-defined in some way. By 'meaningful DNA Intelligence', this means DNA profile information that can be provided to the client that could lead to an identification of a person potentially associated to the alleged matter.

6.3. Experiment 3: Datamine of the difference in pre- and post-Microcon® Quantification values

Intent
Evaluate the difference between the values obtained from the Quantification process in samples that have had a Microcon® concentration step applied.

As this is purely a datamining experiment, only the samples that have yielded a result of 'success' was examined.

Data Analysis

The samples applicable to this experiment had Quantification values above 0.001ng/µL where the final result was 'success'.

The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/µL and 0.015ng/µL were examined.

This range was considered by the author to be able to provide a sufficient demonstration of the trend of the data.

~~6.~~7. Results and Discussion

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7.1 Assessment of 'auto-microcon' results

For samples in the 'auto-microcon' Quantification range, the total number of samples that were processed this way (excluding certain samples as per Section 5.1) was N= 1449 samples.

The percentage of samples that resulted in a determination of 'fail' was 89.4% (Fig 1). As expected, the number of 'fails' increased when the Quantification decreased and approached the Limit of Detection of Quantification ie. 0.001ng/uL (Fig 2). This was considered to be due to there being less DNA detected in the extract, and therefore less DNA to concentrate.

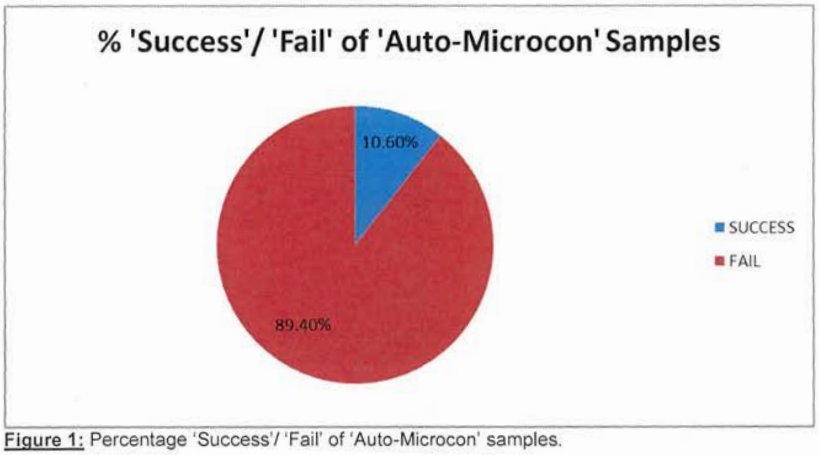


Figure 1: Percentage 'Success'/ 'Fail' of 'Auto-Microcon' samples.

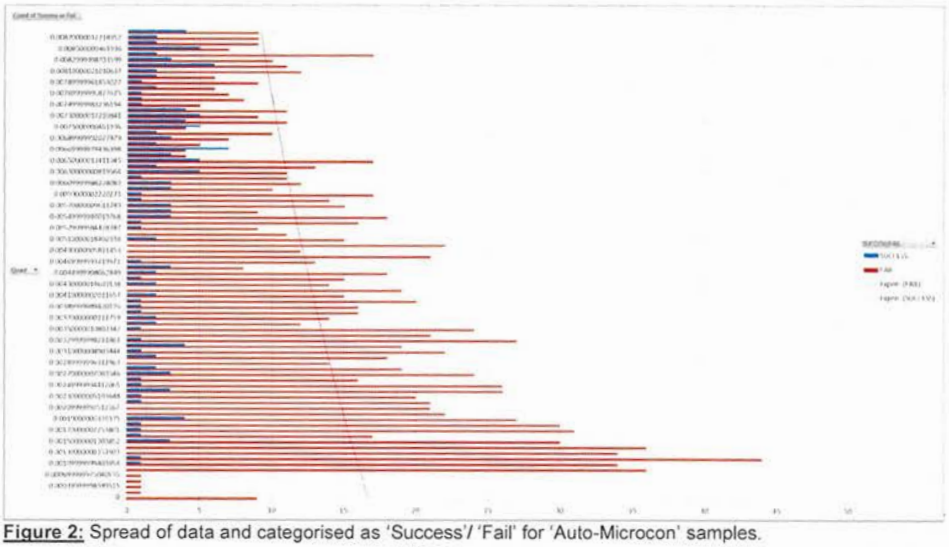


Figure 2: Spread of data and categorised as 'Success'/ 'Fail' for 'Auto-Microcon' samples.

If samples were not processed through the 'auto-microcon' process, what DNA Intelligence would the client miss out on? To evaluate this, the 'success' data was drilled down to the samples that had some NCIDD interaction and in particular, where they were the only samples in the case that were NCIDD-suitable for that particular profile (Fig 3). This represented 1.86% of all 'auto-microcon' samples. In looking at samples that provide *new* Intelligence, that is DNA information available for future linking, or has provided a cold-link, this equated to 1.45% of all 'auto-microcon' samples.

This 1.45% of samples would be the pertinent value for the client to consider if the 'auto-microcon' process was not performed. In considering this, it would be important to evaluate the time and cost for processing, and the opportunity to concentrate efforts on other higher yielding samples. In saying this, with the ease of communication through the Forensic Register, these samples could process if the client has no other Forensic Intelligence assisting the matter, or if the item is considered to be of critical priority.

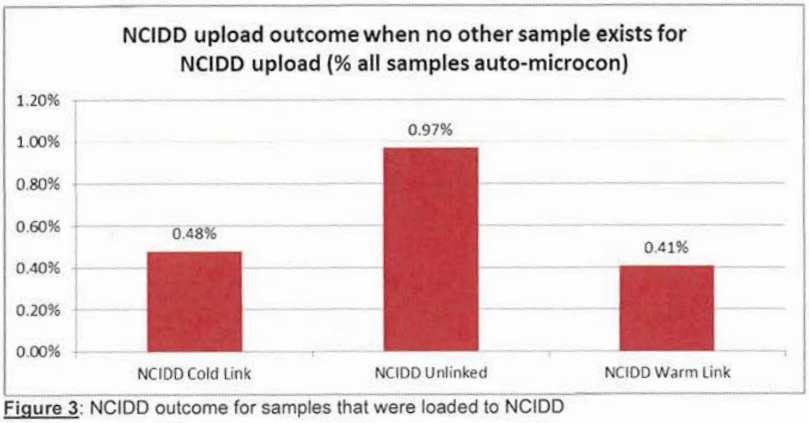


Figure 3: NCIDD outcome for samples that were loaded to NCIDD

The 'success' data was further evaluated to see if any particular substrate type or possible biological source, was more likely to lead to meaningful interpretations after an 'auto-microcon'. The data set for this evaluation was N=154 samples. These samples were broken down into three general interpretation outcomes:

- Profiles matching assumed known contributors. These were either single source DNA profiles, or mixed DNA profiles where the profile was conditioned with no information available for comparison in the remaining contribution (ie. peaks visible sub-threshold or the profile has allelic imbalance suggesting a mixture);

- Single source. These were DNA profiles that were attributed to unknowns, or matched reference DNA profiles, or were from items where ownership could not be confirmed; and,

- Mixtures where no statistical interpretation (NSIP) was performed or were suitable for comparison to reference DNA profiles for Likelihood Ratio (LR) purposes.

Figures 4 displays the DNA profile outcome as a function of the possible biological type, and Figure 5 displays the DNA profile outcome as a function of the substrate.

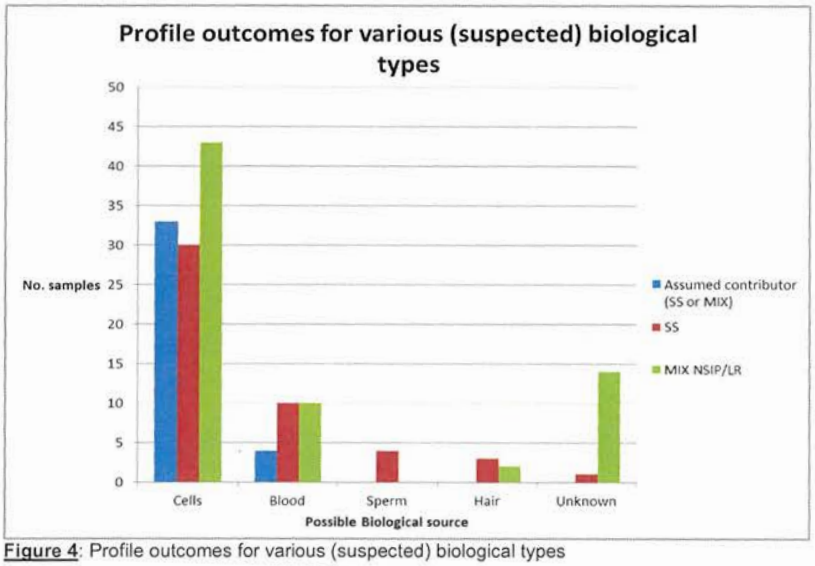


Figure 4: Profile outcomes for various (suspected) biological types

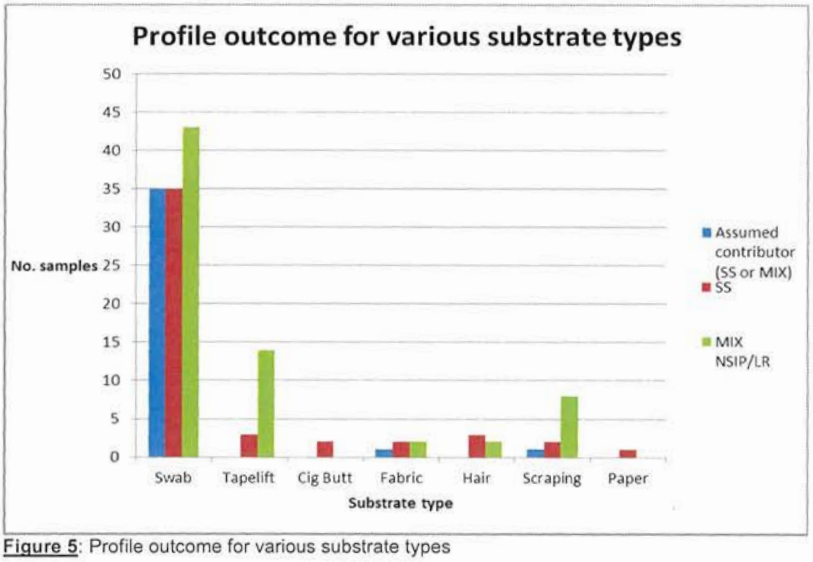


Figure 5: Profile outcome for various substrate types

Figures 4 and 5 show that there do not appear to be any obvious trends in the data. It is not unexpected to have a variety of DNA profile outcomes for different biological source types, and not unexpected for a variety of DNA profile outcomes for different substrate types. Interestingly, the number of 'assumed known contributors' is almost one-third of DNA profile outcomes for the most numerous suspected biological type (cells), and substrate type (swab). It could

be argued that this DNA profile outcome is not meaningful to the client as the results are not unexpected.

What this means is that if the client requested a Microcon® process on a particular sample that was initially in the 'auto-microcon' Quantification range, there does not appear to be a predictive element to the likely success of the microcon rework for a particular biological source type, nor substrate type.

Ultimately, for approximately 90% of samples that underwent an 'auto-microcon' process, there is arguably negligible DNA profile Intelligence for the client. If the 'auto-microcon' was not applied as a streamlining strategy, there would be the following advantages, including but not limited to:

-the potential to make available at least 1449 processing positions for other samples including further available positions that would have been used for reworks. It must be noted that it is not unusual for low-quantification samples to reworked further before determining if the profile is suitable for comparison to reference DNA profiles.

-the lack of a need for the considerable efforts required to prepare and process Microcon® (and further rework) batches for this number of samples,

-consumable and labour savings in the end-to-end processing of these samples, and

-time and effort could be redirected in the laboratory workflow to other activities including service extensions like Y-STR profiling.

7.2 Assessment of all DNA profile results from extracts that have had a concentration step.

All samples from 2016 that had a Microcon® process were determined. The total number of samples was N= 2201 samples, excluding certain samples as per Section 5.1.

The percentage of samples that resulted in a determination of 'fail' was 78.5% (see Fig 6). As expected, in looking at the spread of the 'combined' data, the number of 'successes' increased when the Quantification increased (Fig 7).

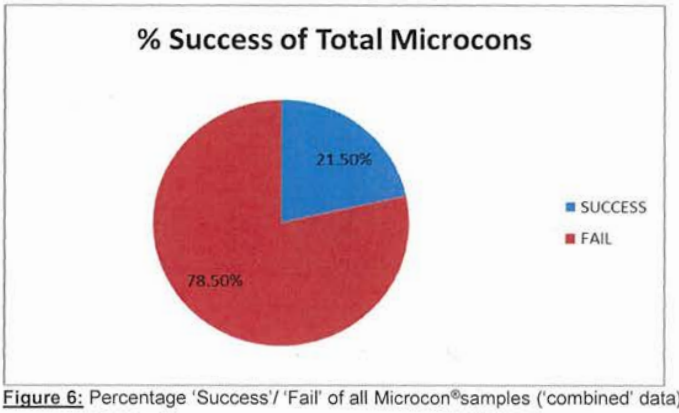


Figure 6: Percentage 'Success'/ 'Fail' of all Microcon®samples ('combined' data).

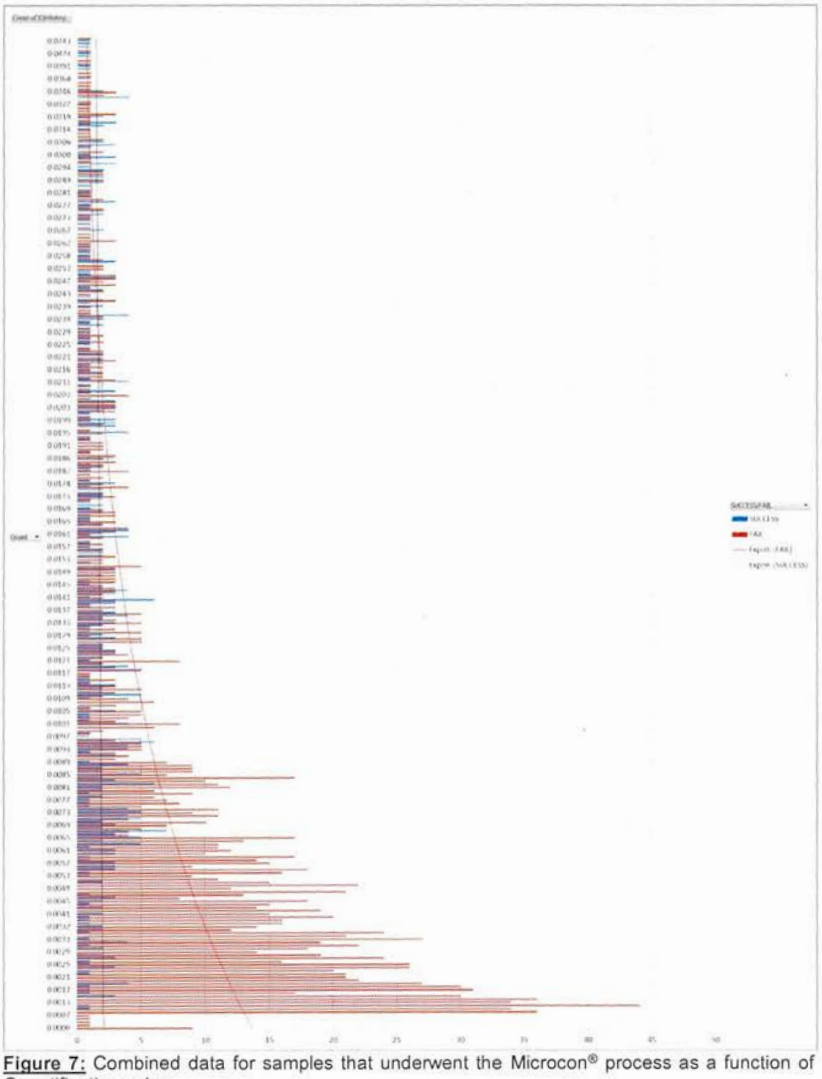


Figure 7: Combined data for samples that underwent the Microcon® process as a function of Quantification value.

As mentioned in Section 5.2, the Quantification value where there was roughly the same number of 'success' and 'fail' samples was approximately 0.02ng/uL. It must be noted that this is a rough estimate *at this* particular Quantification value, and it is based on limited samples that returned that Quantification value. It can be argued that taking a range of Quantification values to look at the overall success/fail percentages could provide the client with approximate likelihoods of obtaining meaningful DNA Intelligence.

A number of ranges were looked at to determine the percentage 'success' of samples with Quantification values in various ranges (Fig 8). The ranges were established up to the highest Quantification value of 0.02ng/uL. As expected, the percentage 'success' increased as the Quantification increased due to the higher amount of DNA in the extract available to be concentrated.

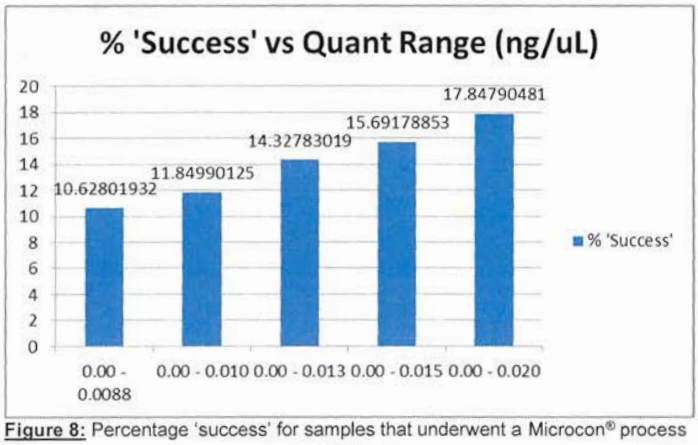


Figure 8: Percentage 'success' for samples that underwent a Microcon® process

In viewing the data in Fig 8, a limitation is that all samples that fell in the 'auto-microcon' range, had a Microcon® process performed, whereas there are samples that are in higher Quantification ranges that might not have required a Microcon® concentration rework step to yield useful DNA profiles. These samples were not evaluated.

A lower Quantification value to where the number of 'successes' roughly equalled the 'failures' was chosen to be the upper end of data ranges that were evaluated further. The value chosen was 0.015ng/uL. Table 1 and Figure 9 describe the risk to NCIDD upload for samples in these ranges if Microcon® concentration steps were not performed.

Table 1: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

	% No other samples to Upload in Quantification ranges (Q)		
	Q = 0.00ng/uL to 0.01ng/uL (total samples in range = 1519)	Q = 0.00ng/uL to 0.0133ng/uL (total samples in range = 1696)	Q = 0.00ng/uL to 0.015ng/uL (total samples in range = 1778)
NCIDD Cold link	0.92	0.88	1.01
NCIDD Unlinked	0.53	0.77	1.24
NCIDD Warm Link	0.46	0.83	0.90

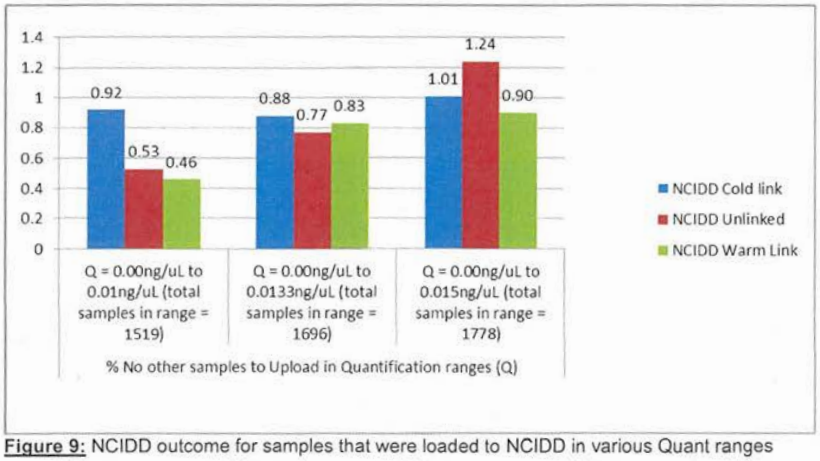


Figure 9: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

Approximately 1.45% of samples in the Quantification range up to 0.01ng/uL resulted in 'new' DNA Intelligence. This percentage is the same as that found in the 'auto-microcon' range. This percentage increased to 1.65% and 2.25% for the Quantification ranges up to 0.0133ng/uL and 0.015ng/uL respectively.

7.3 Datamine of the difference in pre- and post- Microcon® Quantification values

The samples applicable to this experiment had Quantification values above 0.001ng/µL where the final result was 'success'. The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/µL and 0.015ng/µL were examined.

As the Microcon® process concentrates the DNA extract from approximately 100uL to approximately 35uL, in theory it would be a reasonable expectation to obtain approximately two to three-fold increases in DNA Quantification after

concentration. Figure 10 shows the plot of the differences found for samples that resulted in 'success'.

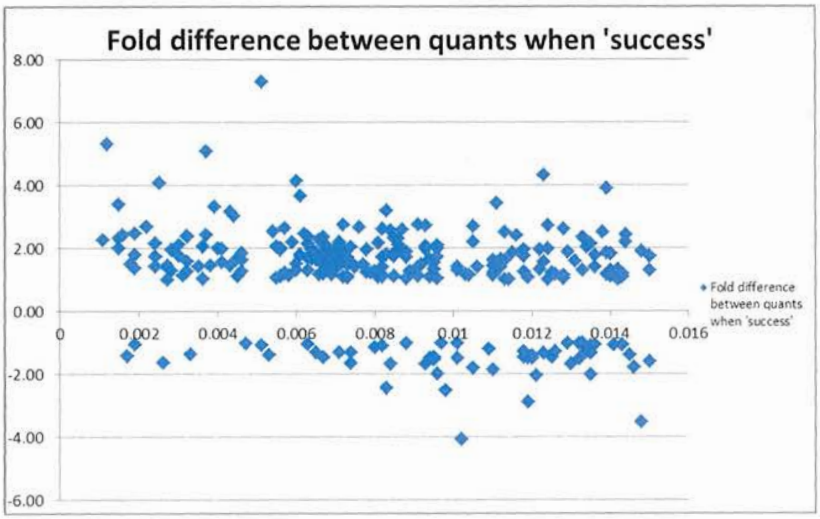


Figure 10: Quantification differences pre and post concentration

The findings are not unexpected as the scatter focusses mostly around two-fold increases in Quantification. It was also not unexpected to observe the variable results. Anecdotally, variability in success rates is found at profile management stage when assessing results of samples that have had this concentration step.

DNA can be lost in the process as seen in Fig 10 where the Quantification values decreased after concentration. Variability in results could be attributed to a number of things, including but not limited to the slight differences between operators and instrumentation, the differences in substrate type and level of degradation, and the variability in Quantification result.

8. Conclusion and Recommendations

The data analysis demonstrated that there was arguably minimal value in performing the 'auto-microcon' concentration step. This opinion was formed by analysing the data from 2016 where it was found that for all samples that underwent the 'auto-microcon' step, 89% did not yield results suitable for meaningful interpretation (or 'success' in this report).

It was found that in considering *all* samples that underwent a Microcon® step at some stage in 2016, 78.5% did not yield results suitable for meaningful interpretation. As expected, when the Quantification value increased, the percentage of meaningful results increased. However, it was also demonstrated in the data analysis that the Quantification values did not always improve after Microcon®, but where they did, the magnitude of change was roughly equivalent to the change in volume (from neat to concentrated sample).

Based on the data analysis, the following recommendations are offered:

1. ~~1.~~ Cease 'auto-microcon' (Quant range: 0.001ng/uL to 0.0088ng/uL) processing for all P3 samples ~~with the following exceptions:~~

    ~~a. Priority 1 samples (Critical Priority); and~~

    ~~b. Coronial/DVI samples where profiles are mostly single-source. Quite often incomplete profiles may be enough to provide Intelligence on possible identity.~~

2. Automatically send result information via the Forensic Register to QPS at Quantification stage for samples in the Quant range: 0.001ng/uL to 0.0088ng/uL. This result information is recommended to be the exhibit result line of 'DNA Insufficient for Further Processing'. This recommendation is an extension to the current 'No DNA Detected' process, which looks at Priority 2 samples yielding Quantification results of less than the Limit of Detection (0.001ng/uL). This new EXH line is intended to act as a flag to QPS to assess the sample within the case context and decide if rework is desired/required, per recommendatioin 4 below.

3. After a six month period of processing, re-analyse samples that have had a Microcon® process performed and were in the initial Quantification range greater than 0.0088ng/uL, to evaluate whether the range from Recommendation 1 can be extended for P3 samples, and potentially include P2 samples (this needs to be examined from P2 interp rules perspective).

4. Communicate the change in process to QPS and ensure that QPS are aware that for samples in the range mentioned in Recommendations 1,

that they could be requested for Microcon® concentration steps at any point in time. This request can be made via the Forensic Register after they have received the 'DNA insufficient...' result line.

~~7.~~9. References

Formatted: Bullets and Numbering

[1] QIS 19544v11 – Concentration of DNA Extracts Using Microcon Centrifugal Filter Devices

[2] PowerPlex® 21– Amplification of Extracted DNA Validation. Megan Mathieson, Thomas Nurthen, Cathie Allen. December 2012. Forensic DNA Analysis.

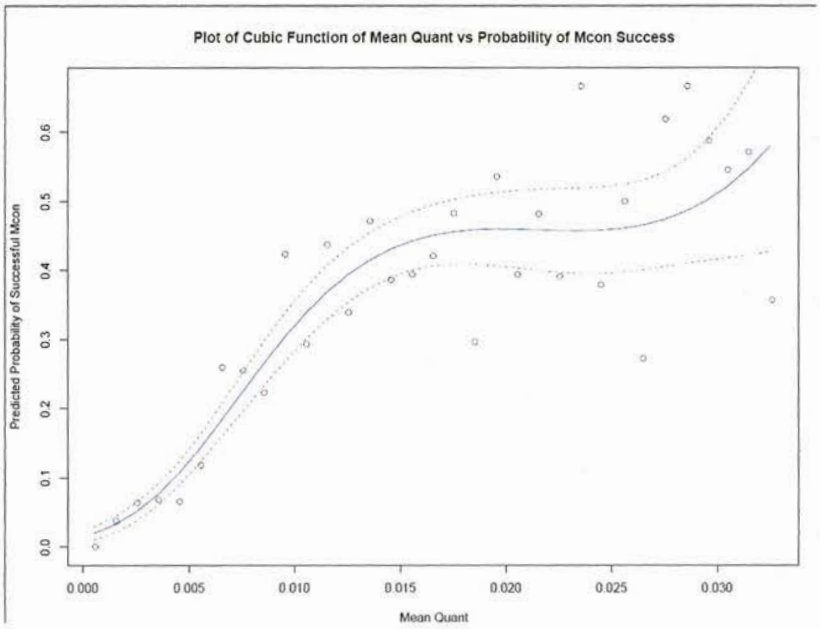
[3] Project #163 - Assessment of results obtained from 'automatic-microcon' samples. Josie Entwistle, Allison Lloyd, Kylie Rika, Thomas Nurthen, Cathie Allen. August 2015. Forensic DNA Analysis.

- To note is the use of percentages and non-normalized data to draw conclusions from the data that are not valid.
  - By not normalizing the very low quant (<0.0088ng/uL; n=1449) data which represents the bulk of the samples(n_{total}=1731), percentages derived from data combined with the above very low quant samples (eg. Figure 8 and figure 9) are artificially skewed by the large number of close-to-zero quant values. Thus, it would not be expected for there to be an insignificant increase in the percentage of successful microcons as presented in figures 8 & 9). Even if 100% of the microcons in the 0.015-0.020 range were successful (n=94), this would have little effect on the mean success rate of the n=1492 samples that have lower quants (94/1492 = 6.4%) at maximum.
  - The data needs to be normalized by obtaining the probability for the mean quant using a frequency distribution for a range of quant values.
  - My own analysis of the data shows that the data can be best modelled by a third order regression of the success/fail probability against the quant. I developed the data as a frequency distribution based on divisions of 0.001 ng/uL. The probability of success was calculated based on the outcome of all samples within a single division, thus normalizing the data. This reduced the data to 33 points. The data was analysed as a binomial distribution as is appropriate with binomial data and the 95% confidence intervals calculated.
  - These outcomes are presented in graphical and tabular form in the attached pages suggests a very different set of conclusions.
  - As can be seen from the results there is a mean success rate of approximately 30% at 0.010ng/uL up to approximately 43% at 0.015ng/uL. This is at odds with the conclusions drawn in section 7.2 of the project and with the justification for the use of 0.015ng/uL in the introduction to Experiment 2 (pg 8).
- As such, I conclude that setting the cut-off for no processing at 0.0088ng/uL is probably too high.

- Additionally, conclusion drawn from percentage values derived from non-normalized data cannot be trusted as the data is clearly skewed towards very low-level quants.

Table 1. 95% confidence intervals for the microcon success probabilities for all quant ranges. (eg. Line 6 represents the probability of success for all samples with a quant between 0.0055 and 0.0064.)

	Mean Quant for range	lower	Estimated Prob of Success	upper
1	0.001	0.061921	1.984695	2.907470
2	0.002	2.111484	3.275817	4.440151
3	0.003	3.746543	5.116828	6.487114
4	0.004	6.038001	7.574229	9.110456
5	0.005	8.936327	10.645507	12.354687
6	0.006	12.277503	14.244627	16.211752
7	0.007	15.868023	18.210662	20.553300
8	0.008	19.552401	22.337853	25.123304
9	0.009	23.205051	26.415076	29.625101
10	0.010	26.709850	30.259965	33.810081
11	0.011	29.959510	33.738579	37.517648
12	0.012	32.862823	36.769795	40.676767
13	0.013	35.350065	39.319138	43.288211
14	0.014	37.375481	41.387961	45.400441
15	0.015	38.919212	43.002380	47.085547
16	0.016	39.989907	44.204209	48.418510
17	0.017	40.625908	45.044506	49.463105
18	0.018	40.891674	45.579421	50.267168
19	0.019	40.869451	45.867744	50.866037
20	0.020	40.649724	45.969556	51.289388
21	0.021	40.323576	45.945520	51.567465
22	0.022	39.977440	45.856505	51.735570
23	0.023	39.689097	45.763385	51.837673
24	0.024	39.523421	45.726976	51.930532
25	0.025	39.526412	45.808084	52.089757
26	0.026	39.716517	46.067684	52.418852
27	0.027	40.074323	46.567177	53.060032
28	0.028	40.538169	47.368584	54.198998
29	0.029	41.021312	48.534376	56.047440
30	0.030	41.456547	50.126451	58.796354
31	0.031	41.839757	52.203470	62.567183
32	0.032	42.240691	54.815589	67.390487
33	0.033	42.793029	57.995491	73.197953


Plot of Cubic Function of Mean Quant vs Probability of Mcon Success
Predicted Probability of Successful Mcon
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.000
0.005
0.010
0.015
0.020
0.025
0.030
Mean Quant

KR-04

[redacted]

From: Justin Howes
Sent: Thursday, 30 November 2017 12:50 PM
To: Allan McNevin; Amanda Reeves; Cathie Allen; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone; Wendy Harmer
Subject: Project #184 for review
Attachments: Report_Evaluation of the efficacy of Microcons_v1.doc

Hi all

Please find attached a report for Project #184 – Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

This has a due date of **Wednesday 20 December** for feedback. Please be mindful of this due-date and schedule time to review.

Thanks
Justin

Justin Howes
Team Leader – Forensic Reporting and Intelligence Team

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

[redacted]

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KR-04-1

[redacted]

From: Cathie Allen
Sent: Monday, 31 July 2017 11:01 AM
To: Allan McNevin; Justin Howes; Kirsten Scott; Kylie Rika; Matthew Hunt; Paula Brisotto; Sharon Johnstone; Megan Mathieson; Saan Orion
Cc: Luke Ryan; Wendy Harmer
Subject: FW: Proposal #184
Attachments: Project Proposal_Evaluation of the efficacy of Microcons_July2017.doc; Budget_July2017.xls; Project Plan_Evaluation of the efficacy of Microcons_July2017.doc

Follow Up Flag: Follow up
Due By: Thursday, 10 August 2017 12:00 PM
Flag Status: Flagged

Hi Everyone

Please find attached a Project Proposal, Project Plan and Budget for Project #184 – Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

These documents are held in I:\Change Management\Proposal#184 - Evaluation of the efficacy of Microcons

ACTION: Please consider the documents, undertake a risk assessment for your team and add this to the Project Plan and provide feedback to Justin Howes by Thursday, 17th of August 2017.

Cheers
Cathie

Cathie Allen
Managing Scientist – Police Services Stream

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

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KR-04-2

[redacted]

From: Justin Howes
Sent: Wednesday, 30 August 2017 9:25 AM
To: Kylie Rika
Subject: Microcon project

Hey Kylie,
I am only waiting on your feedback for the proposal #184.

Please fill in risks to the Project Plan in I:\Change Management\Proposal#184 - Evaluation of the efficacy of Microcons

I want to print the Proposal for Mgt Team in next day or so.

Thanks
JAH

Justin Howes
Team Leader – Forensic Reporting and Intelligence Team

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

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

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KR-04-3

[redacted]

From: Justin Howes
Sent: Thursday, 30 November 2017 12:50 PM
To: Allan McNevin; Amanda Reeves; Cathie Allen; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone; Wendy Harmer
Subject: Project #184 for review
Attachments: Report_Evaluation of the efficacy of Microcons_v1.doc

Hi all

Please find attached a report for Project #184 – Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

This has a due date of **Wednesday 20 December** for feedback. Please be mindful of this due-date and schedule time to review.

Thanks
Justin

Justin Howes
Team Leader – Forensic Reporting and Intelligence Team

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

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w | Queensland Health e | [redacted]

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KR-04-4

From: Justin Howes
Sent: Monday, 8 January 2018 9:04 AM
To: Kerry-Anne Lancaster; Allan McNevin; Amanda Reeves; Cathie Allen; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone; Wendy Harmer
Cc: Allison Lloyd
Subject: Project #184

Hi all
I will have my door shut for most of today now that I have all feedback on v1 of the report.

I intend on sending v2 out today for urgent review by you all by 11am tomorrow. I don't think I am stepping on Paula's toes (for ERQ reviewers) by asking for this to be your No. 1 Priority as you all know how urgent this is now.

There will be some additions and removals as usual with reports.

Thanks
Justin

Justin Howes
Team Leader – Forensic Reporting and Intelligence Team

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

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KR-04-5

[redacted]

From: Justin Howes
Sent: Monday, 8 January 2018 4:47 PM
To: Kerry-Anne Lancaster; Allan McNevin; Amanda Reeves; Cathie Allen; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone; Wendy Harmer
Subject: #184 report v2
Attachments: Report_Evaluation of the efficacy of Microcons_v2.doc

Hi all
I am after your swift review please by **1pm Tues 9 January**. This is to allow any further adjustments, hopefully by the end of the day.

I have made some changes:

- Removed the data and discussion on reworks
- Added evaluation of the 'success' samples – looked at profile outcome vs substrate type, and poss biological origin
- Revised the ranges to keep simple for both priority types – just the auto-mic range. All manual mics to be assessed again at a future date.
- Added some definitions
- Tried to fix labelling of graphs, but alas I couldn't for everything due to my use of pivot tables.

Thanks
Justin

Justin Howes
Team Leader – Forensic Reporting and Intelligence Team

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

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

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KR-05

HealthSupport
Queensland
Forensic and Scientific Services

Project Plan

Stage 2

		Project #:	184
Name/s of Project Staff :	Justin Howes	**Start Date:**	25/07/2017
		Due Date:	09/08/2017
Name Project Team Leader :	Justin Howes	**Contact Phone Number:**	[redacted]
Technical Reviewer/s	Rhys Parry		
Project Title:	An Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.		
Project type	☐ Administration ☐ IT/LIMS ☐ Laboratory ☒ Data mining/analysis ☐ External Project ☐ Other_____		

Project Background (may include a literature review):

The use of Microcon® filters to concentrate extract has been a standard post-extraction process within Forensic DNA Analysis to reduce the volume of extract from approximately 100uL to ≤20µL for AmpFℓSTR® Profiler Plus® and ≤35µL for PowerPlex® 21 (PP21) -requested samples.

Since the implementation of PP21 amplification kit within Forensic DNA Analysis for casework samples in December 2012, extracts with low Quantification values were recommended to be concentrated. Templates of <0.132ng were found to exhibit marked stochastic effects after amplification. Consequently, a workflow that directed extracts automatically to a concentration step based on Quantification value was implemented ('auto-microcon' process).

Anecdotally, the suitability to provide the Queensland Police Service (QPS) with DNA profile intelligence from extracts that have been concentrated has been noted to be limited. Furthermore, extracts that are of low quant value that have been automatically concentrated have been observed to rarely yield DNA information for QPS.

Project #163 – *Assessment of results obtained from 'automatic-microcon' samples* was conducted to evaluate the results of samples that were processed with the 'auto-microcon' process. A recommendation of this project was to re-evaluate after the introduction of the Forensic Register in conjunction with the use of Quantifiler® Trio DNA Quantification Kit.

The purpose of this project is to evaluate the suitability for interpretation of DNA profiles that may be obtained after the post-extraction concentration step using the Microcon® centrifugal filter devices. This evaluation will include an assessment of those samples that underwent the 'auto-microcon' process.

Benefit of Project:

This evaluation will be based on a data mine of extracts in the year 2016 that were concentrated with Microcon® centrifugal filter devices, and will assess the 'suitability' of PP21 profile outcomes as a function of quant values obtained from using the Quantifiler® Trio DNA Quantification Kit.

This evaluation will look at two data sets (from 2016) as a function of the quantification value:
- PP21 DNA profile outcomes from extracts that were processed through the 'auto-microcon' process;
- PP21 DNA profile outcomes from all extracts that were concentrated with the Microcon® filter devices.

Potentially, a new workflow could be designed based on the success/fail rates observed in the data. This could create time and cost savings for the laboratory, and increase the ability to process other higher DNA-yielding samples more quickly.

Proposed Methodology:

The evaluation will look at two data groups:

1. Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 through the 'auto-microcon' workflow.The samples applicable to this experiment will have quantification values in the range 0.001ng/uL to 0.0088ng/uL.

2. Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 and underwent a post-extraction concentration step using Microcon® centrifugal filter devices. The samples applicable to this experiment will have quantification values in the above 0.001ng/uL.

DNA profile interpretation outcomes will be grouped into either 'success' or 'fail' as a function of the quantification value.

- A percentage of samples that fall into these categories will be determined.

- Of the DNA profile interpretation outcomes of 'success', the type of outcome will be broken down further to determine:

    1. The percentage of these samples that were reworked; and,
    2. The percentage of samples that led to an upload of DNA information to NCIDD.

Expected Outcome:

It is expected that the data, especially the data generated for 'auto-microcon' samples will match the anecdotal information from case managers which has been gathered from years of experience. It is expected that the vast majority of DNA profile outcomes would be in the 'fail' category ie. mostly reported as 'complex unsuitable for interpretation'.

It is expected that there will be some 'success' and that this would include DNA profiles that would have been loaded to NCIDD and possibly obtained linking information for the QPS.

It is an expectation that any recommendations are communicated with QPS in order to agree on possible new workflow strategies. This could include not automatically processing low quant samples

with microcons, but to hold and communicate 'low DNA quant' to QPS. Samples could be processed upon request based on case assessment by QPS.

It is an expectation that Critical Priority (P1) samples be processed with the 'auto-microcon' process.

Outputs and Project Milestones: (Ensure that the Change Management Milestone Register is filled out I:\Change Management\Change Management Milestone Register.xls)

Description of Outputs/Milestones:	Expected due date:	Completed date:
1.Data generation and compilation	02/08/2017	
2. Report writing and submission to Mgt Team	04/09/2017	
3. Workflow strategy communication and decisions	03/10/2017	
4.Implementation of any agreed decisions	06/11/2017	
5.		

If expected due date/s not met - explanation of reason required:

Project Budget: Prepare using QIS 31052 (and attach to Project Plan)	**Total Project Budget**
	$5085

Gantt Chart (for large projects): If required, refer to Quality team for help preparing (and attach to Project Plan)

RISK ASSESSMENT:
If a risk is identified: Refer to QIS document 29100 and 29106 for further information on risk identification and management.

Team:	Details of Risk/s Identified	Type of Risk/s:
Evidence Recovery :		☐ Business Risk ☐ OH&S Signature Line Manager
Analytical :		☐ Business Risk ☐ OH&S Signature Line Manager

Intel :		☐ Business Risk ☐ OH&S **Signature Line Manager**
Reporting 1:		☐ Business Risk ☐ OH&S **Signature Line Manager**
Reporting 2 :		☐ Business Risk ☐ OH&S **Signature Line Manager**
Quality and Projects (includes OO) :		☐ Business Risk ☐ OH&S **Signature Line Manager**
Admin :		☐ Business Risk ☐ OH&S **Signature Line Manager**
Team Leader ER &Quality :		☐ Business Risk ☐ OH&S **Signature Team Leader**
Team Leader FRIT :	Potential risks of samples not going to NCIDD – expected to be a low percentage of samples. Samples could always be microconned if the case circumstances warrant eg. P1	☐ Business Risk ☐ OH&S **Signature Team Leader**

	case. Collaboration with QPS and communication of risks to occur.	JAH

Project Proposal approved by:			
Signature Team Leader ER and Quality:		**Date:**	
Signature Team Leader FRIT:		**Date:**	
Signature Managing Scientist:		**Date:**	

Comments:

Please send to Quality Team [redacted] after completion

KR-06

[redacted]

From: Justin Howes
Sent: Thursday, 9 June 2016 11:02 AM
To: Kylie Rika
Subject: RE: today

Hi Kylie, I appreciate that and want to chat to you sometime today. I will be in touch later to see if you are available.

jah

Justin Howes BSc BA MSc (For Sci)
Team Leader – Forensic Reporting & Intelligence Team
Forensic DNA Analysis | Police Services Stream
Forensic and Scientific Services | Health Support Queensland
Department of Health | Queensland Government
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PO Box 594, ARCHERFIELD QLD 4108
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e. [redacted] | www.health.qld.gov.au

HealthSupport Queensland

From: Kylie Rika
Sent: Thursday, 9 June 2016 11:00 AM
To: Justin Howes
Subject: today

Hi Justin

Just to let you know that I felt very scared and intimidated in today's mgmt. meeting because of Allan.

I hope he does not do that ever again.

thanks

Kylie Rika Dip Mgt BSc PGrad Dip (Forensic)
Senior Scientist - Forensic DNA Analysis
Police Services Stream | Forensic & Scientific Services | Health Support Queensland
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KR-07

sample	result after RW	NCIDD upload?	new result for the case?	sfrac?	sperm seen?	initial quant	quant after RW
[redacted]	complex	no	no	no	N/A	0.00727	0.01258
	complex	no	no	no	N/A	0.00866	0.01347
	3p	no	no	no	N/A	0.00378	0.00919
	3p 1 mill support her on him (penis)	no	best result for female in male SAIK	no	N/A	0.00872	0.01156
	3p 100 bill support him on her (SAIK)	no	best result for male in vaginal swabs	yes	yes	0.00873	0.0181
	SS him on her cheek	no	no	yes	yes	0.00331	0.00409
	SS him on her cheek	no	no	yes	yes	0.00417	0.01218
	2p him on condom	no	ask AAP	no	N/A	0.00402	0.00828
	3p	no	no	yes	yes	0.00337	0.00644
	complex	no	no	no	N/A	0.00877	N/A
	3p 100 bill support for a ref	no	ask AAP	no	N/A	0.00608	N/A
	2p UKM1 to NCIDD	yes	ask CG	no	N/A	0.00624	0.01987
	2p	no	no	yes	yes	0.00536	0.00857
	2p 1000 support him on her (SAIK)	no	no	yes	no	0.004	0.00366
	2p 1000 support him on her (SAIK)	no	no	yes	no	0.00436	0.00631
	CPMU	No	No	No	N/A	0.00491	0.00497
	2p UKM2 on her (SAIK)	yes	Yes, new UKM2 upload (not suspect) from HVS	yes	yes	0.0084	N/A
	2p	no	no	yes	yes	0.00164	N/A
	3p 100 bill support him on her (SAIK)	no	no	yes	yes	0.0019	0.00261
	2p 100 bill support him on her (SAIK)	no	no	yes	yes	0.00101	0.00144
	complex	no	no	no	N/A	0.00108	0.00398
	complex	no	no	no	N/A	0.00419	0.00745
	complex	no	no	no	N/A	0.00178	0.00433
	complex	no	no	no	N/A	0.00206	0.00303
	complex	no	no	no	N/A	0.00162	0.00218
	complex	no	no	no	N/A	0.00477	0.00627
	complex	no	no	no	N/A	0.00216	0.00237
	complex	no	no	no	N/A	0.00367	0.00664

[redacted]	3P	no	yes	no	N/A	0.00554	0.0078
	complex	no	no	no	N/A	0.0013	0.00257
	complex	no	no	no	N/A	0.00187	0.00217
	3P	yes	yes	no	N/A	0.00822	0.01008
	complex	no	no	no	N/A	0.00243	0.003132
	complex	no	no	no	N/A	0.00436	0.00861
	complex	no	no	no	N/A	0.00203	0.00216
	3P	yes	yes	no	N/A	0.00814	0.01825
	complex	no	no	no	N/A	0.00527	0.01177
	2P	no	no	no	N/A	0.00134	0.00513
	complex	no	no	no	N/A	0.0025	0.0081
	complex	no	no	no	N/A	0.00458	0.01439
	2P	yes	yes	no	N/A	0.00514	0.00748
	4P	yes	yes	no	N/A	0.00758	0.01031
	4P	no	yes	no	N/A	0.00542	0.01028
	complex	no	no	no	N/A	0.00305	0.00284
	complex	no	no	no	N/A	0.00348	0.00698
	complex	no	no	yes	yes	0.00217	0.00149
	complex	no	no	no	N/A	0.00126	0.00366
	4P	no		no	N/A	0.00507	0.01321
	3P	no		no	N/A	0.00202	0.00391
	3P	no		no	N/A	0.00294	0.0066
	4P	no	Yes	no	N/A	0.00456	0.015
	complex	no	no	no	N/A	0.00606	0.01178
	complex	no	no	no	N/A	0.00123	0.00344
	SS	no	no	yes	yes	0.00527	0.00438
	complex	no	no	no	N/A	0.00636	0.01129
	SS psti	no	no	yes	yes	0.00423	0.00297
	3P	no	no	no	N/A	0.00728	0.02165
	complex	no	no	no	N/A	0.00079	0.00169
	complex	no	no	no	N/A	0.00176	0.00374
	2p	no	no	no	N/A	0.00775	0.02641
	3p rem dec'd from cartridge case	no		no	N/A	0.00564	0.01147

[redacted]	SS UKM6	yes	yes			0.00121	
	2p 100 bill support for ref					0.00584	
	SS 100 bill support for ref	yes				0.00204	0.0054
	SS UKM8	yes	yes			0.00471	
	SS 100 bill support for ref	yes				0.0029	
	4p 1 mill support for ref	no				0.00591	
	2P cond comp, rem match def	no	no	yes	yes	0.00392	0.009
	2P cond comp, rem match def	no	no	yes	yes	0.00728	0.01
	complex - is a decent profile though	no	no	no	N/A	0.00877	0.009
	2P >100b support REF	no	no	yes	yes	0.007	0.013
	SS >100b support REF	yes	no	yes	yes	0.008	MCON
	CMPU	no	no	yes	yes	0.004	0.001
	SS AKC (victim)	no	no	yes	yes	0.002	0.002
	SS AKC	no	no	yes	yes	0.008	0.01
	CMPU	no	no	yes	yes	0.007	0.004
	CMPU	no	no	yes	yes	0.003	0.004
	SS suppot REF	no	no	yes	yes	0.004	0.005
	CMPU	no	no	yes	yes	0.001	0.001
	3P supports 2x REF (>100b; 98000)	no	potentially given case details	yes	yes	0.002	0.007
	3P supports 3x REF (>100b; <10; <10)	no	potentially given case details	yes	yes	0.002	0.004
	CMPU	no	no	yes	yes	0.003	
	SS >100b support REF	yes	potentially given case details	yes	yes	0.008	MCON
	SS >100b support REF	yes	yes	yes	yes	0.007	0.016
	2P >100b support REF	no	no	no	N/A	0.036	
	2P >100b support REF	no	potentially given case details	yes	no	0.002	0.003
	2P COND non support REF	no	no	no	N/A	0	0.001
	3P >100b support REF	no	no	no	N/A	0.008	0.037
	SS AKC	no	no	no	N/A	0.007	0.009
[redacted]	2P >100b support REF	no	no	yes	yes	0.007	0.006

[redacted]	CMPU 5P+ (high RFU)	no	no	no	N/A	0.007	0.022
	single source matching deceased	no	no	no		0.00474	0.01
	2p (UKM1 + another)	no (already uploaded)	no	yes	yes	0.004	0.011
	3mx ref >100b	no (already uploaded)	no	no	no (obvious blood staining)	0.008	0.014
	3PMIX, Ref >100b, 2 refs fav contrib	no	no	no	no	0.00624	M'con to full
	4P Mix, Ref>100 billion, 4 refs favouring contrib	no	no	no	no	0.00425	M'con to full
	2mx cond ref>100 bil	no (already uploaded)	no	no		0.008	0.005
	2mx cond ref>100 bil	no (already uploaded)	no	no		0.003	0.01
	SS AKC	no	no	no	no	0.006	0.013
	2mx cond rem unsuit for NCIDD	no	no	no		0.009	0.033
	2MX NSIP	no	no	no		0.006	0.17
	3mx cond ref>100 bil	no	no	yes	yes	0.003	0.008
	2mx cond rem unsuit for NCIDD, ref excl	no	no	no		0.001	0.004
	2mx cond ref>100 bil	yes	no	yes	yes, 1+	0.008	0.022
	2mx cond, ref excluded	no	no	no		0.004	0.014
	2mx cond, ref = non cont	no	no	no		0.003	0.008
	3mx cond , ref = non cont	no	no	no		0.005	0.012
	3mx cond, not other refs	no	no	yes	yes	0.008	0.03
	2mx cond, UKM1 rem	yes	yes	yes	yes	0.004	0.01
	3mx cond, ref = low support	no	no	no		0.005	0.01
	2mx	yes	y	yes	y	0.004	M'con to full
	3mx cond	? No	? No	no		0.005	M'con to full

Comments

KR-08

[redacted]

From: Kylie Rika
Sent: Friday, 23 February 2018 11:32 AM
To: Justin Howes
Subject: RE: Auto-microcons

Hi Justin

Just following up on your thoughts re below

thanks

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**

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From: Kylie Rika
Sent: Friday, 9 February 2018 9:27 AM
To: Justin Howes
Subject: FW: Auto-microcons

Hi Justin

This is a concern.

I guess it's one thing for the QPS to understand this risk (if they do) but it's not full testing/disclosure for the case from our lab.

Perhaps the process needs to be re-assessed?

thanks

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**

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From: Emma Caunt
Sent: Thursday, 8 February 2018 4:56 PM
To: Kylie Rika
Subject: RE: Auto-microcons

Hi Kylie

I understand from a conversation with Justin that the DNA Insuff process will continue as per the no DNA detected process so samples won't be assessed taking into account the circumstances of the case. I just want to pass on one example.

Rape case
Nothing on the SAIK
Underpants – EFRAC had auto microcon and gave 2 pers mixture of complainant and defendant
Only other sample in the case was defendant on a shoe found in a park
In this case the auto-microcon gave the only evidence to substantiate the claims of the complainant
[redacted]

Thanks

Emma

From: Emma Caunt
Sent: Thursday, 8 February 2018 9:37 AM
To: Justin Howes
Cc: Kylie Rika
Subject: RE: Auto-microcons

Hi Justin

I've been thinking about this a bit more. I want to say from the outset that I am not necessarily opposed to stopping the auto-microcon process, but I do think that there is a risk that we are able to manage.

I am assuming that the 'DNA insuff for processing' line will be added automatically and that it will be added to a list for validation. My question is, how will the validation process be managed?

My personal opinion is that the line should not be validated until the whole case has been assessed to see if processing of this sample would be of benefit, particularly as the quant value reaches the upper range. Obviously at the statement stage, the reporter can assess these samples, but the gap will be if no statement is requested. Since we case manage on a sample by sample basis the 'DNA insuff' results won't be monitored during the normal case management process.

Thanks

Emma

From: Justin Howes
Sent: Wednesday, 7 February 2018 4:14 PM
To: Emma Caunt
Cc: Kylie Rika
Subject: RE: Auto-microcons

Hi, yes I will be changing the expanded comment as I know it is not exactly what we mean. The wording will be similar to the statement wording and making it clear that requests can be actioned.

QPS will have their processes expanded to enable this as well as including how to request further work. The expanded comment change will be added to the current SOP as a comment.

JAH

Justin Howes
Team Leader – Forensic Reporting and Intelligence Team

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

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From: Emma Caunt
Sent: Wednesday, 7 February 2018 4:07 PM
To: Justin Howes
Cc: Kylie Rika
Subject: RE: Auto-microcons

Hi Justin

I've had a look at the reports for this and, NCIDD aside, it shows that 10% of samples that went through the auto-microcon gave interpretable results.

The expanded comment for the 'DNA Insufficient for further processing' line states the following:

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.

This indicates to scientific staff that there is nothing further that can be done with this sample, which is not the case for 10% of samples. It also does not give them the option to request for this sample to be processed further. Can I request that we update the expanded comment to be clear that there may be a chance of getting a usable profile and that they have the option of requesting this? We should probably bring this expanded comment in line with your suggested statement wording as they say different things.

Thanks

Emma

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**

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KR-09

[redacted]

From: Paula Brisotto
Sent: Friday, 27 April 2018 9:35 AM
To: Kylie Rika; Justin Howes
Subject: RE: no DNA detected process and dilutions

Hi all,

User story 715 refers to the enhancement requested.

Thanks,
Paula

From: Kylie Rika
Sent: Thursday, 26 April 2018 3:30 PM
To: Paula Brisotto; Justin Howes
Subject: RE: no DNA detected process and dilutions

Thanks Paula

If the samples are being inhibited, shouldn't we dilute them more not less?

In your email you say perhaps 1/50 and 1/60 instead of 1/100 and 1/120 but this would make them more concentrated???

Unless I am missing something.....

thanks

Kylie Rika DipMgt PGradDipForensic BSc
Senior Scientist Reporting – Forensic DNA Analysis

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

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From: Paula Brisotto
Sent: Thursday, 26 April 2018 3:12 PM
To: Justin Howes; Kylie Rika
Subject: RE: no DNA detected process and dilutions

Hi all,

Thanks for raising this Kylie.

I am going to submit an enhancement to VSTS to ensure the Analytical note re: the dilution is pulled from the parent item to the dilution subsample so it is clear on the quant transition page. This is the page where all samples are directed from – to STR amp, NDNAD or DNA insuff. This will be an additional flag to ensure the sample is assessed accordingly and an appropriate quant transition is made.

For the two samples listed below, the quant values appear to be extremely high (~43 and 58ng/ul). The IPC CT values for these two samples is 21 and 22 (normally ~27-29). This may indicate so much DNA is present in the sample it is impacting/reducing the internal positive control – caused by competition in the rxn. This may therefore also impact on the CT of the samples themselves. We know with quantification, extremely high concentrations of DNA may result in less accurate quant values, therefore it may be best to do a different dilution factor for each of these samples (maybe 1/50 and 1/60 instead of the 1/100 and 1/120....?). These dilution sub-samples will then be quanted and from there hopefully proceed to amp if the quant value is sufficient.

Please let me know if you have any questions regarding the enhancement or if I can show you the quant transition page I am referring to above.

Thanks,
Paula

From: Justin Howes
Sent: Thursday, 26 April 2018 10:57 AM
To: Kylie Rika; Paula Brisotto
Subject: RE: no DNA detected process and dilutions

Thanks Kylie, will look into the NDNAD.

Justin

Justin Howes
Team Leader – Forensic Reporting and Intelligence Team

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

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w | Queensland Health e | [redacted]

From: Kylie Rika
Sent: Thursday, 26 April 2018 10:42 AM
To: Justin Howes; Paula Brisotto
Subject: no DNA detected process and dilutions

Hi both

Please have a look at samples [redacted] and [redacted]

Both of these samples are apparent bloodstains and both gave very high quant values – such that they needed to be diluted. The quants of the dilutions are very small such that no DNA detected/insuff DNA has been entered

We have had a query from QPS about why we have no DNA from some bloodstained shorts.

I guess two things to look into here

1. Dilutions/quants
2. Checking of the info before sending back no DNA detected/insuff DNA lines

thanks

Kylie Rika DipMgt PGradDipForensic BSc
Senior Scientist Reporting – Forensic DNA Analysis

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

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KR-10

[redacted]

From: Kylie Rika
Sent: Friday, 13 November 2020 1:45 PM
To: Cathie Allen; Justin Howes; Paula Brisotto; Luke Ryan; Allan McNevin; Kirsten Scott; Sharon Johnstone; Allison Lloyd
Subject: Implementation Plan for 3500xL PP21 Casework_13Nov2020
Attachments: Implementation Plan for 3500xL PP21 Casework_13Nov2020.docx

Good afternoon Management Team,

Please find attached the Implementation plan for 3500xL PP21 Casework.

It is my understanding that the STRmix report pertaining to PP21 on 3500xL will be out next week, therefore, can you please review and provide feedback to me by COB 20 Nov 2020.

Thanks
Kylie

Kylie Rika
Senior Scientist - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream
Forensic & Scientific Services, Health Support Queensland, Queensland Health

Please note that I may be working from a different location during the COVID-19 Pandemic. The best contact method is via email.

p [redacted]
a 39 Kessels Road, Coopers Plains, QLD 4108
e [redacted] w www.health.qld.gov.au/healthsupport/businesses/forensic-and-scientific-services

KR-11

[redacted]

From: Kylie Rika
Sent: Monday, 11 January 2021 2:30 PM
To: Cathie Allen; Paula Brisotto; Justin Howes; Allan McNevin; Luke Ryan; Belinda Andersen; Kirsten Scott; Allison Lloyd; Sharon Johnstone
Subject: Project 230 - Implementation Plan for 3500/PP21 CW
Attachments: Project 230 Implementation Plan v4KDR.doc

Good afternoon Management Team,

Please find attached the latest version of the Implementation Plan for 3500/PP21 CW.

Can you please review and provide your final feedback by COB 13 Jan 2021.

Many thanks
Kylie

Kylie Rika
Senior Scientist - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream
Forensic & Scientific Services, Health Support Queensland, Queensland Health

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KR-12

[redacted]

From: Justin Howes
Sent: Thursday, 10 February 2022 12:23 PM
To: Kylie Rika
Subject: RE: DIFP

Hi Kylie, no there is no movement on reassessing quant ranges to my knowledge. I am aware that there were a large number of further processing requests from QPS and FSS in this matter, which is showing a good use of the FR and rework decisions. There are a variety of outcomes as expected as well.

What do you think Claire means by 'backlash'? Is this just a turn of phrase or something?

Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health

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From: Kylie Rika <[redacted]>
Sent: Thursday, 10 February 2022 12:09 PM
To: Justin Howes <[redacted]>
Subject: FW: DIFP

Hi Justin

I haven't replied to Claire yet. Before I do, I just wanted to check that there hasn't been any more movement on re-assessing quant ranges for DIFP process. I think we last talked about this in the mgmt. team meeting on 11 November 2021 Ops meeting?

What wasn't included in the minutes was the discussion around the fact that we need QPS/BDNA to do the data dump for us which could be challenging due to cost involved etc....

Thanks

Kylie

From: Claire Gallagher <[redacted]>
Sent: Thursday, 10 February 2022 9:06 AM
To: Kylie Rika <[redacted]>
Subject: RE: DIFP

No. Its not a new upload or anything, so no immediate backlash. It's the same SS profile that's on that same item. Just highlighting that maybe we need to look into our quants for DIFP. Sorry I didn't include the barcode.

[redacted]

Thanks,
Claire

From: Kylie Rika <[redacted]>
Sent: Thursday, 10 February 2022 8:55 AM
To: Claire Gallagher <[redacted]>
Subject: RE: DIFP

Thanks Claire

Was this a new "result" for the case?

From: Claire Gallagher <[redacted]>
Sent: Wednesday, 9 February 2022 3:09 PM
To: Kylie Rika <[redacted]>
Subject: DIFP

Hi Kylie

This sample from Adrian's P1 case was DIFP. It got reworked and has come back as a 20L profile matching a ref sample. The quant was on the high side, but given it was DIFP, it wouldn't have been considered for a rework initially. It was 0.00783ng/uL.

Thanks,
Claire

Claire Gallagher
Scientist - Forensic Reporting and Intelligence Team

Forensic & Scientific Services
Prevention Division, Queensland Health

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KR-13

Queensland Health

Forensic and Scientific Services

Forensic DNA Analysis Management Team Operational Focus Meeting – Minutes

Date: 11 November 2021
Time: 11:30am
Venue: Conf Room 103
Meeting Commenced at:

Name	Initials	Position	Attending
Committee Members			
Cathie ALLEN (Chair)	CJA	Managing Scientist, PSS	No
Justin HOWES (Chair)	JAH	A/Managing Scientist, PSS	Yes
Paula BRISOTTO	PMB	Team Leader, Forensic DNA Analysis	Yes
Sharon JOHNSTONE	SMJ	A/Team Leader, Forensic DNA Analysis	Yes
Allison LLOYD	AKL	Senior Forensic Scientist	Yes
Adrian Pippia	AAP	A/Senior Forensic Scientist	Yes
Kylie RIKA	KDR	Senior Forensic Scientist	Yes
Luke RYAN	LBR	Senior Forensic Scientist	Yes
Kirsten SCOTT	KDS	Senior Forensic Scientist	Yes
Wendy HARMER	WAH	Administration Support Officer	No
Participants			
Guests -			

Item	Topic	Lead	Paper Attached
1	**Welcome and apologies**	Chair	
1.1	**Acknowledgement of Country** I would like to acknowledge the Yuggera peoples and Turrbal peoples as the Traditional and Cultural Custodians of the lands upon which we meet today Meanjin Brisbane and pay respect to Elders past, present and emerging.	Chair	

1.2	**Confirmation of attendees and apologies**	Chair	N/A
2	**Review and acceptance of previous minutes and update on actions register**	Chair	
2.1	Minutes of previous meeting - Accepted via email 1 Nov 2021		
2.2	**Action Register:** **Forensic DNA Analysis Management Action Register**	Chair	See link for list
3	**Standing Agenda Items**		
3.1	**HR Update** HR Stats for October – will be available soon, WAH will send via email (WAH)	Mgmt Team	
3.2	**Workplace Health and Safety** 11/11/2021: Kristina on training to be the lab rep.	Mgmt Team	
3.3	**Operational Initiatives / Ideas** **Business cases**: **HTER**: one item outstanding - StorStar **Capital funding:** Request for funding for a walk-in Freezer	Mgmt Team	
3.4	**Teams Updates around Workflow Impacts, Risks & Mitigation** Team wins: Tip box basketball; EOI for CA closes 11/11/2021 Current Priorities: Nothing noted. Team challenges and impacts: FR downtime, URL unavailability. KDR: TAT impacts – P1 cases, defence requests, court appearances, higher duties, validation and project work. JAH: Most of these impacts have been communicated to A/ED Lara Keller and QPS and acknowledged. Performance: (KPIs etc) Nothing noted.	Mgmt Team	
3.5	**Communications from relevant meetings** - Quality Community of Practice (QCoP) – nil to update - FSS Leadership meeting –	Mgmt Team	

	Finance: all HTER items should be purchased by Dec 2021, if this is unable to be achieved, please advise Gemma Mockler on the possible date of purchase. HR: Mandatory COVID vaccinations for QH staff in clinical care environments, FSS staff are encouraged to add their COVID vaccination certificate to the Hub. QIRC made a ruling on the 20/21 State wage increase and this will be applied from Sept 2021 (2.5%). WfQ Survey results are in and Lara Keller discussed FSS results on Monday 1st of Nov. Team results supplied to management team after that meeting. Safety – still some areas of FSS that are required to complete the FSS Hazard Register – has Forensic DNA Analysis completed this? SMJ- perhaps something the new OHS delegate could look into? Minor update on Business Case for Significant Change – it is a whole of PQFSS approach, there are some proposed structural changes and some proposed reviews to look at longer term items. A/EDFSS will discuss these with the relevant affected direct reports prior to wider communication. No further detail has been provided on this. - FSS/FSG meeting – Nil - FSS/FSG re: FR – Nil - Other – Human Ethics Committee (KDS) – first meeting attended but nil to update relevant to Forensic DNA Analysis.		
3.6	**Budget –** Chair At the end of September, Forensic DNA Analysis overspent by $51,000		

Profit and Loss Report (All)

	Sept 21 Actual	Sept21 Budget	Variance	YTD Actual	YTD Budget	YTD Variance	Full Year Budget
Revenue	**-348,020**	**-378,508**	**-30,488**	**-1,114,565**	**-1,135,524**	**-20,959**	**-4,543,731**
User Charges	-348,020	-378,508	-30,488	-1,114,565	-1,135,524	-20,959	-4,543,731
Labour Expenses	**624,978**	**626,289**	**1,312**	**1,858,379**	**1,835,505**	**-22,874**	**7,408,463**
Labour - Health Practitioners	541,163	538,283	-2,881	1,601,234	1,577,612	-23,621	6,377,559
Labour - Managerial & Clerical	28,826	27,010	-1,816	82,307	78,312	-3,995	311,944
Labour - Operations					0	0	0
Labour Related Taxes	146		-146	438		-438	
Other Employee Related Expenses				427		-427	
Workcover Premiums	1,912	1,756	-156	5,467	5,268	-199	21,072
Labour-Clinical Assistants	52,930	59,240	6,311	168,507	174,313	5,806	697,888
Non Labour Expenses	**148,615**	**161,975**	**13,360**	**498,621**	**490,925**	**-7,696**	**2,014,707**
Building Services	1,081	0	-1,081	1,081	4,200	3,119	16,400
Catering And Domestic	1,218	1,333	115	5,222	3,999	-1,223	15,996
Clinical Supplies	119,101	129,671	10,570	396,359	389,013	-7,346	1,556,049
Communication	1,756	1,827	71	5,483	5,481	-2	21,924
Computers	10,099	7,391	-2,708	32,150	21,973	-10,177	137,992
Non Capitalised Asset Related Costs		0	0	3,761	1,000	-2,761	5,000
Other Supplies And Services	810	690	-120	3,594	2,070	-1,524	8,590
Travel Expenses	69		-69	100		-100	
Repairs And Maintenance	14,440	21,063	6,623	50,196	63,189	12,993	252,756
Repairs And Maintenance - Building				637		-637	
Miscellaneous	40		-40	40		-40	
Depreciation	**23,287**	**23,367**	**80**	**71,414**	**71,660**	**246**	**284,303**
Depreciation & Amortisation	23,287	23,367	80	71,414	71,660	246	284,303
Operating Position (Surplus)/Deficit	**448,860**	**433,124**	**-15,736**	**1,313,850**	**1,262,566**	**-51,284**	**5,163,742**

4	**Project Updates**		
	Project updates provided prior to meeting and the updated below to be read prior to the meeting. Any significant progress to be discussed. Weeks of nil update to be tracked.		
4.1	**Project #199 Validation of Proflex** 10/11/2021 - Report with Mgt Team for review 11/11/2021: LBR: feedback focus mainly on stutter data – the limited number of samples/data size can affect SD. What do we want to see in the experimentt? Perhaps looking at how much of the data is over current threshold? Ie. Tally the numbers and loci where over the existing thresholds. Noted that there was data below threshold as well. Aim of testing was to see if the values were similar between each other, and comparable to 9700. Any proposed alternatives to look at this data, please speak to LBR.	LBR	
4.2	**Project # 206 – Y Filer Plus** *To be reviewed at both Strategy & Operational Meetings* 09/11/2021 - TEN, KDS and KDR having MS Teams meeting with AFP next week (90min session to receive YSTR FR demo and chat). Sharelle making up mixtures in the lab. Some YPWG email discussions centred on the following	KDR	

	questions: How do you report Y database links (both when autosomal info supports or doesn't support the link)? Do you report Y links with one mismatch (e.g. as a possible familial link)? Does this link get reported even if an autosomal familial search has not been done? If there is one Y mismatch and the familial search has been done but has not linked the samples does the Y mismatch get reported?		
4.3	**Project #213 – Verifiler Plus** 09/11/2021 – 1. *Testing the Impact of Pre-Prepared VeriFiler™ Plus PCR Amplification Reagents on PCR Efficiency and Quality.* Primary author - CKS. - Finalised 2. *Testing of VeriFiler™ Plus PCR Amplification Reagent Stability at Room Temperature* Primary author - CKS. Final report with Verifiler team for review. - Finalised 3. *VeriFiler™ Plus – Full Volume Amplification.* Primary author - LMF. - Finalised 4. *VeriFiler™ Plus – Stutter.* Primary author - CLJ. **Management has reviewed,** back for additional edits post feedback 5. *VeriFiler™ Plus – Direct Amplification.* Primary author - AF. Drafted report: with Luke and Megan for review before going to VF team for review 6. *VeriFiler™ Plus – Half Volume Amplification.* Primary author - Revised estimated date to provide report to VF team ~ before Christmas 7. *VeriFiler™ Plus – Testing for D10S1248.* Primary author - MMA. Submitted to VF feedback completed by 21st Oct. Pending edits and to management team this week 8. *VeriFiler™ Plus – STRmix.* Primary author - EJC. Still pending analysis of data. 9. *VeriFiler™ Plus – Mixtures.* Primary author - SMJ. Still pending analysis of data	KDS	
4.4	**Project #216 – Validation of Ion Chef and S5** *To be reviewed at both Strategy & Operational Meetings* 10/11/2021 - Training this week. EOI for PQ progressing. EOI at QEII out.	LBR	
4.5	**Project #221 – Impact of magnetic fingerprint powders on bead-based trace DNA extraction (collab with QPS)** 10/11/2021 - Exp Design in draft.	LBR	
4.6	**Project #227 – Baseline Method Trial** 11/11/2021: nil update	PMB	

4.7	**Project #229 – Paternity Index Distributions in PP21** 09/11/2021 – report is written and with JAH for review before going to the mgt team.	SMJ	
4.8	**Project #233 – Bone sampling and demineralisation protocol** 10/11/2021 – nil update	AKL	
4.9	**Project #234 – Process mapping of interpretation and reporting (SMJ)** 09/11/2021 – It's on hold at the moment	SMJ	
4.10	**Project #235 - 2021 FR version upgrade**	Mgmt Team	
4.11	**Project #236 – Exhibit Result Line Revision** 11/11/2021: To close this project as it now will roll into FR version upgrade.	JAH	
5	**Projects on Hold – to be reviewed at Strategy focussed meeting as well**		
	Nil		
6	**Matters for discussion / decision**		
6.1	Requests/suggestions for audit topics 2022 (KDS) 11/11/2021: some previous suggestions to follow, possibly in 2023 include – VFP, Proflex, NIFA. Suggestions: audit Difference of Opinion Process, lubricant testing process, continuity of samples, equipment and calibrations, statement production via paperless process. Any more to KDS please.		
7	**Matters for noting**		
7.1	**ANZFSS 25th International Symposium call for Abstracts:** https://www.anzfss2022.com/submit-abstract/ Invitation for submission of abstracts for original work (either Oral presentation or Poster presentation): **Submission date is Monday 7 February 2022.**	JAH	

	Author notifications: April 2022.		
7.2	**Familial Testing challenge in South Australia** Challenge heard in a Voir Dire that took evidence from Dr Duncan Taylor. Challenge included legality of familial search using covert sample. Pending voir dire decision, familial testing has been halted at FSSA. The testing was not via NIFA, was performed during a trial of using familial searches more proactively. DNA results (not familial results yet) are able to proceed to committal.	JAH	
8	**Other Business**		
8.1	**DNA Insufficient for Processing (DIFP) process** KDR collecting samples where better results obtained after case manager requested concentration, including profiles for NCIDD. General discussion ensued that this possibility was communicated and accepted by QPS, and that they could request processing any time and that the case manager may rework if case circumstances indicate worthwhile. Value for DIFP determined from PCR (PP21 validation); values may be different with VFP which is more sensitive. Suggestion from LBR that may be worthwhile if moving to VFP that we profile above this value and then after collecting enough data (eg. last data was a year of data), review the findings to see if a threshold could be determined. KDS mentioned if collecting data, need to balance with the number that do not eventuate with profiles (as many get requested by QPS monthly for reactivation).	KDR	

Next Meeting: Thursday 25 November 2021

KR-14

[redacted]

From: Kylie Rika
Sent: Wednesday, 7 September 2022 8:24 AM
To: Lara Keller; Justin Howes; Cathie Allen; Paula Brisotto
Subject: FW: data

Thanks Lara,

Justin, Cathie and Paula, please see thread below. Are we able to please get an update yet? With all that is going on with the media and COI around DIFP, I think it would be good for reporters to know any outcomes to this new data analysis to help prepare them for questions in court.

Thanks
Kylie

From: Lara Keller <[redacted]>
Sent: Wednesday, 7 September 2022 7:57 AM
To: Kylie Rika <[redacted]>
Subject: RE: data

Good morning Kylie
Sorry I will need to direct you to Cathie, Justin or Paula for this. All science-related discussions should be with them.
Kind regards
Lara

From: Kylie Rika <[redacted]>
Sent: Thursday, 1 September 2022 10:22 AM
To: Lara Keller <[redacted]>
Subject: FW: data

Morning Lara

I was just wondering if the A/ED office had an update on whether we are able to see the recent data analysis/outcomes of the DIFP based on the last ~4 years' worth of data? See thread below.

Many thanks
Kylie

From: Justin Howes <[redacted]>
Sent: Friday, 19 August 2022 10:48 AM
To: Kylie Rika <[redacted]>
Subject: RE: data

Hi Kylie,
I have followed up with Helen Gregg as we would take the direction from A/ED office with this work. I am advised that there isn't anything to share with Mgt team at this stage. If I am advised of anything to share with Mgt Team, or further with Reporting Scientists, then I would let you know.

Thanks
Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health

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From: Kylie Rika <[redacted]>
Sent: Thursday, 18 August 2022 12:55 PM
To: Justin Howes <[redacted]>
Subject: RE: data

Hi Justin

Just following up on this. It would be good for reporters to know any outcomes to help them prepare for questions in court.

Thanks
Kylie

From: Kylie Rika
Sent: Monday, 11 July 2022 3:03 PM
To: Justin Howes <[redacted]>
Subject: RE: data

OK, thank you

Kylie

From: Justin Howes <[redacted]>
Sent: Monday, 11 July 2022 1:43 PM
To: Kylie Rika <[redacted]>
Subject: RE: data

Hi
I will find out what is ready to share on this Kylie.

Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health

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From: Kylie Rika <[redacted]>
Sent: Monday, 11 July 2022 11:23 AM
To: Justin Howes <[redacted]>
Subject: data

Hi Justin

I was just wondering if we were able to get an update on the data analysis that you and Allan did recently?

Thanks
Kylie

Kylie Rika
Senior Scientist, Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health

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KR-15

Kylie Rika

From: Kylie Rika
Sent: Wednesday, 8 July 2015 4:43 PM
To: Justin Howes
Subject: CONFIDENTIAL FW: Project plan Proposal #163 Auto Mic

When I was last acting for you, Paula and I discussed a data dump to look at this. It was never classified as a formal project. Then it was put on hold as per your advice. Then the green light came from you and Cathie (re reducing TATs) to go ahead with the "m'con project". So I did. I already had the green light from you and Cathie - it wasn't like a project plan was going to stop the work from happening if the other mgmt team members didn't like it.

There was also a bit of pressure to have some results for your QPS meeting - so what first - the work or the plan - what would QPS have appreciated more?

I can never get an email from her without some little dig in it...

I know, I know....suck it up.....

Kylie Rika BSc. PGDip (Forensic Science)
Senior Scientist - Forensic DNA Analysis
Police Services Stream | Forensic & Scientific Services | Health Support Queensland
Department of Health | Queensland Government
39 Kessels Road Coopers Plains QLD 4108
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t. [redacted]
e. [redacted] | www.health.qld.gov.au

From: Cathie Allen
Sent: Wednesday, 8 July 2015 4:06 PM
To: Kylie Rika
Subject: RE: Project plan Proposal #163 Auto Mic

Hi Kylie

I would recommend that an Acceptance Criteria is included in the project proposal. Something like 'Recommendation to be put forward to the Decision Making Group if there is a clear trend which highlights a different quant value to use which may achieve a DNA profile after Microcon'. I'm sure you'll have better wording, but was thinking that some type of qualifier would be of value.

For future projects, could the project proposal be circulated and signed off prior to the commencement of the work.

Cheers
Cathie

From: Kylie Rika
Sent: Tuesday, 23 June 2015 4:18 PM
To: Justin Howes; Kirsten Scott; Amanda Reeves; Allison Lloyd; Luke Ryan; Allan McNevin; Emma Caunt; Cathie Allen
Subject: Project plan Proposal #163 Auto Mic

Hello

Please find attached the project plan for proposal # 163.

Your feedback ASAP would be appreciated.

thanks

KR-16

[redacted]

From: Justin Howes
Sent: Monday, 6 June 2022 1:55 PM
To: Kylie Rika; Sharon Johnstone
Cc: Paula Brisotto
Subject: FW: DNA Insufficient - Quant transition to Amp

Importance: High

Hi
Please note the DIFP process is currently suspended (the range correction to below is 0.001-0.0088ng/uL). Any new samples in this range will go directly for amp.

Previously reported DIFP that are requested for a restart, will go to microcon as per current process.

P3 samples will continue to be case managed in the same way as always – without rework unless not amped at max (of which the samples in the pertinent range will be amped at max).

Regards
Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health

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From: Paula Brisotto <[redacted]>
Sent: Monday, 6 June 2022 1:23 PM
To: Justin Howes <[redacted]>
Subject: FW: DNA Insufficient - Quant transition to Amp
Importance: High

FYI

From: Luke Ryan <[redacted]>
Sent: Monday, 6 June 2022 1:20 PM
To: Adam Kaity <[redacted]>; Alanna Darmanin <[redacted]>; Amy Cheng <[redacted]>; Belinda Andersen <[redacted]>; Biljana Micic <[redacted]>; Generosa Lundie <[redacted]>; Lai-Wan Le <[redacted]>; Lisa Farrelly <[redacted]>; Maria Aguilera <[redacted]>; Melissa Cipollone <[redacted]>; Nicole Roselt <[redacted]>; Pierre Acedo <[redacted]>; Sharelle Nydam <[redacted]>; Tara Prowse <[redacted]>
Cc: Paula Brisotto <[redacted]>; Cathie Allen <[redacted]>
Subject: DNA Insufficient - Quant transition to Amp
Importance: High

Afternoon All
The premier has requested we test (amp) all samples in the current DNA Insufficient Range (i.e. above 0.001 – 0.088 ng/µL).

When transitioning Quant batches, please ensure all samples in the DNA Insufficient range are transitioned to the Amp WL. We are not reporting DNA Insufficient result lines as of now.

Please also ensure when reviewing No DNA Detected samples, look for samples with the DNA Insufficient result which have not been transitioned to the Amp WL. Please reallocate these to the Amp WL. I will go through the No DNA review list now and allocate these to the Amp WL.

There is no change to rules for No DNA Detected samples.

FR will be modified so that these rules are incorporated into the Quant transition page, but this will be a manual process until these changes are made.

Thanks
Luke

Luke Ryan
Senior Scientist – Analytical Team

Forensic DNA Analysis, Forensic and Scientific Services
Prevention Division, Queensland Health

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KR-17

[redacted]

From: Sharon Johnstone
Sent: Monday, 6 June 2022 3:13 PM
To: Adrian Pippia; Alicia Quartermain; Angela Adamson; Anne Finch; Cassandra James; Emma Caunt; Jacqui Wilson; Josie Entwistle; Kerry-Anne Lancaster; Rhys Parry; Allan McNevin; Angelina Keller; Claire Gallagher; Deborah Nicoletti; Ingrid Moeller; Matthew Hunt; Penelope Taylor; Tegan Dwyer; Thomas Nurthen
Cc: Kylie Rika; Allison Lloyd; Luke Ryan
Subject: FW: DNA Insufficient - Quant transition to Amp

Importance: High

Hi all,
Please see below instructions stemming from today's announcements. These have been agreed to by QPS.
Please also note that any sample that has already been DNA insufficient is to be continued to be reported as such at statement stage. These results are known to the QPS. If it is their wish to have them restarted they will let us know.

Regards,
Sharon

Sharon Johnstone
Senior Scientist – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream
Prevention Division, Queensland Health

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From: Justin Howes <[redacted]>
Sent: Monday, 6 June 2022 1:55 PM
To: Kylie Rika <[redacted]>; Sharon Johnstone <[redacted]>
Cc: Paula Brisotto <[redacted]>
Subject: FW: DNA Insufficient - Quant transition to Amp
Importance: High

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Regards
Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
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From: Paula Brisotto <[redacted]>
Sent: Monday, 6 June 2022 1:23 PM
To: Justin Howes <[redacted]>
Subject: FW: DNA Insufficient - Quant transition to Amp
Importance: High

FYI

From: Luke Ryan <[redacted]>
Sent: Monday, 6 June 2022 1:20 PM
To: Adam Kaity <[redacted]>; Alanna Darmanin <[redacted]>; Amy Cheng <[redacted]>; Belinda Andersen <[redacted]>; Biljana Micic <[redacted]>; Generosa Lundie <[redacted]>; Lai-Wan Le <[redacted]>; Lisa Farrelly <[redacted]>; Maria Aguilera <[redacted]>; Melissa Cipollone <[redacted]>; Nicole Roselt <[redacted]>; Pierre Acedo <[redacted]>; Sharelle Nydam <[redacted]>; Tara Prowse <[redacted]>
Cc: Paula Brisotto <[redacted]>; Cathie Allen <[redacted]>

Subject: DNA Insufficient - Quant transition to Amp
Importance: High

Afternoon All
The premier has requested we test (amp) all samples in the current DNA Insufficient Range (i.e. above 0.001 – 0.088 ng/µL).

When transitioning Quant batches, please ensure all samples in the DNA Insufficient range are transitioned to the Amp WL. We are not reporting DNA Insufficient result lines as of now.

Please also ensure when reviewing No DNA Detected samples, look for samples with the DNA Insufficient result which have not been transitioned to the Amp WL. Please reallocate these to the Amp WL. I will go through the No DNA review list now and allocate these to the Amp WL.

There is no change to rules for No DNA Detected samples.

FR will be modified so that these rules are incorporated into the Quant transition page, but this will be a manual process until these changes are made.

Thanks
Luke

Luke Ryan
Senior Scientist – Analytical Team

Forensic DNA Analysis, Forensic and Scientific Services
Prevention Division, Queensland Health

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e [redacted] w www.health.qld.gov.au/healthsupport/businesses/forensic-and-scientific-services

KR-18

[redacted]

From: Justin Howes
Sent: Friday, 19 August 2022 4:54 PM
To: Allison Lloyd; Cathie Allen; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone; Wendy Harmer; Adrian Pippia; Alicia Quartermain; Allan McNevin; Allison Lloyd; Angela Adamson; Angelina Keller; Anne Finch; Cassandra James; Claire Gallagher; Deborah Nicoletti; Emma Caunt; Ingrid Moeller; Jacqui Wilson; Josie Entwistle; Justin Howes; Kerry-Anne Lancaster; Matthew Hunt; Penelope Taylor; Rhys Parry; Tegan Dwyer; Thomas Nurthen
Subject: Process following A/DG memo
Attachments: DG Memo - Reversion to concentration of all Priority 2 samples in range.pdf; Extract 19.4 from SOP 17117V19.pdf

Hi all
Following this memo, the information below will be added to 17117 which will be sent to review early next week:

When seeking written approval from QPS for additional work if considered beneficial, send a Request/Task via the Forensic Register to the relevant Forensic Officer found by the field below. Add the Forensic Officer's ID number to the Action Officer field, and link the relevant crime scene barcode to the Request/Task.

Location / Owner
From the front driver seat adjustment levers

Exam Source
Vehicle: [redacted] Black Nissan Elgrand, Van

Exhibit Notes & Analysis Advice

Parent Barcode Property Tag Current Location

Suggested Template for wording:

Hello, a DNA profile has been obtained from the linked crime scene sample. I am seeking approval for additional work to be undertaken on the sample, in an attempt to obtain a suitable DNA profile for interpretation. Please be advised if this additional work is approved, the DNA extract will be consumed. This means there will be no opportunity for further processing in this laboratory, or elsewhere if alternative technologies are under consideration. We understand that consultation with the Investigating Officer may be necessary and will await the outcome of those discussions. Once finalised, please advise via return Request/Task if the additional work is approved. If approval is not provided, the DNA profile obtained will be reported.

When sending the Request/Task, the exhibit result line *SOHAA – Sample on hold, awaiting advice* should be added, and validated by a second operator.

When QPS respond, the exhibit result line *TRQ – Testing restarted on advice from QPS* should be added irrespective of whether approval for further processing has been granted or not. The result will either be reported based on the one amplification result, or will be reported after the further processing.

Regards

Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health

[redacted]

Please note that I may be working from a different location during the COVID-19 Pandemic. The best contact method is via email.

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

From: Helen Gregg <[redacted]>
Sent: Friday, 19 August 2022 3:33 PM
To: Abigail Ryan <[redacted]>; Adam Kaity <[redacted]>; Adrian Pippia <[redacted]>; Alanna Darmanin <[redacted]>; Alicia Quartermain <[redacted]>; Allan McNevin <[redacted]>; Allison Lloyd <[redacted]>; Amy Cheng <[redacted]>; Amy Morgan <[redacted]>; Angela Adamson <[redacted]>; Angelina Keller <[redacted]>; Anne Finch <[redacted]>; Belinda Andersen <[redacted]>; Biljana Micic <[redacted]>; Cassandra James <[redacted]>; Cathie Allen <[redacted]>; Cecilia Flanagan <[redacted]>; Chantal Angus <[redacted]>; Chelsea Savage <[redacted]>; Cindy Chang <[redacted]>; Claire Gallagher <[redacted]>; Dasuni Harmer <[redacted]>; Deborah Nicoletti <[redacted]>; Emma Caunt <[redacted]>; FSS.FDNA.Admin <[redacted]>; Generosa Lundie <[redacted]>; Helen Williams <[redacted]>; Ingrid Moeller <[redacted]>; Jacqui Wilson <[redacted]>; Janine Seymour-Murray <[redacted]>; Josie Entwistle <[redacted]>; Julie Brooks <[redacted]>; Justin Howes <[redacted]>; Kerry-Anne Lancaster <[redacted]>; Kevin Avdic <[redacted]>; Kim Estreich <[redacted]>; Kirsten Scott <[redacted]>; Kristina Morton <[redacted]>; Kylie Rika <[redacted]>; Lai-Wan Le <[redacted]>; Lisa Farrelly <[redacted]>; Luke Ryan <[redacted]>; Madison GULLIVER <[redacted]>; Maria Aguilera <[redacted]>; Matthew Hunt <[redacted]>; Melissa Cipollone <[redacted]>; Michael Goodrich <[redacted]>; Michael Hart <[redacted]>; Michelle Margetts <[redacted]>; Naomi French <[redacted]>; Nicole Roselt <[redacted]>; Paula Brisotto <[redacted]>; Penelope Taylor <[redacted]>; Phillip McIndoe <[redacted]>; Pierre Acedo <[redacted]>; Rhys Parry <[redacted]>; Ryu Eba

<[redacted]>; Sandra McKean <[redacted].au>; Sharelle Nydam <[redacted]>; Sharon Johnstone <[redacted]>; Stephanie Waiariki <[redacted]>; Suzanne Sanderson <[redacted]>; Tara Prowse <[redacted]>; Tegan Dwyer <[redacted]>; Thomas Nurthen <[redacted]>; Valerie Caldwell <[redacted]>; Vicki Pendlebury-Jones <[redacted]>; Wendy Harmer <[redacted]>; Yvonne Connolly <[redacted]>
Cc: Alison Slade <[redacted]>; FSS Corro <[redacted]>; Lara Keller <[redacted]>; Keith McNeil <[redacted]>; Petra Derrington [redacted]
Subject: FW: C-ECTF-22/13557 - DG MEMO - from Dr David Rosengren, Acting Director-General, Queensland Health - Subject of memorandum

Good afternoon everyone,

Please see attached memo. I have asked for an enhancement to FR to assist with this change.

Please hold all quants effective immediately, until the FR enhancement is complete. Paula has specific details for the analytical team.
For batches that have already progressed beyond quant, proceed as per this morning's processes.

Could you please update SOPs asap.

Contact me if you have any queries.

Regards
Helen

Helen Gregg
A/Executive Director

Forensic and Scientific Services
Prevention Division, Queensland Health

[redacted]

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

Good Afternoon

Please see attached the Memorandum from Dr David Rosengren, Acting Director-General, Queensland Health, for your attention.

Should you have any questions in relation to this advice, please contact Professor Keith McNeil, Acting Deputy Director-General on telephone [redacted]

Kind Regards

Ministerial & Executive Services Unit, Office of the Director-General | Queensland Health

E [redacted]

W health.qld.gov.au

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KR-19

From: Justin Howes <[redacted]>
Sent: Tuesday, 23 August 2022 2:46 PM
To: Kylie Rika <[redacted]>; Sharon Johnstone <[redacted]>
Cc: Paula Brisotto <[redacted]>
Subject: RE: Exhaustion of extract

Hi
Please try this workflow first Kylie which has been made available to Helen Gregg. I did this to get my head around it and am hoping that this is clear on what samples go where, and the overriding principle. This is in 17117 as an Appendix which is currently in review.

Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team
Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health
[redacted]
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From: Kylie Rika <[redacted]>
Sent: Tuesday, 23 August 2022 2:28 PM

To: Justin Howes <[redacted]>; Sharon Johnstone <[redacted]>
Cc: Paula Brisotto <[redacted]>
Subject: RE: Exhaustion of extract

Thanks Justin

I am wondering if a meeting with staff would be a good way for staff to better understand the changes? and allow all questions to be answered in one go.

Thanks
Kylie

From: Justin Howes [redacted]
Sent: Tuesday, 23 August 2022 2:02 PM
To: Kylie Rika <[redacted]>; Sharon Johnstone <[redacted]>
Cc: Paula Brisotto <[redacted]>
Subject: Exhaustion of extract

Hi
I know there have been some questions regarding the A/DG Memo and extract volumes. I just spoke to Helen Gregg who asked if I thought the message on extract availability is clear with staff.

I said there have been some questions to me, and perhaps more with seniors but that I would reiterate the message that the overarching principle in any situation (eg. whether second amp post mic, or consideration of mic to full) from the DG memo is that the DNA extract cannot be exhausted without QPS approval. She was happy with this and I mentioned it is already in the draft SOP for further review (17117v21.4).

Could you pls ensure that staff understand the key principle?

Thanks
Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team
Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health
[redacted]

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