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 :	Nil risks to ER team, as noted below there is some risk of samples not being loaded to NCIDD however these are mitigated against and are offset by process efficiency meaning results should be more timely	☐ Business Risk ☐ OH&S **Signature Line Manager** ARM 04/08/2017
Analytical :	Nil risks to the Analytical team, if anything it could potentially decrease the post-extraction workload in the team. Low risk of samples not being concentrated and loaded to NCIDD however this might be determined on the outcome of the project.	☐ Business Risk ☐ OH&S **Signature Line Manager** MLM 10/08/2017

Intel :	Nil risks in the Intel team for the running of this project.	☐ Business Risk ☐ OH&S **Signature Line Manager** SMJ 28/08/2017
Reporting 1:	Nil risk in conducting this study and assessing the efficacy of microcons. Following the proposed data interrogation we can then assess any risk or trade-off associated with a process change such as curtailing the standard use of the microcon step.	☐ Business Risk ☐ OH&S **Signature Line Manager** MOH 31/08/2017 [redacted]
Reporting 2 :	Nil risk and agree with comments of Reporting team 1	☐ Business Risk ☐ OH&S **Signature Line Manager** KDR [redacted]
Quality and Projects (includes OO) :	Nil OHS risks. Business risk is that we do not concentrate/microcon and profile a sample where a loadable profile could be obtained. The risk of this is low and will need to be balanced with the cost implications of processing all samples in this way. Result of this project to specifically address this risk.	☐ Business Risk ☐ OH&S **Signature Line Manager** KDS [redacted]
Admin :	Hi Justin As discussed, no business or OHS implications for admin staff. Kind regards **Saan Orion** A/Administration Support Officer	☐ Business Risk ☐ OH&S **Signature Line Manager** SO
Team Leader ER &Quality :	Potential risks of loadable sample not going to NCIDD. Low risk as case assessment would still be performed, and a determination of post-extraction processing requirements can be made at that time taking into consideration any other samples/results and circumstances of the case.	☐ Business Risk ☐ OH&S **Signature Team Leader** PMB 03/08/2017
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:	[redacted]	**Date:**	31-08-2017
Signature Team Leader FRIT:		**Date:**	31-08-2017
Signature Managing Scientist:	Cathie Allen	**Date:**	04-09-2017

Comments:

Please send to Quality Team [redacted] after completion

Justin Howes

From: Kylie Rika
Sent: Wednesday, 3 January 2018 11:54 AM
To: Justin Howes
Subject: Report_Evaluation of the efficacy of Microcons_v1KDR feedback
Attachments: Report_Evaluation of the efficacy of Microcons_v1KDR feedback.doc

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:

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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

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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.

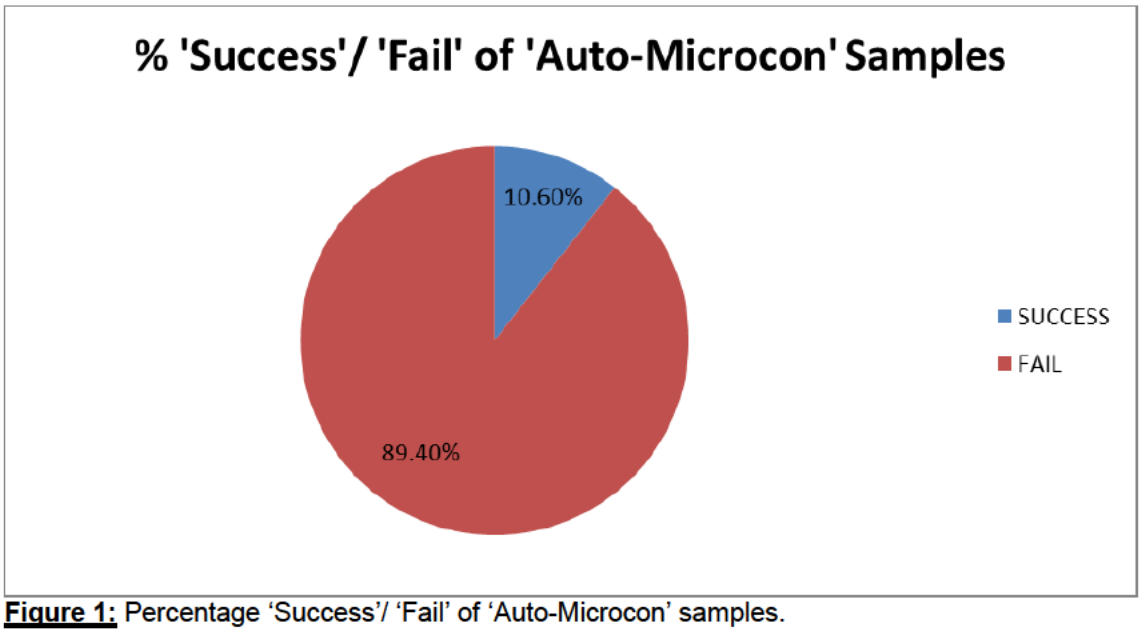

Figure 1: Percentage 'Success'/ 'Fail' of 'Auto-Microcon' samples.

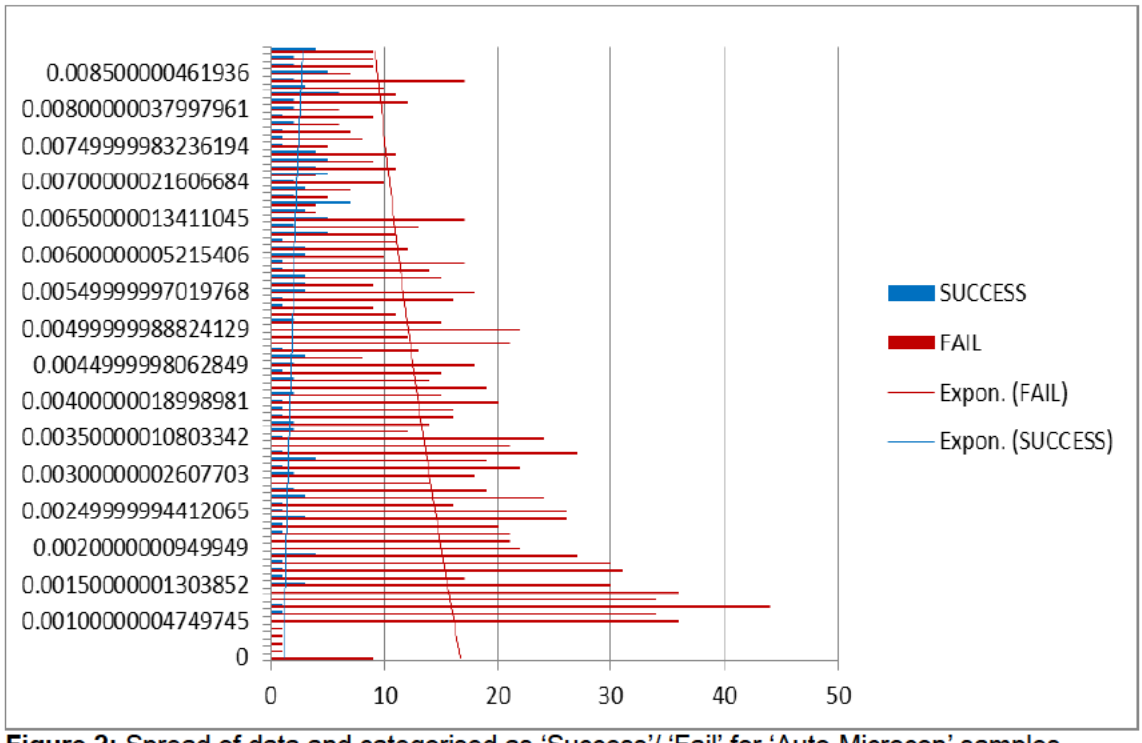

Figure 2: Spread of data and categorised as 'Success'/ 'Fail' for 'Auto-Microcon' samples.

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

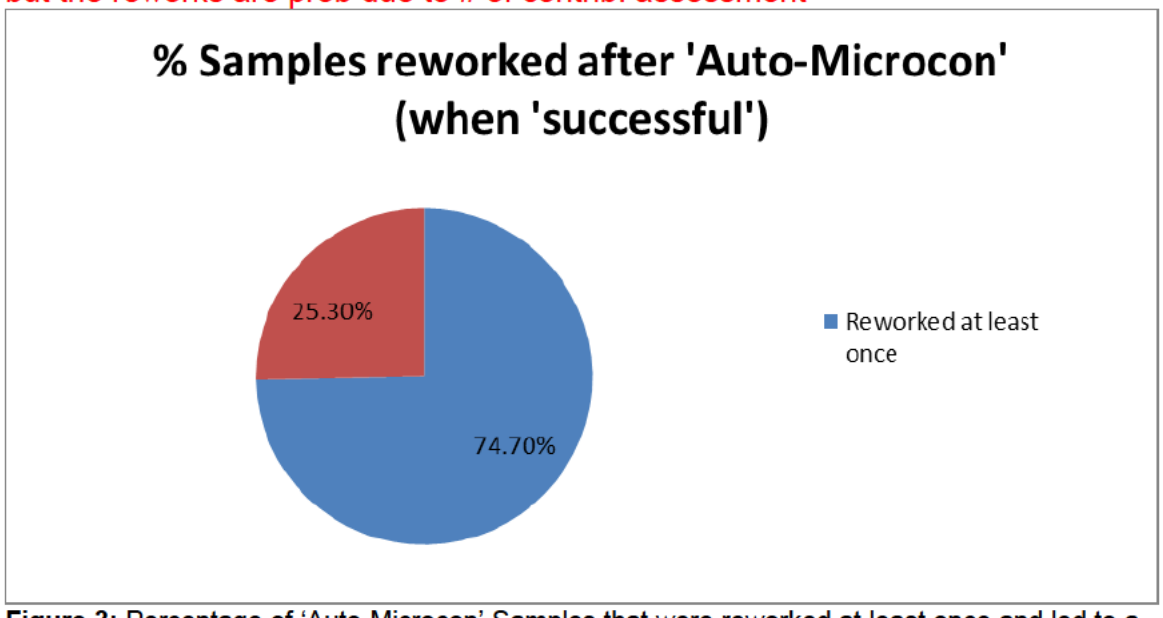

Figure 3: Percentage of 'Auto-Microcon' Samples that were reworked at least once and led to a 'successful' DNA profile outcome.

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. 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.

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.

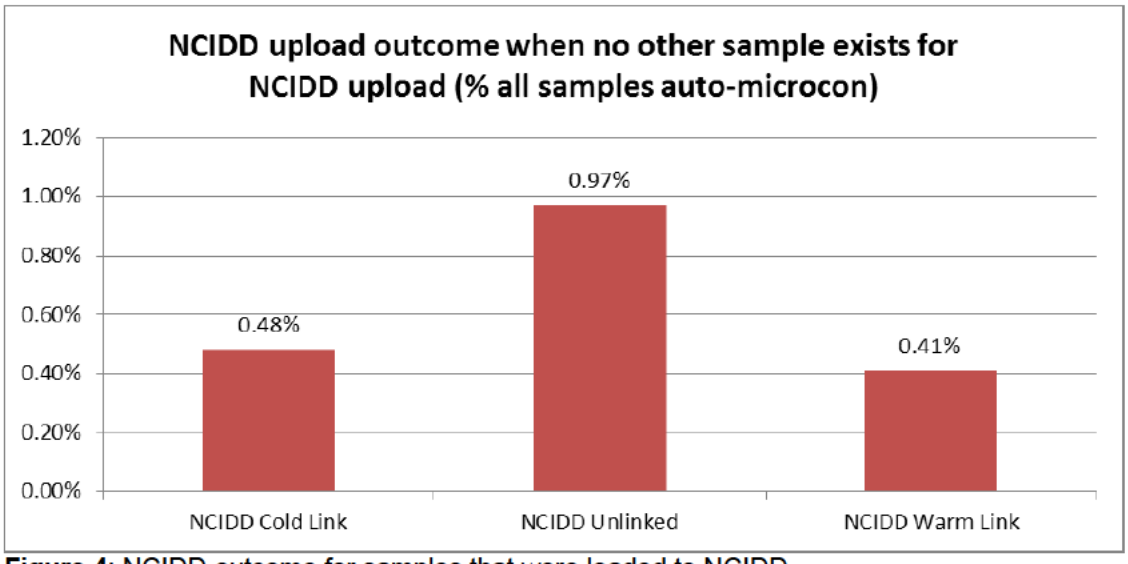

Figure 4: NCIDD outcome for samples that were loaded to NCIDD

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?) 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?

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).

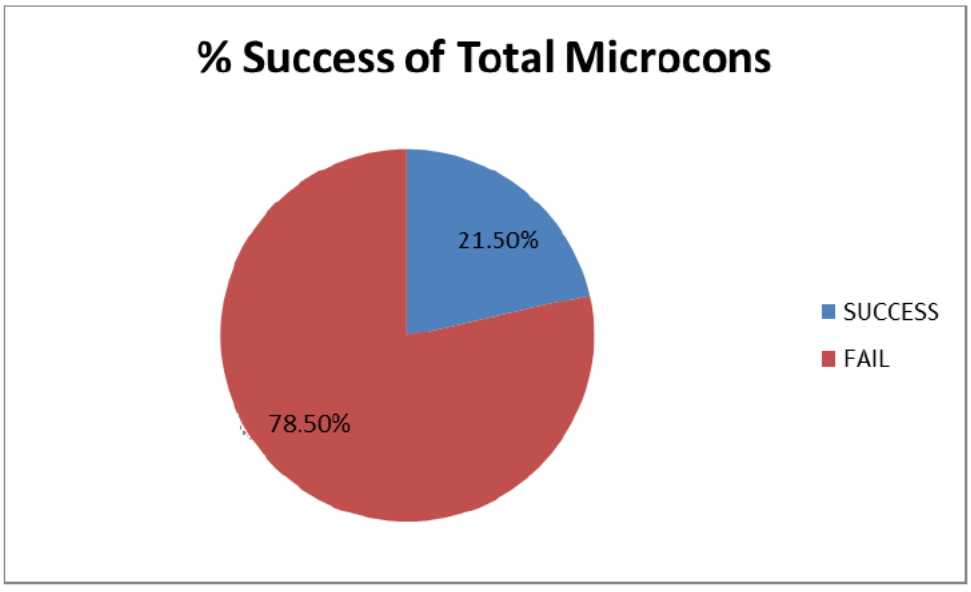

Figure 5: Percentage 'Success'/ 'Fail' of all Microcon® samples ('combined' data).

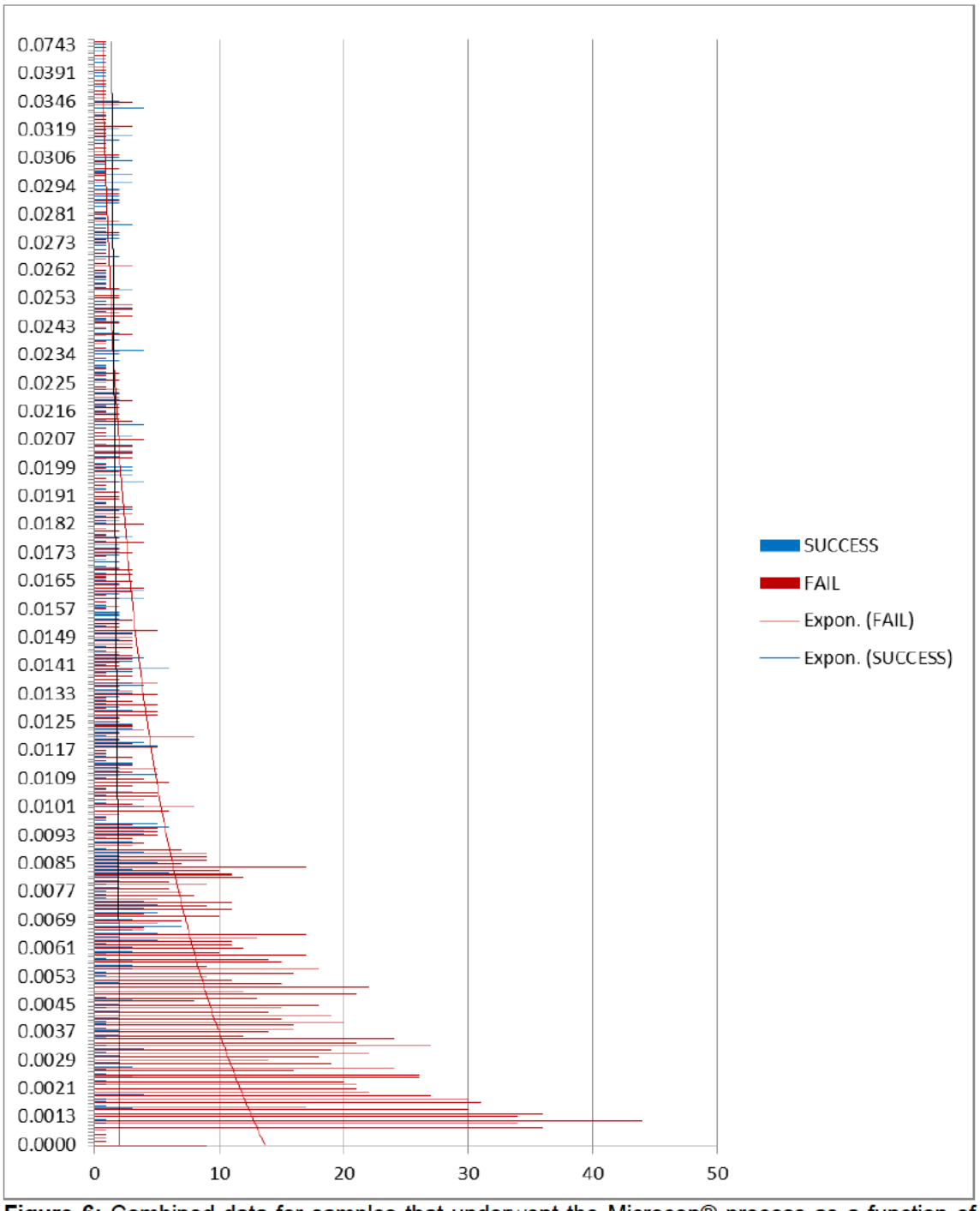

Figure 6: Combined data for samples that underwent the Microcon® process as a function of Quantification value.

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.

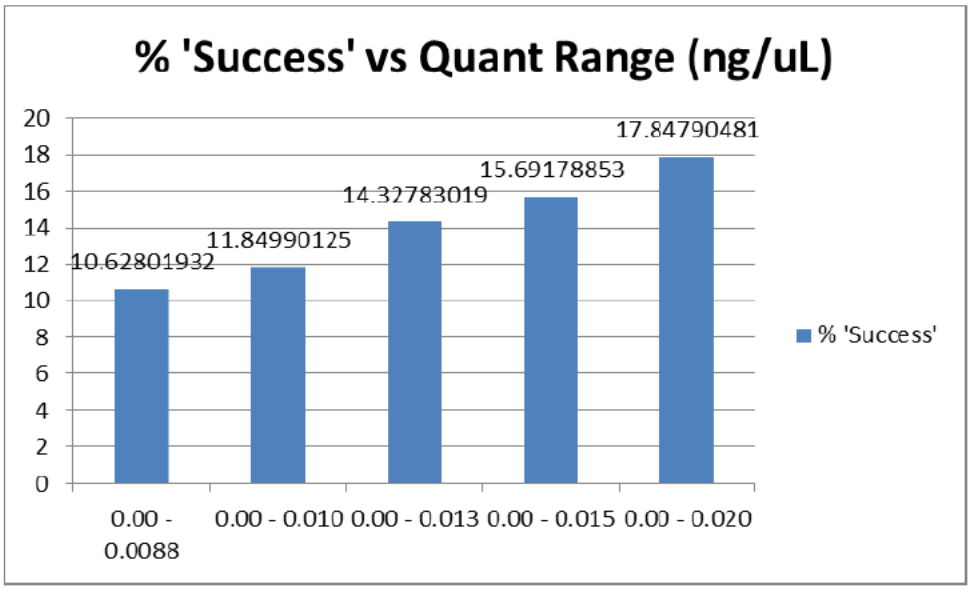

Figure 7: Percentage 'success' for samples that underwent a Microcon® process

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

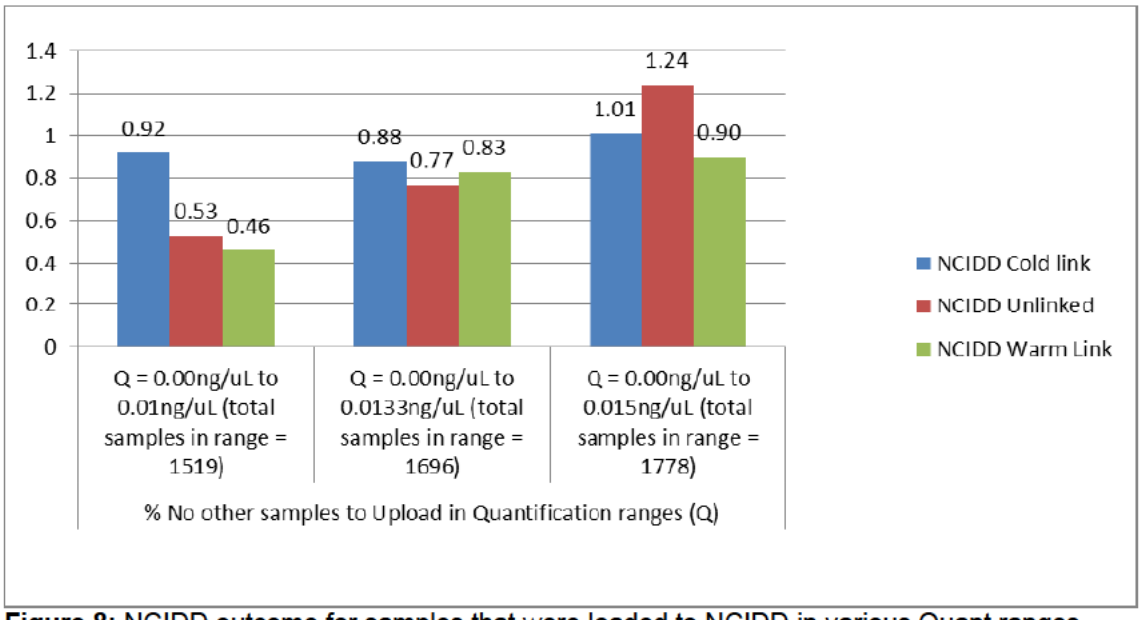

Figure 8: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

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

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.

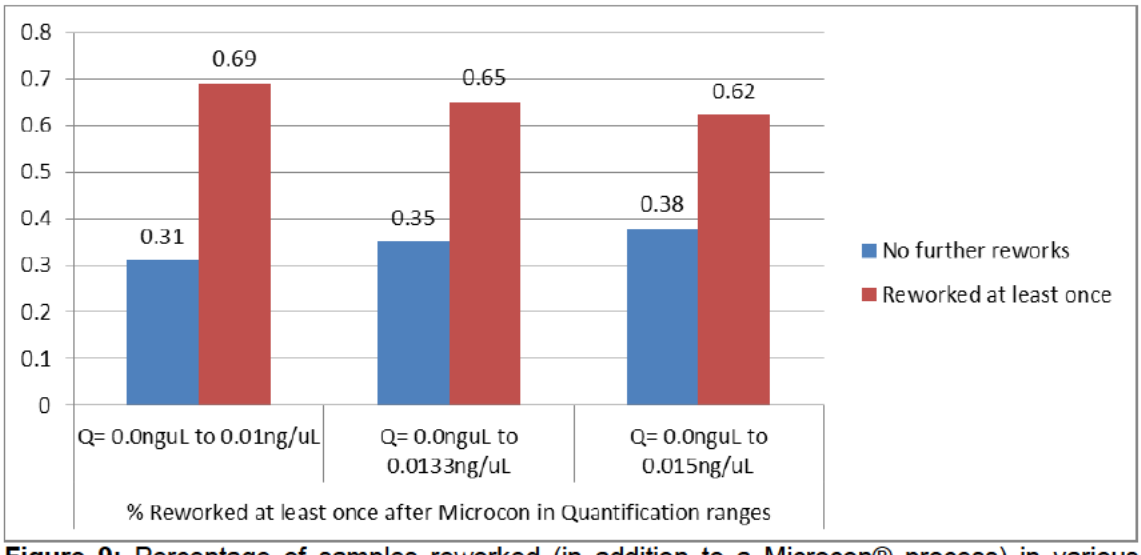

Figure 9: Percentage of samples reworked (in addition to a Microcon® process) in various Quantification ranges.

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'.

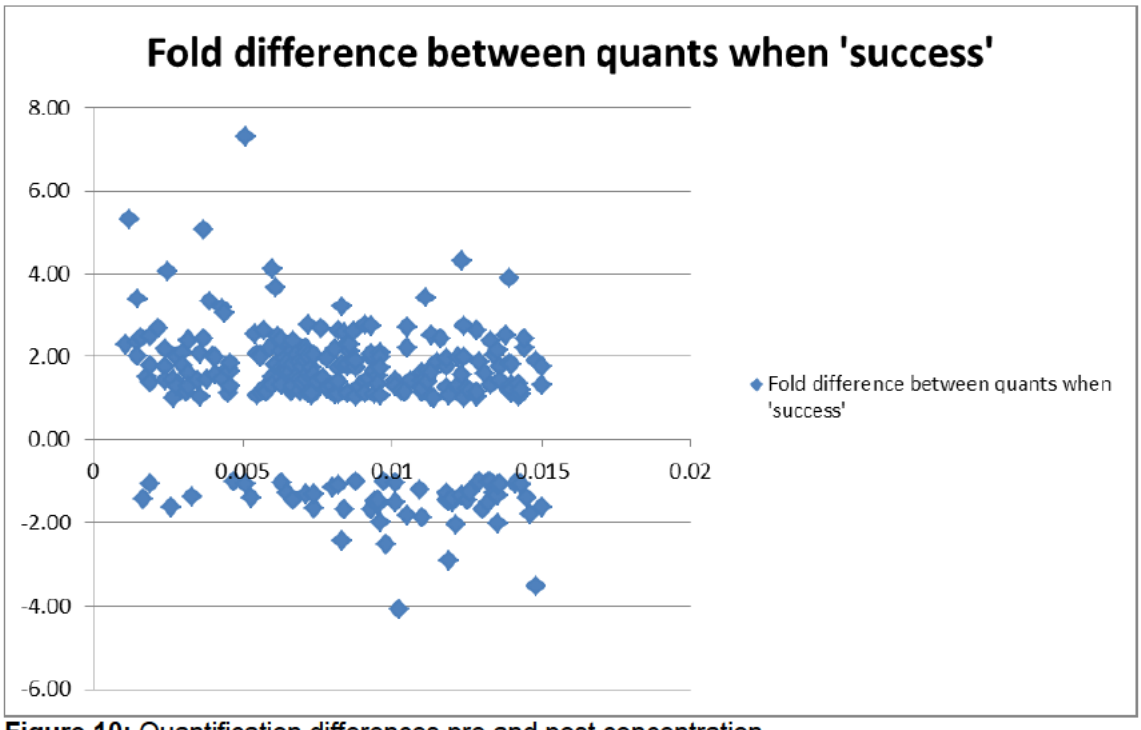

Figure 10: Quantification differences pre and post concentration

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

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.

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.

8. References

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

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

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

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

November 2017

Justin Howes and Cathie Allen

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

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

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Document Details

Contact for enquiries and proposed changes

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Document sign off

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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.

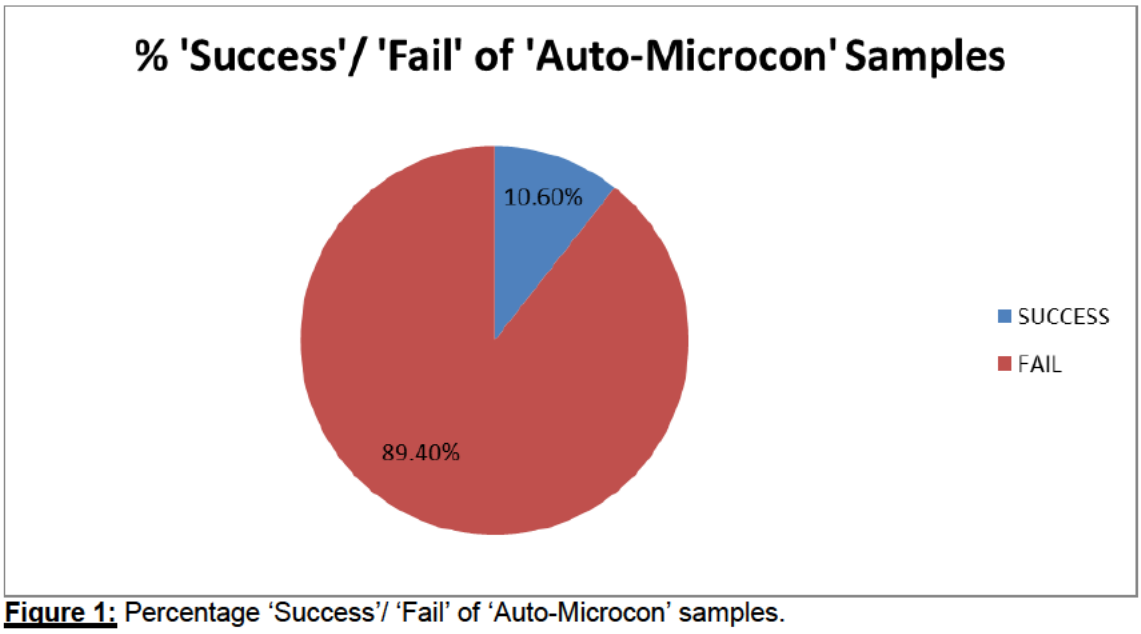

Figure 1: Percentage 'Success'/ 'Fail' of 'Auto-Microcon' samples.

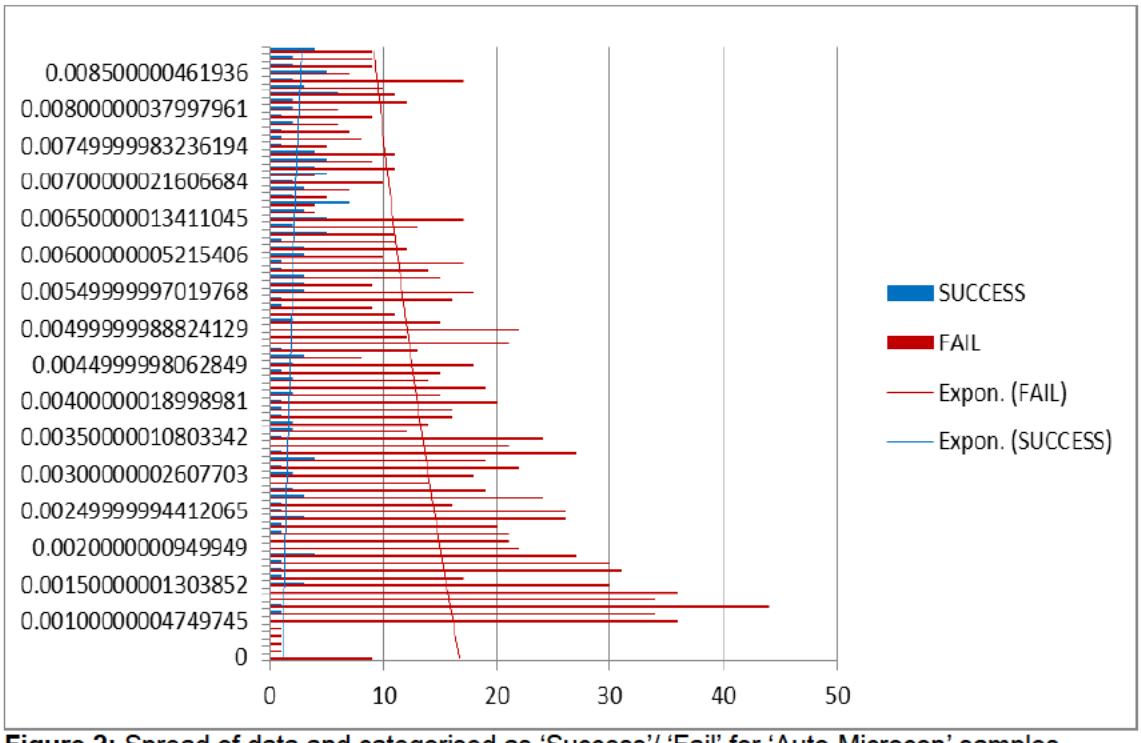

Figure 2: Spread of data and categorised as 'Success'/ 'Fail' for 'Auto-Microcon' samples.

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.

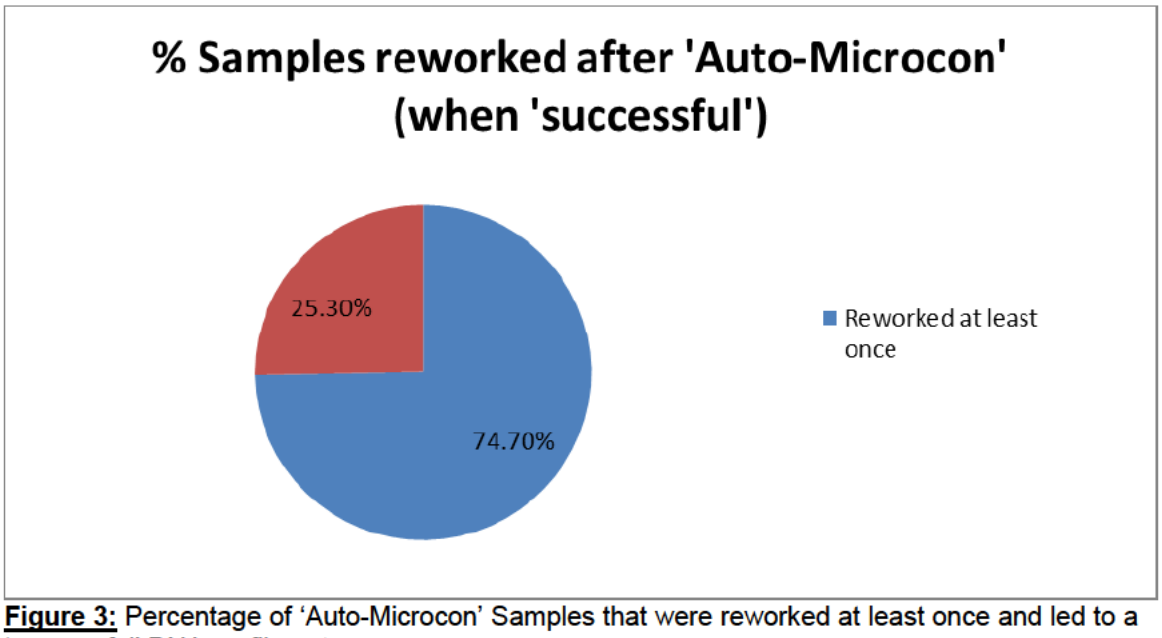

Figure 3: Percentage of 'Auto-Microcon' Samples that were reworked at least once and led to a 'successful' DNA profile outcome.

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.

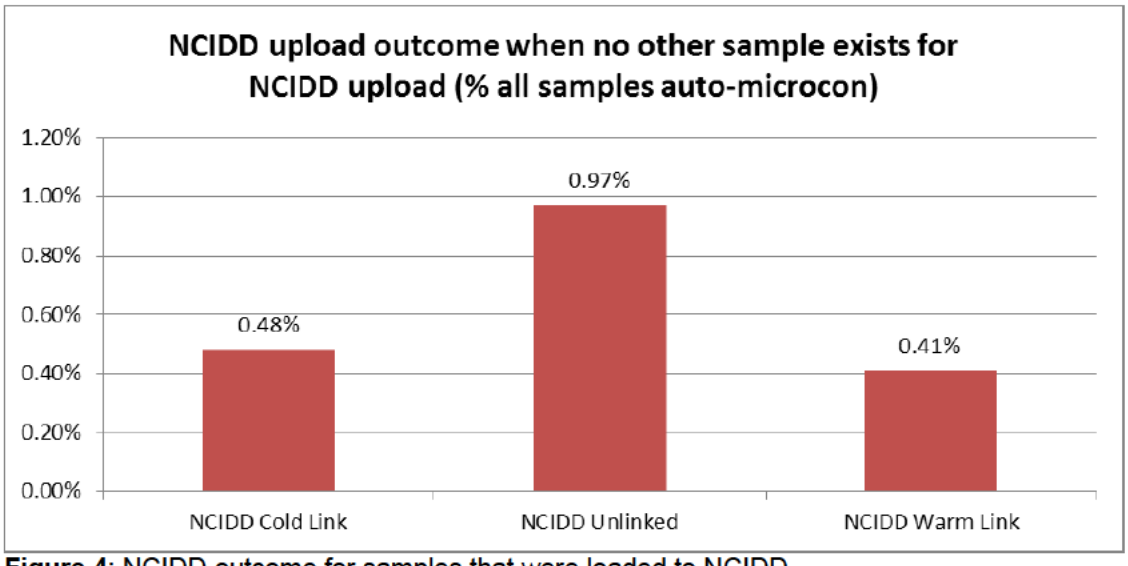

Figure 4: NCIDD outcome for samples that were loaded to NCIDD

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).

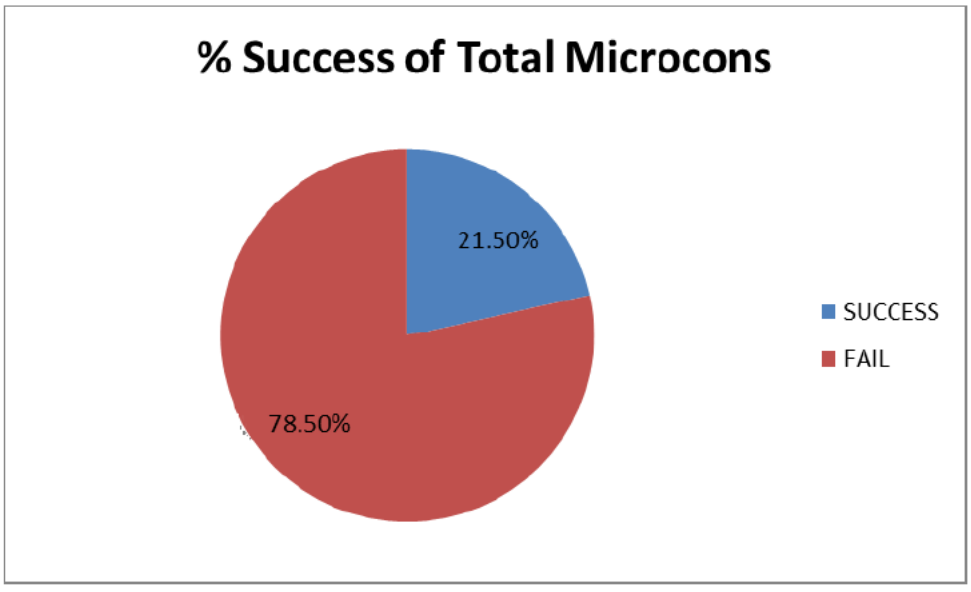

Figure 5: Percentage 'Success'/ 'Fail' of all Microcon® samples ('combined' data).

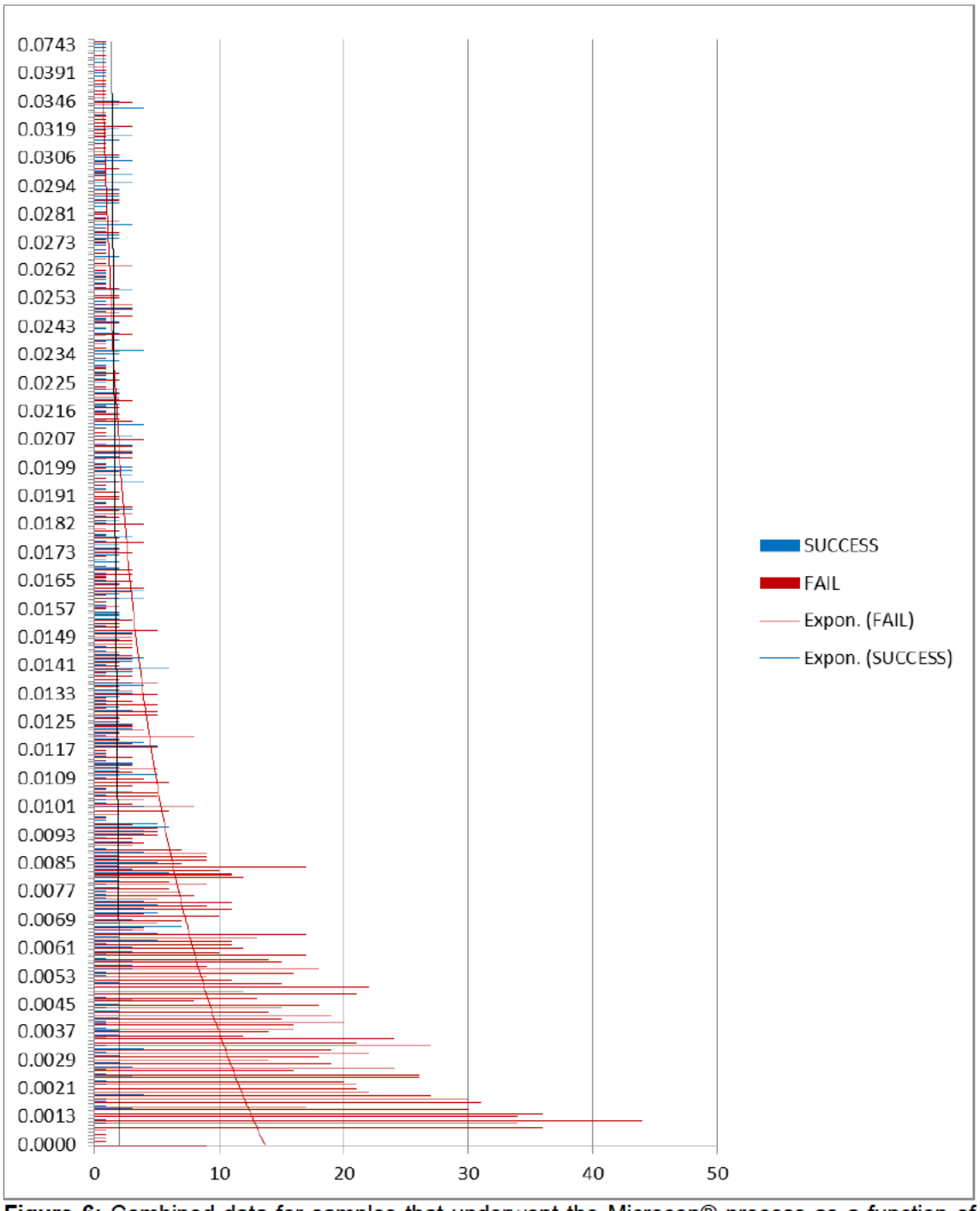

Figure 6: Combined data for samples that underwent the Microcon® process as a function of Quantification value.

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.

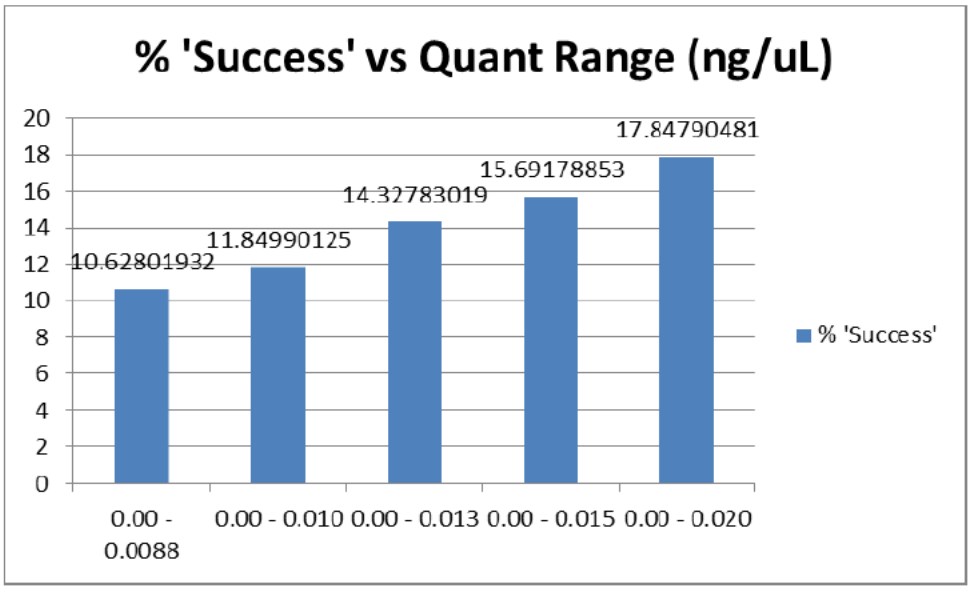

Figure 7: Percentage 'success' for samples that underwent a Microcon® process

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

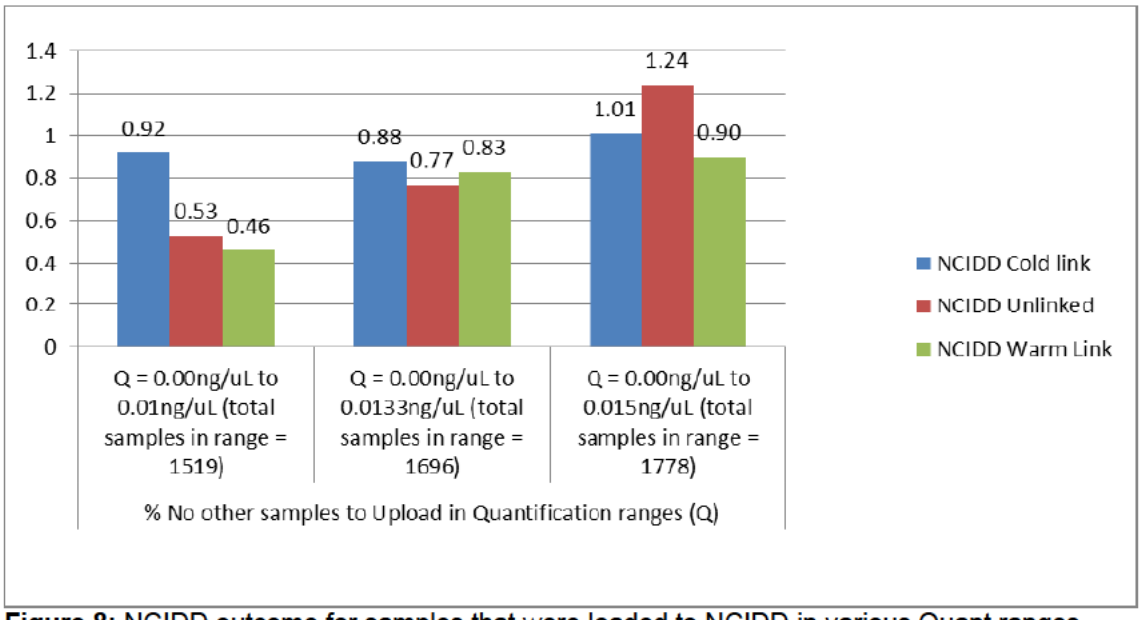

Figure 8: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

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.

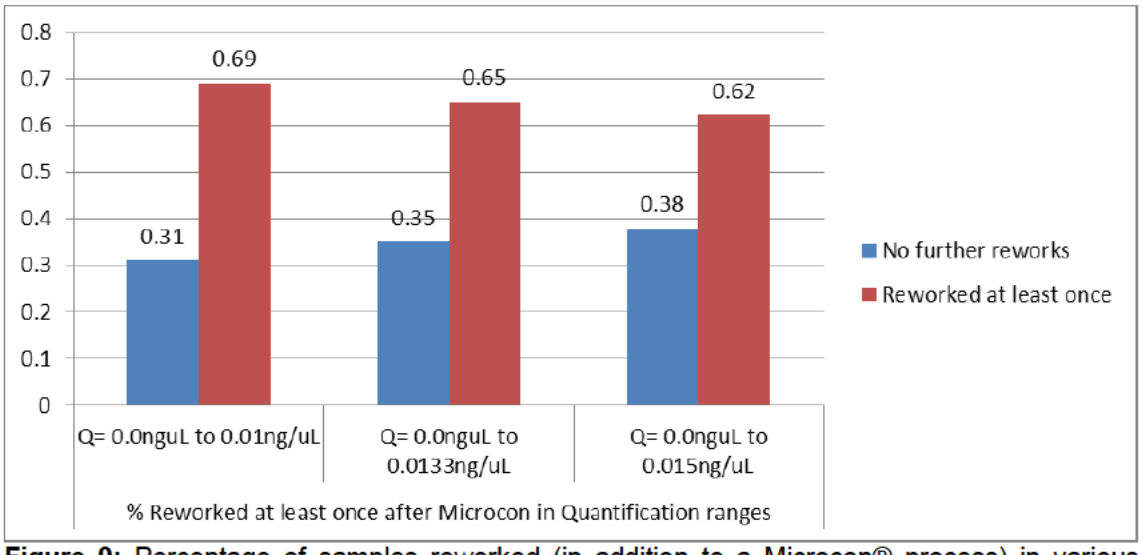

Figure 9: Percentage of samples reworked (in addition to a Microcon® process) in various Quantification ranges.

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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'.

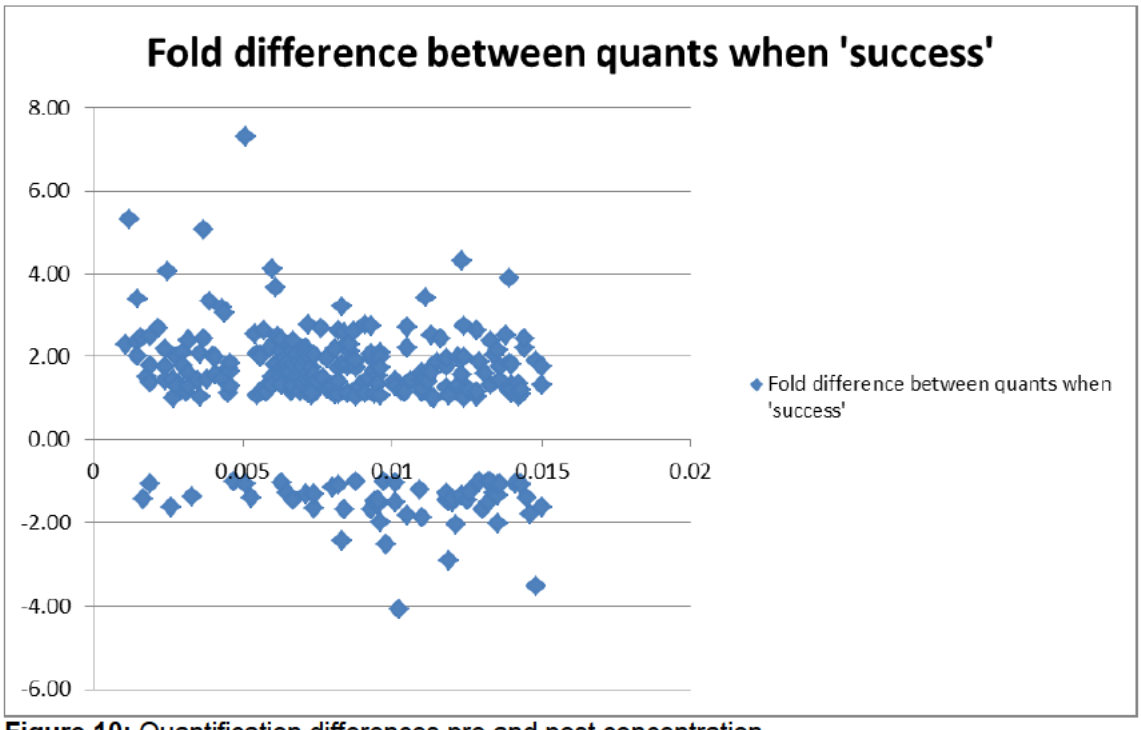

Figure 10: Quantification differences pre and post concentration

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.

8. References

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

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

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

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

January 2018

Justin Howes and Cathie Allen

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

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Document Details

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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.

4. Resources

The following resources were required for this validation/project:

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

5. Methods

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.

6. Experimental Design

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.

7. Results and Discussion

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.

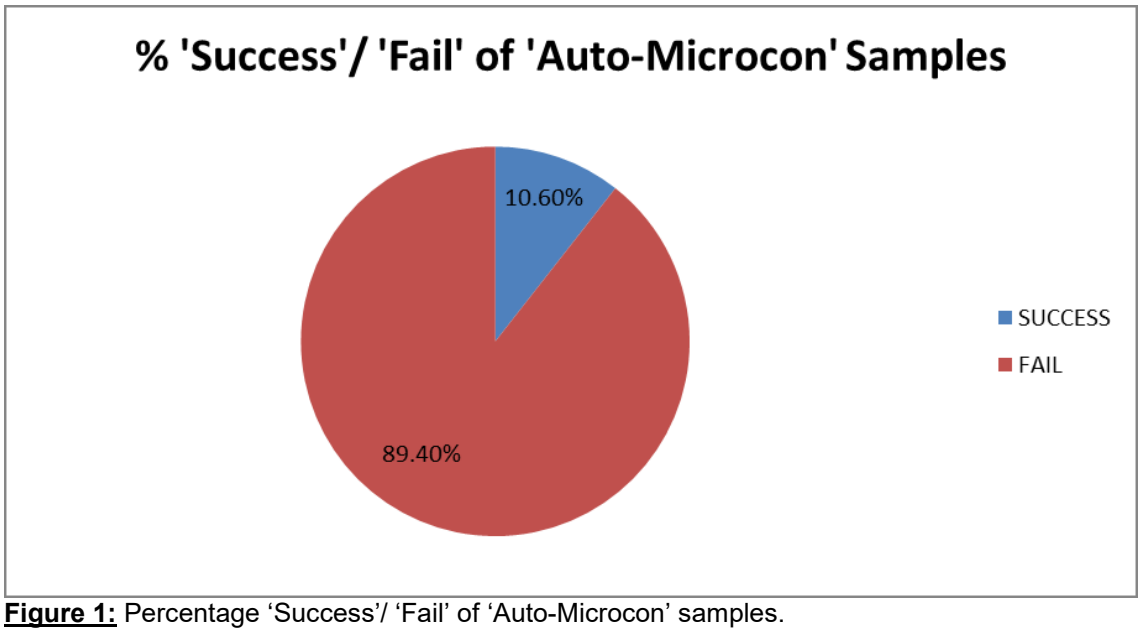


Figure 1: Percentage 'Success'/ 'Fail' of 'Auto-Microcon' samples.

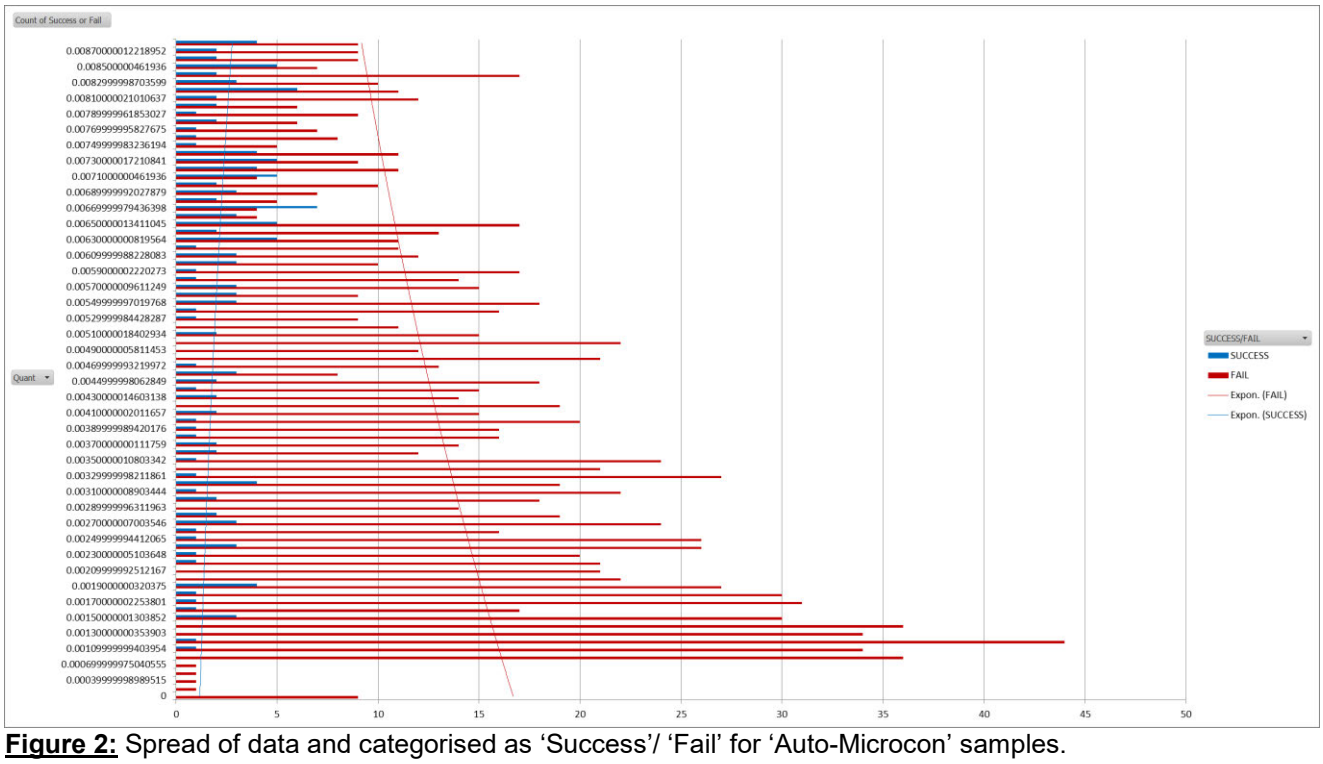


Figure 2: Spread of data and categorised as 'Success'/ 'Fail' for 'Auto-Microcon' samples.

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.

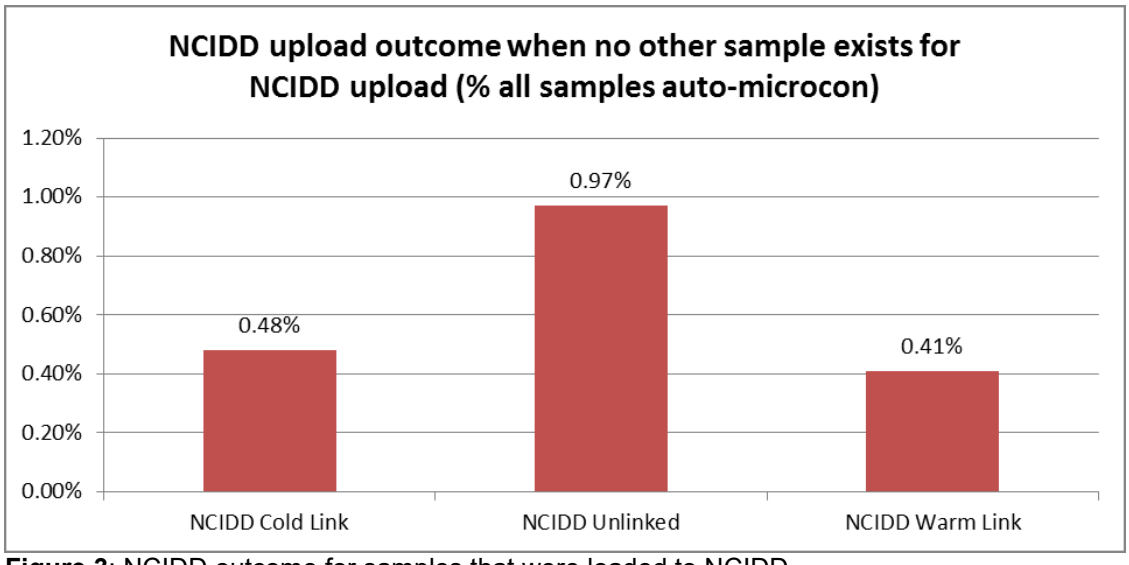


Figure 3: NCIDD outcome for samples that were loaded to NCIDD

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.

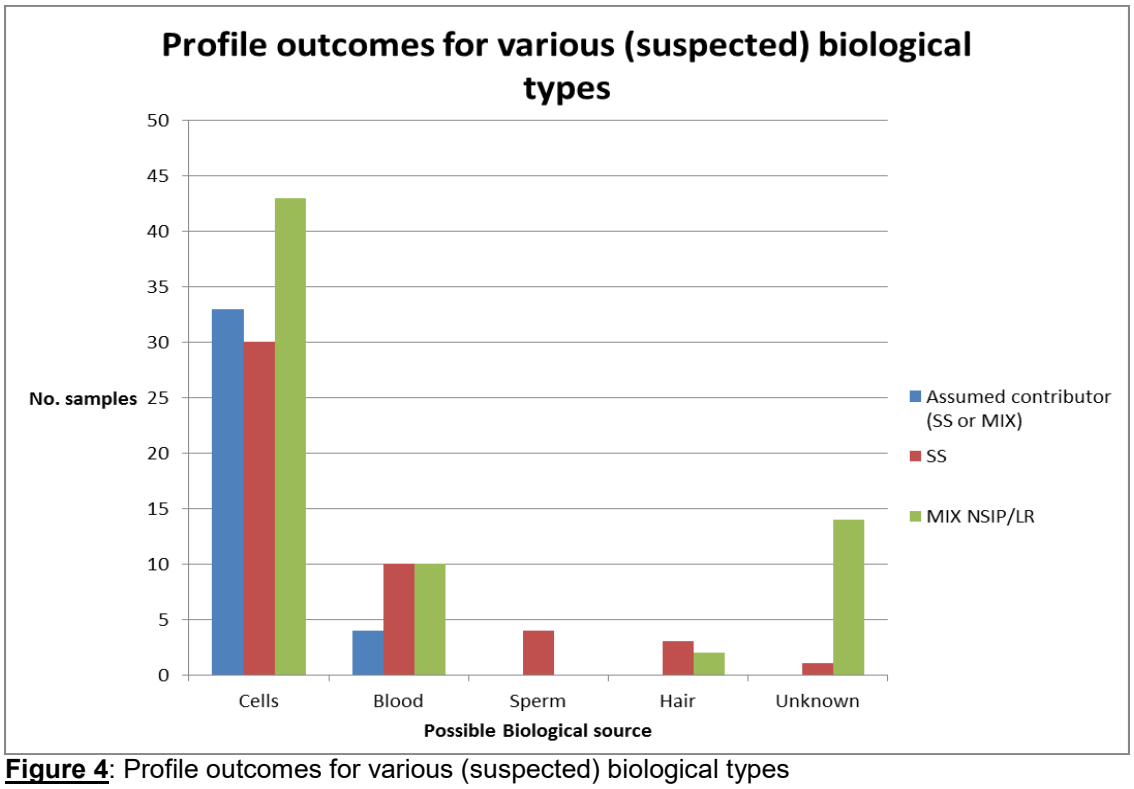


Figure 4: Profile outcomes for various (suspected) biological types

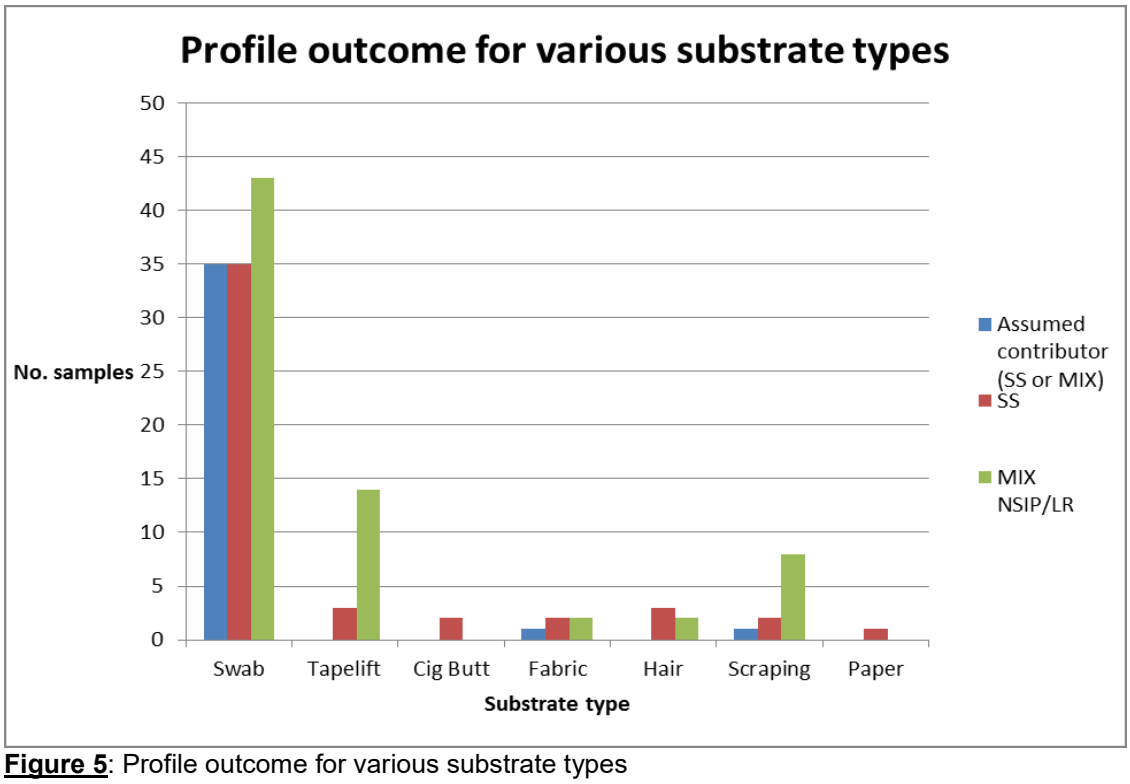


Figure 5: Profile outcome for various substrate types

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).

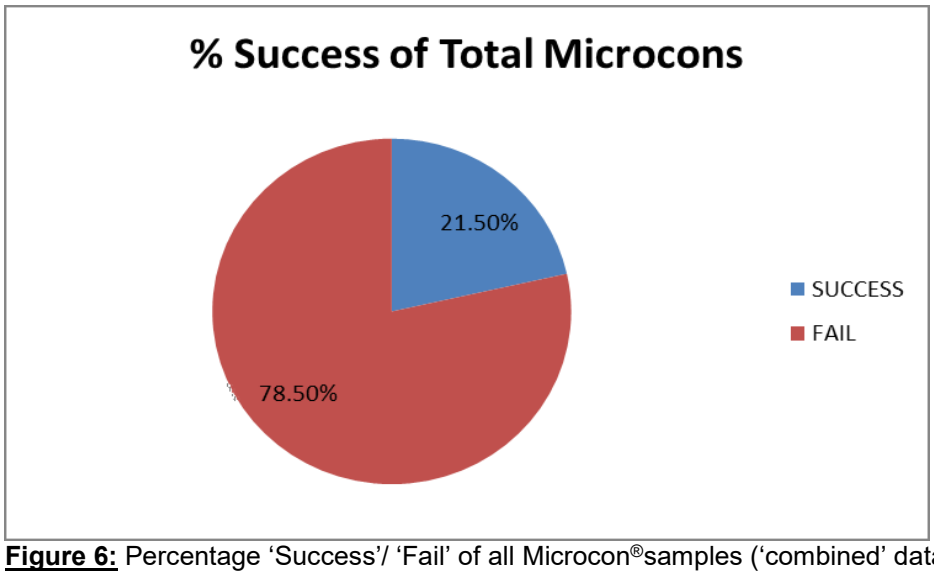


Figure 6: Percentage 'Success'/ 'Fail' of all Microcon®samples ('combined' data).

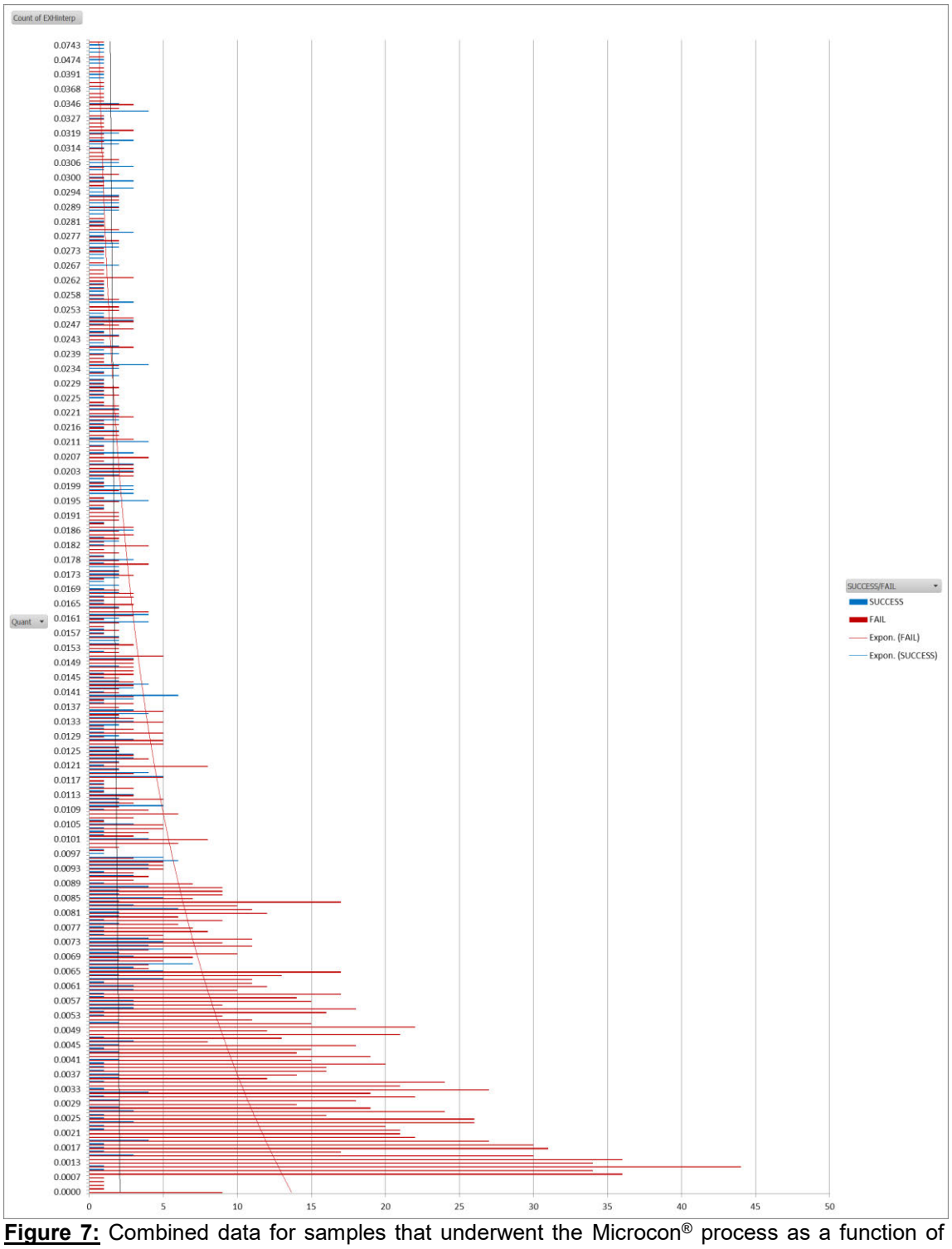


Figure 7: Combined data for samples that underwent the Microcon® process as a function of Quantification value.

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.

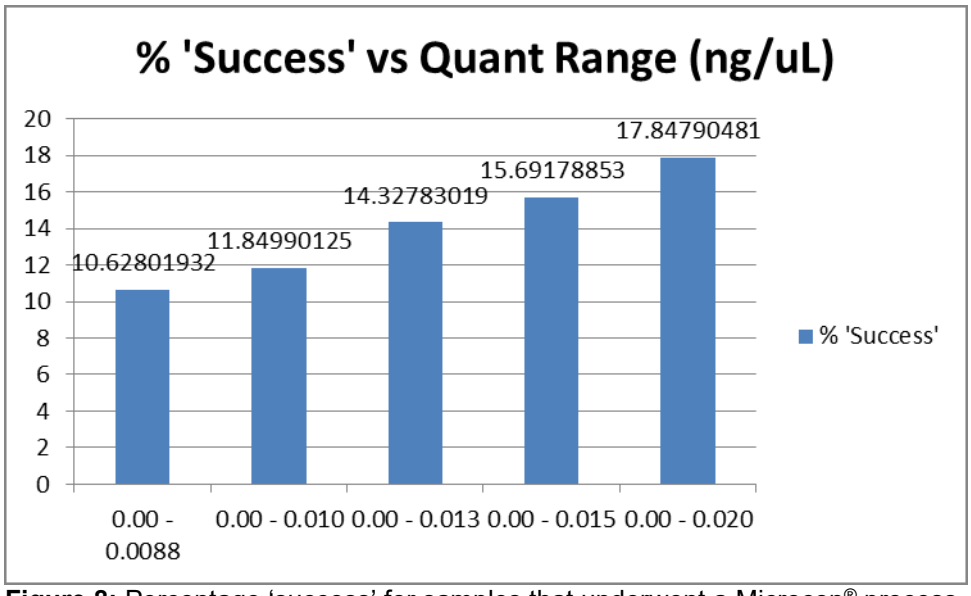


Figure 8: Percentage 'success' for samples that underwent a Microcon® process

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

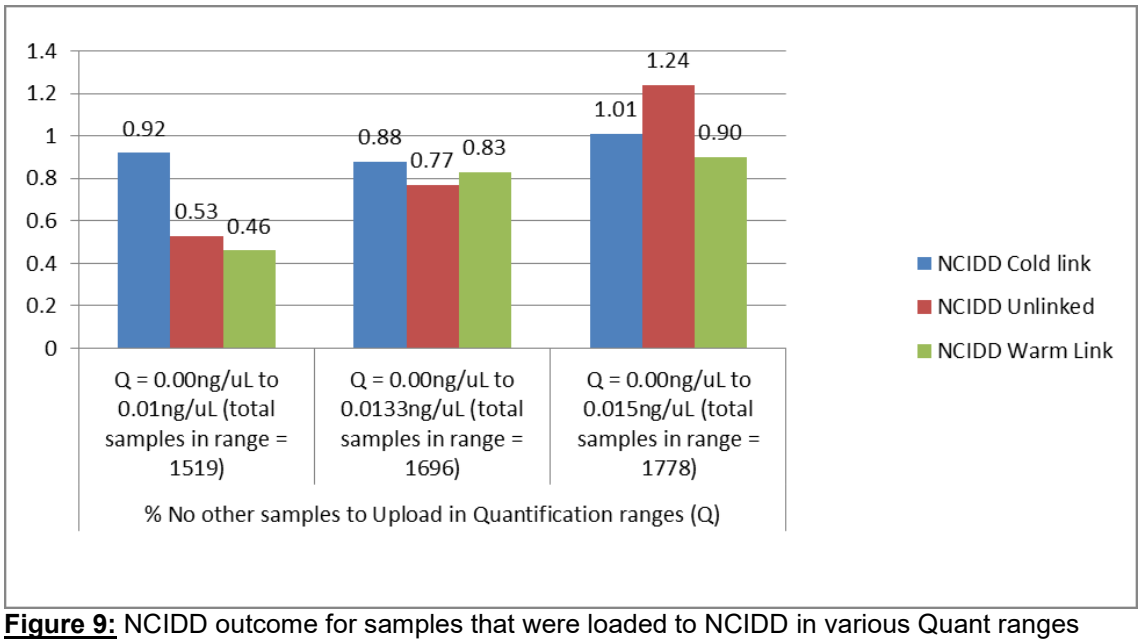


Figure 9: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

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'.

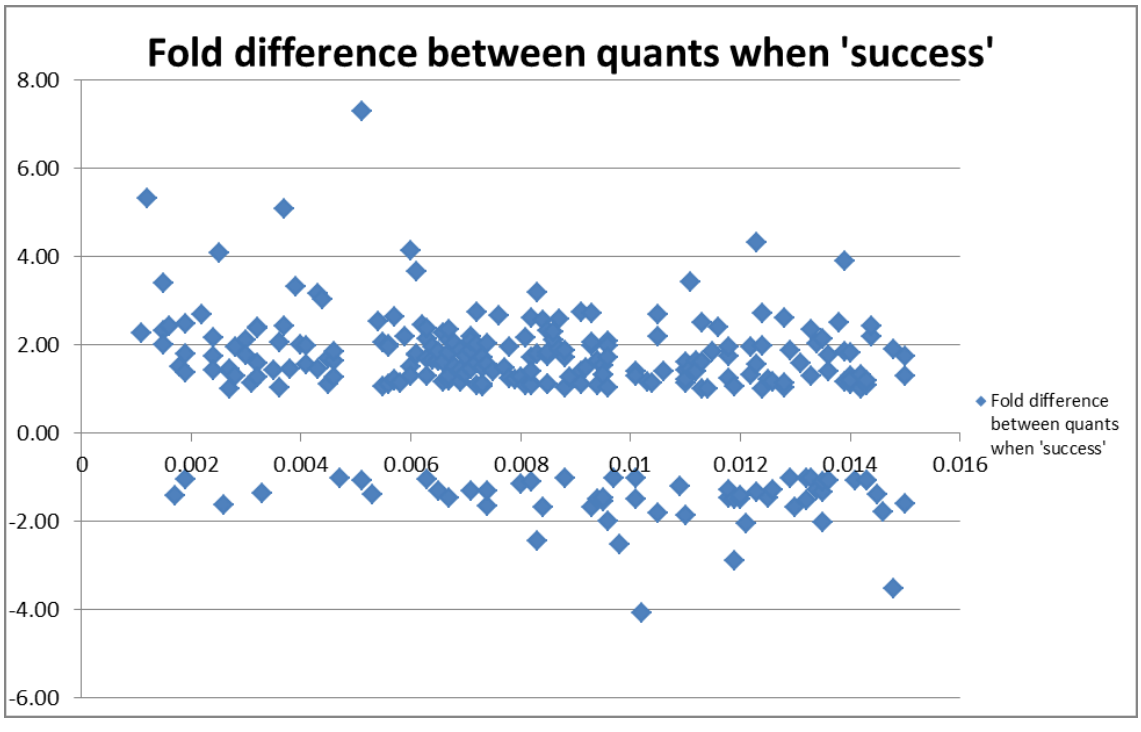


Figure 10: Quantification differences pre and post concentration

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.~~ 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.

9. References

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

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

[3] 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.

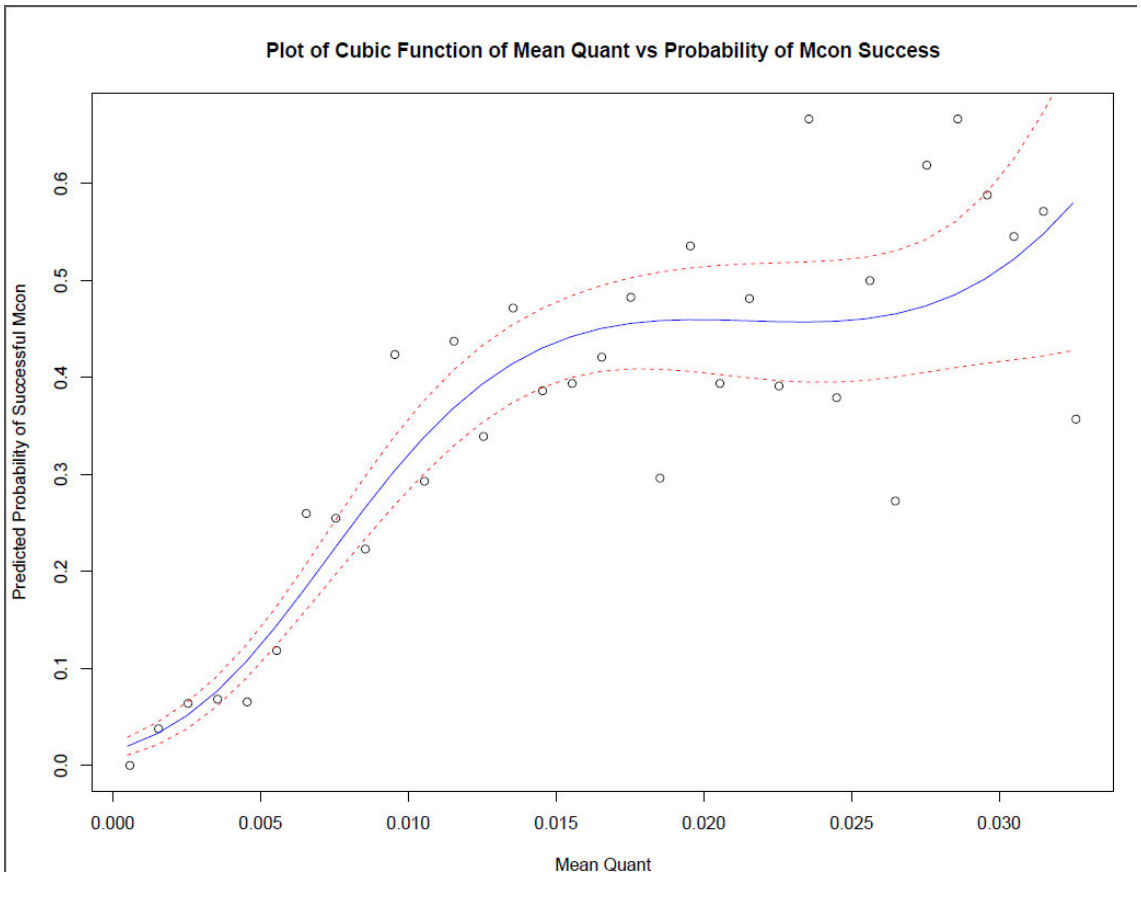
- To note is the use of percentages and non-normalized data to draw conclusions from the data that are not valid.
  - By not normalizing the very low quant (<0.0088ng/uL; n=1449) data which represents the bulk of the samples(n_{total}=1731), percentages derived from data combined with the above very 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

Justin Howes

From: Amanda Reeves
Sent: Tuesday, 9 January 2018 1:11 PM
To: Justin Howes
Cc: Kylie Rika
Subject: 184 final feedback
Attachments: Reporting_final_Report_Evaluation of the efficacy of Microcons_v2seniors.doc

Hi JAH

KDR and I have combined our feedback, given the short timeframe involved. I have also included some extra feedback from Rhys, after our conversation the other day in your office.

Please find attached.

Thanks

AJR and KDR

Amanda Reeves Dip Mgt BSc MSc For Sci
Senior Reporting Scientist – Forensic Reporting and Intelligence Team

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

p | 07 [redacted]
a | 39 Kessels Road, Coopers Plains, QLD 4108
w | www.health.qld.gov.au e [redacted]

2018

WEEK 1 4-361

2018

JANUARY

Friday 5

J A N

5-360 WEEK 1

8:00 am

8:30

Ask feedback on Mic project received (was due 20/12/17)
- mostly readability & definitions.
- discussed what samples were 'success'

2018

WEEK 2 8-357

2018

JANUARY

Tuesday 9

JAN

9-356 WEEK 2

8:00 am

Feedback on #184x12 received
— some points verbal eg.. 13 was decided in PI21 validation

8:30

9:00

From: Chris Gasteen [redacted] >
Sent: Tuesday, 20 September 2022 10:07 AM
To: Jess Wellard
Cc: James Mann; Kylie Schulte; Samantha Gray
Subject: CIDNA Notice 2022/00204 - rESPONSE

Dear Jess

Commission of Inquiry Notice 2022/00204

I am instructed that in relation this Notice:

- *Item 1*- As advised yesterday in relation to his statement, [redacted]. Until he returns to his role, QH will be unable to make sufficient enquiries to ensure a response to this Item is complete.

- *Item 2*- Staff of the Office of the ED FSS have thoroughly searched all physical areas of the office, including physically reviewing all paper records and notebooks in the office, and no such notebook was discovered. For completeness contact has been made with the recently retired Executive Support Officer (who worked in the Office of the ED at the relevant time), and she has no recollection of any such notebook. We understand no archived copies of this notebook exist.

Regards,

Chris Gasteen
Special Counsel
Native Title, Resources and Dispute Resolution Branch
Crown Law
[redacted]
A 50 Ann Street, Brisbane QLD 4000 **W** www.crownlaw.qld.gov.au

****

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Procedure for Change Management in Forensic DNA Analysis

1 Purpose and Scope

This document describes the change management procedure that is to be used within Forensic DNA Analysis, to ensure that all process changes and projects occur in a controlled and timely manner. This procedure applies to all process changes or projects that:

- involve the validation/verification of equipment
- involve the validation/verification of technical procedures
- are projects with external funding
- are internal projects (minor or major) which impact on sample reporting/processing
- involve major LIMS function/configuration changes
- impact on multiple stakeholders
- require staff training to be implemented
- significantly alter workflow procedures

This procedure does not apply to:

- routine document updates/alterations
- minor technical changes which do not impact on sample reporting/processing (e.g. changes in specimen type, storage configuration changes)

2 Definitions and Abbreviations

For a comprehensive list of abbreviations refer to QIS 23849 Common DNA Analysis Terms and Acronyms.

LIMS: Laboratory Information Management System used to record information and track exhibits/case files.
FSS: Forensic Scientific Services
IT: Information Technology
NATA: National Association of Testing Authorities

3 Principle

Changes within Forensic DNA Analysis have the potential to impact on our clients, on stakeholders (internal/external to FSS) and may impact on compliance with NATA. As such changes which occur with Forensic DNA Analysis must be carefully considered and documented. There are a number of types of changes that may occur within Forensic DNA Analysis; for the purpose of documentation - these are classified into five types: administrative change, IT/LIMS change, minor project, major project, and external projects.

Administrative changes: are restricted to changes in processes/workflows that impact on documentation or administration processes only. These changes will most likely occur

within the Administrative team within Forensic DNA Analysis. It does not include any changes of a technical nature.

IT/LIMS change: An IT change would apply to the introduction of new software into Forensic DNA Analysis, in some instances for upgrades in software versions or the introduction of new hardware. This type of change would require collaboration with IT services. A LIMS project would include any alteration that required a change in the LIMS function, or major configuration changes. It would not include minor changes such as storage configurations, or minor changes to specimen types etc.

Minor Project: are general defined as projects that have a duration of <6 weeks and a budget of <$5,000. These projects have a minor impact on sample processing/reporting. Any project which major impact on workflow or sample reporting should be considered under major projects.

Major Project: are generally defined as projects that have a duration of >6 weeks and/or a budget of >$5,000. Major projects require significant planning and detailed consideration of project impacts and implementation procedures.

External Projects: is to be used for all projects which have been externally funded. Where there are no documentation requirements for an externally funded project – standard change management document as described in this document apply. For RDAC projects, RDAC documentation requirements apply with the additional requirements of:

- A change management number will be assigned within Forensic DNA Analysis
- Management Team are to indicate that they have reviewed all RDAC proposals by adding their name to the Excel sheet included within the project folder

The change management procedure utilises a three step process: the initial request (Step 1), minor change (Step 2) and project plan (Step 3). The utilisation of these steps is dependent on the type of change (administrative, IT/LIMS, minor, major and external) and on the progression of the change management process. Refer to Section 4 for details.

4 Actions

Prior to the preparation of any change management documentation it is recommended that ideas are discussed at the work unit level to determine the merit of each idea or proposal. If the process of change management is initiated it will need to follow the documentation requirements as listed in sections 4.1 to 4.9 and the workflow as shown in Appendix 1.

An exception is made for projects that are a mandatory requirement for the laboratory e.g. validation/verification of a new process or equipment item. In these cases it is possible to proceed directly to full project plan (section 4.3).

Technical Review:
For major projects and for validations it is a requirement for the project to have a technical reviewer. The role of the technical reviewer is to 'peer view' critical technical aspects of the project (e.g. new instrument programs/settings, new analytical procedures) and/or to review data analysis with the project (e.g. Excel data transformations, formula's and calculations etc.). The technical reviewer/s are nominated by the team leader and/or management team as project proposal stage (section 4.3). The technical review is completed either during the project or at the completion of the laboratory work and data analysis - but prior to final report being presented to the management team. The technical review should provide to the Management Team as a written document that outlines the aspects of the project reviewed and general findings.

4.1 Initial Request (Step 1)

Change requests can be initiated by any staff member within Forensic DNA Analysis, and are to be recorded on an **Initial Request Form** (QIS 31543). Submission of an initial request requires the following actions:

- Complete the **Initial Request Form** (QIS 31543). The initiator is required to complete the blue sections of the form only.
- Print the form and submit it to the Quality Team.
- Quality will allocate the request a proposal number, and then distribute it to the Line Manager of the person initiating the request. The Line Manager is to complete the red sections of the form.

The Line Manager will assess and sign the initial request recommending either:

- **Abandon process at Initial Request** (Refer to section 4.6)
- **Proceed to Step 2:**
  - **Minor Change** (Refer to section 4.2)
    or
  - **Project Proposal** (Refer to section 4.3)

  If the line manager wants to recommend proceeding to a full project proposal – they will need to seek Management Team approval.

If the initial request is abandon - no further action or documentation will be required.

All hardcopies of documents to be forwarded to Quality

4.2 Minor Change (Step 2)

The minor change form is used to document the purpose, method and date of change. If the Line Manager recommends that the change management is to proceed as a minor change, the project initiator must complete the blue sections of the **Minor Change Form** (QIS 31548) and submit it to their line manager.

The Line Manager must then complete to the following actions:

- **Add the change to the Minor Change Register** located in I:\Change Management
- Print the minor process change form 31548, sign it and submit it to the quality team.
- **Inform all stakeholders of the change** (e.g. SOPs, team meetings, emails).

All hardcopies of documents to be forwarded to Quality

4.3 Project Plan (Step 3)

If the Management Team recommends that a change management should proceed as a full proposal (administrative, IT/LIMS, major change or external project) the project leader is required to complete the following project documents:

1. **Project Plan Form** (QIS 22872): The level of detail entered into the project plan will depend on the size/importance of the project. This document includes the Risk Assessment for the project.

2. **Milestones register:** Ensure that the milestones register is filled out. This will include the Outputs/Project Milestones and relevant dates (expected due date and completed date) as entered into page 2 of the Project Plan Form (QIS 22872). The register is located in I:/Change Management/Change Management Milestones Register.xls.

3. **Project Budget** (QIS 31052): A budget must be prepared and submitted to the Forensic DNA Analysis Management Team - with each project plan. A budget template is provided in QIS 31052. Additional resources for budgeting are located in G:\ForBiol\AAA Administration\Managing Scientist\Forensic DNA Analysis\Costing data\2013 HSSA Finance costings\1st cut

4. **Change Management Project Proposal Document**: In addition to the project plan form (QIS 22872), a project proposal will be required. The project proposal document should include an introduction to the project (including literature review), and detailed materials and methods sections - refer to QIS 23402 for writing guidelines and template for the project proposal (Template http://qheps.health.qld.gov.au/hsq-staff/comms/corporate-id/home.htm). These project proposals will essentially constitute the introduction and materials and methods section of the projects final project report.

   This project proposal must be prepared and submitted to the Forensic DNA Analysis Management Team with a Project Plan Form (QIS 22872) and a Project Budget (QIS 31052) for each change management proposal. This document should cover what all aspects of what the project is proposing to do: purpose/background, methodology and experimental design (either laboratory experiments or data analysis as applicable).

5. **(Optional) Project Gantt Chart**: Preparation of a Gantt Chart is optional - it may be particularly useful for large projects. Refer to the Quality Team if Gantt Chart preparation is required.

After all four (or five) project documents have been prepared (as listed above); risk assessments (if applicable) and LIMS documentation completed (if applicable):

- Submit all documents to your Line Manager and to the Quality Team ([redacted] by email. The Line Manager will submit the documentation to the Forensic DNA Analysis Management Team for consideration (Refer the section 4.4).

  The Line Manager should email the electronic copy of the documents to the Management Team a few days before the next scheduled Management Team meeting - to ensure there is time for pre-reading. A hardcopy of documentation is to be printed/supplied to the meeting – for signatures.

4.4 Forensic DNA Analysis Management Team – Consideration of Project Proposal

The Forensic DNA Analysis Management team will consider the change management project proposal documents as outlined in section 4.3. It is not necessary for all Management Team members to read and approve every proposal; however a quorum of the Management team must approve the proposal. The quorum must include the Managing Scientist, Team Leaders, Quality and Projects Senior Scientist, Senior Scientist that has Line Management of the staff/project and Senior Scientist/s of areas significantly affected

by the project. For major projects and validations a technical reviewer submission should also be provided to the management team for consideration (Refer to section 4).

Consideration of the proposal should include:

1. *A determination the impact of the proposed change on all stakeholders*
2. *Cost/Benefit Analysis of the project*
3. *Risk Assessment (Workplace Health & Safety and Business Risks)*
4. *A communication plan for all project participants and stakeholders*

The Forensic DNA Analysis Management Team will then make a recommendation as follows:

- **Implement proposal.** If the proposal is approved, the project plan documentation will be signed by the Management Team, and the project plan documents returned to the quality team and the project leader/appointed staff can initiate the project.
- **Implement proposal after change.** If the Management Team requires additions/edits to the project plan, the Management team will return the proposal to the project leader/appointed staff with feedback. The project documents will need to be edited and resubmitted (as per section 4.3.) before further consideration by the Management Team.
- **Abandon process.** Refer to Section 4.6 for details.

4.5 Implementation and Final Report (Step 3)

On completion of the change management project - a final report is required, this is usually written by the project leader (Refer to QIS 23402 for report preparation details). An Implementation Plan (Refer to Appendix 2) must also be prepared, and this will be a list of the steps required to be completed either before the change is implemented, or shortly after implementation. Although a proposal may not be implemented on completion, a basic implementation plan that can be refined closer to implementation should still be completed and submitted. On completion of the report and implementation plan, they are to be forwarded by email to your Line Manager. The Line Manager is then to have the technical review completed. On completion of the technical review the Line Manager will submit the final report, technical review and implementation plan to the Forensic DNA Analysis Management Team for consideration/acceptance.

The Line Manager should email the electronic copy of the documents to the Management Team a few days before the next scheduled Management Team meeting to ensure there is time for pre-reading. A hardcopy of documentation is to be printed/supplied to the meeting – for signatures.

If the final report is accepted by the Forensic DNA Analysis Management Team it will be signed and the project/change management process closed (hardcopy to be sent to the Quality Team. If the Management Team requires additions/edits to the final report, it will be returned to the project leader/appointed staff with feedback. The final report will need to be edited and resubmitted for consideration by the Management Team.

After acceptance of the final report the Forensic DNA Analysis Management team will recommend that the:

- **Change is implemented** into routine use (Refer to Appendix 2 for implementation plan for project leaders).

- **Change is accepted but will be implemented at a later date** (Refer to Appendix 2 for implementation plan for project leaders).
- **Change is abandon** (Refer to Section 4.6 for details).

After completion of the project, all stakeholders must receive communications about the findings and outcomes of the project. This may include presentations at meetings, or the provision of final reports to stakeholders. For significant projects, a summary of the project is to be presented at team meetings.

All paperwork is to be submitted to quality on completion of the project for scanning and storing. Quality will also lock data files with a password on submission of final project report.

4.6 Responsibilities in Signing Documentation

When a project plan or report is submitted for review, it is the responsibility of the reviewer to ensure that all feedback is provided by the due date. Any feedback provided after the due date may not be considered (based on the merit of the feedback).

It is acceptable for a reviewer from the Forensic DNA Analysis Management Team to seek advice from other members of staff where it is deemed appropriate (e.g. where another person may have more experience in the subject of the report). In this instance, it is the responsibility of the person seeking the advice to provide the feedback to the project officer and to do so by the due date.

4.7 Abandon/Cancellation

Should a change proposal not be approved, or if at any time the change is no longer required, the change management process may be abandon/cancelled. This shall be recorded on the change management hard copy documents (to be forwarded to the Quality Team).

It is possible to re-start abandon change management processes at a later date, and there are relevant sections in the change management forms to record a restarted process.

4.8 Recording Project Progress

Change Management project progress (i.e. milestones and outputs) is to be recorded in I:\Change Management\Change Management Milestone Register.xls

4.9 Recording Feedback

Project feedback, including feedback on project plans and reports, is to be tabulated and stored in the relevant change management folder.

All email communications regarding the project are also to be stored in the relevant change management folder.

5 Records

- All change management documentation (plans, reports, data etc.) are to be stored electronically in a network drive (e.g. I:Drive), and hardcopies filed in Quality Drawers.
- Quality team will "lock" data files with a password on completion of the project
- Validation reports are to be stored electronically in a network drive (e.g. I:Drive), and hardcopies filed in Quality Drawers on completion.

6 Associated Documentation

QIS: 22872	Project Plan Form for Change Management in Forensic DNA Analysis
QIS: 23401	Forensic DNA Analysis Validation Guidelines
QIS: 23402	Writing Guidelines for Validation and Change Management Reports
QIS: 27592	CISSU Non-Standard Change Form
QIS: 27593	CISSU Request for Standard Change Form
QIS: 27594	CISSU Complex Change request
QIS: 29100	Health & Safety Risk Assessment Form
QIS: 29106	FSS OHS Risk Assessment Procedure
QIS: 31052	Forensic DNA Analysis Unit Change Management Budget
QIS: 31543	Initial Request Form for Change Management in Forensic DNA Analysis
QIS: 31548	Minor Process Change Form for Change Management in Forensic DNA Analysis
QIS: 33017	FSS Research and Development short form
QIS: 33333	Participant Information and Consent Form (PICF) - Common Biological Samples
QIS: 33334	Participant Information and Consent Form (PICF) - Semen Samples
QIS: 33335	Participant Information and Consent Form (PICF) - Vaginal Samples

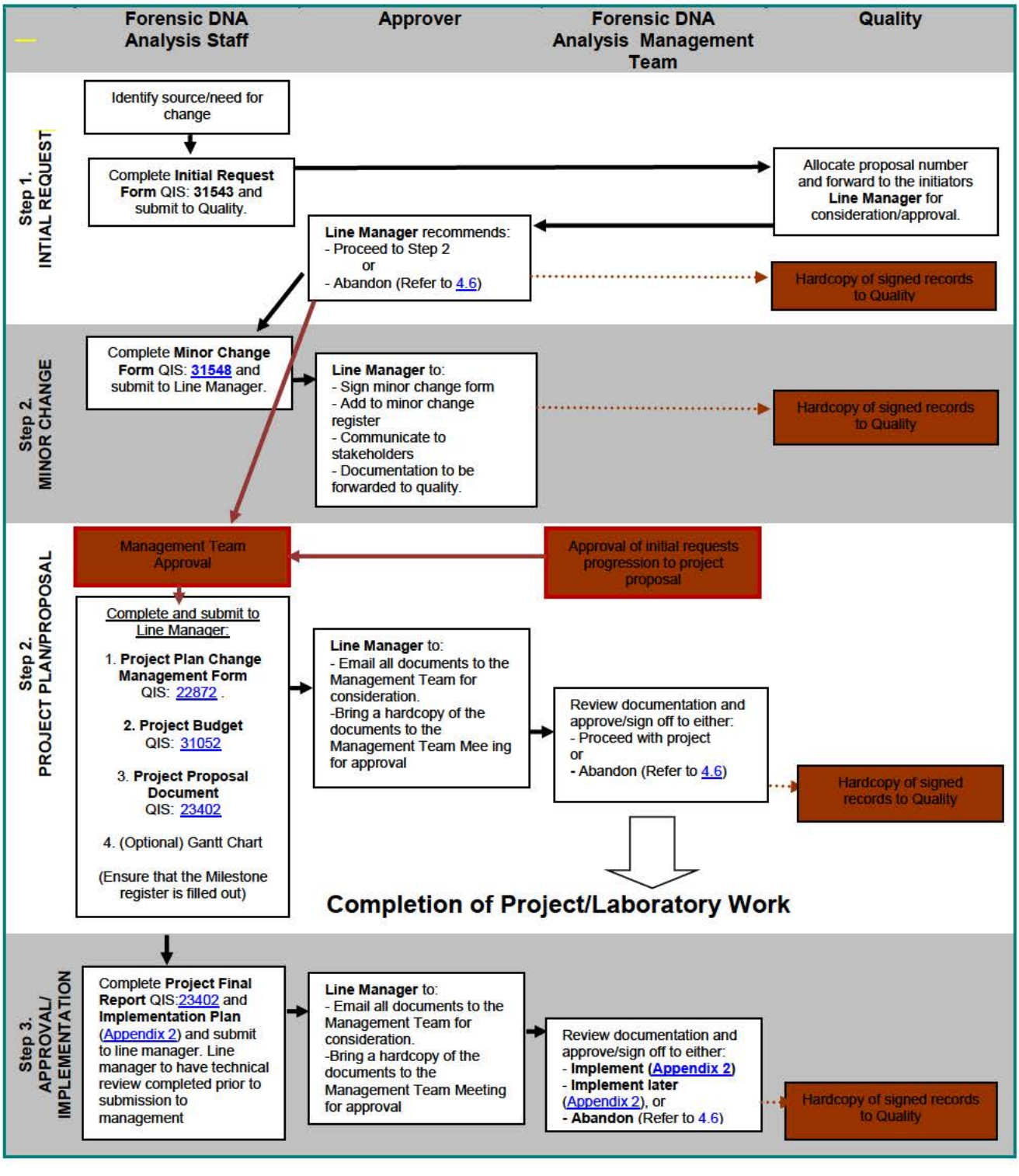
7 Amendment History

Version	Date	Author/s	Amendments
1	25 Aug 2005	Mary Gardam	First Issue
2	27 Feb 2007	Jane Olsson Mary Gardam Vanessa Ientile	Format Changed to include Project Management.
2	April 2008	QIS2 Migration Project	Headers and Footers changed to new CaSS format. Amended Business references from QHSS to FSS, QHPSS to CaSS and QHPS to Pathology Queensland
3	25 Sept 2008	Robyn Smith Crystal Revera	Formatting, Changes made to reflect new Laboratory name, Contact email addresses updated, SOP brought in line with changes made to template.
4	14 May 2012	Shannon Thompson Kirsten Scott	Major revision/re-write as the change management process changed.
5	21 Jan 2013	Kirsten Scott	Update QIS numbers for CM forms, update headers. Add records, additional associated documents and minor edits.
6	26 Mar 2013	Kirsten Scott	Clarify point 3 in section 4.4. Update hyperlinks
7	6 June 2014	Kirsten Scott	Remove Assessment Phase. Change in actions required by line managers for approving initial plan and minor change documents. Change content of appendix 2.
8	19 June 2015	Kerry-Anne Lancaster	Update to new template. Added reference to a milestone register and implementation plan. Changed content of appendix 2. Changed references to AUSLAB to LIMS. Defined project proposal document. Defined responsibilities of the reviewer. Added link to QIS 33017
9	21 Oct 2015	Kirsten Scott	Inclusion of consent forms in associated documents. Option for mandatory projects to proceed directly to project plan. Inclusion of RDAC processes into Change Management. Addition of Quality Checklist for project documentation
10	25 Nov 2015	Kirsten Scott	Inclusion of a technical review for major projects and validations – section 4, and minor text update in other section as a result of technical review
11	20 Sept 2016	Kirsten Scott	Specify implementation plan as mandatory, and add additional implementation examples. Section 4.5 and 5 add a note on locking of data files by quality. Section 3 clarify RDAC documentation requirements

8 Appendices

- APPENDIX 1: Change Management Process
- APPENDIX 2: Implementation Plan for project leaders
- APPENDIX 3: Checklist of documents required for a Change Management Project

8.1 APPENDIX 1: Change Management Process



8.2 APPENDIX 2: Implementation Plan for project leaders

Successful project implementation may require numerous tasks to be completed either prior to implementation, or shortly after the implementation date. Some of the considerations/tasks that may be required are listed below; however this is not intended to be a comprehensive list of tasks as each project will have different implementation requirements. Project leaders should devise and submit a comprehensive implementation plan for management review. Once complete, the checklist should be submitted to the quality team for filing with the signed project documents.

Task	Details	Date Completed
Create new procedures	New SOP 'Operation and Maintenance of the AB Quant Studio RT-PCR Instrument' QIS# 35028 created and submitted for review.	
Update procedures / training modules	Update of SOP 'Preparation & Testing of Quantification Standards, In-house controls, Quantification Kits and Amplification Kits' QIS# 34514. Update of SOP 'Quantification of Extracted DNA using the Quantifiler® Trio DNA Quantification Kit' QIS# 34045. Update of SOP 'DNA Extraction and Quantification of Samples Using the QIAsymphony® SP and AS Modules' QIS# 34132. <u>Training Module</u> Update of Training Module 'Quantification of Extracted DNA using the Quantifiler® Trio DNA Quantification Kit' QIS 33406.	
Staff training	Project members and relevant staff to be issued with CTT statements as required. CTT staff to train other staff/operators who will be issued with RCC statements.	
Equipment tasks	Add QS5 equipment to FR	
Add to minor change register	To be added once implemented	
Communication	Senior Scientist to send email to all staff advising of implementation date.	

8.3 APPENDIX 3: Checklist of documents required for a Change Management Project

Minor Change:

☐ Initial Request Form (31543) (May not be required for mandatory projects)

☐ Minor Change Form (31548)

☐ Added to Minor Change Register

Major Project:

☐ Initial Request Form (31543) (May not be required for mandatory projects)

☐ Project Plan Form (22872)

☐ Project Budget (31052)

☐ Project Proposal Document

☐ Risk Assessment (As applicable for new equipment and laboratory procedures 29100)

☐ (Optional) Gantt Chart

☐ Milestone Register is Complete (if applicable)

☐ Project Final Report

☐ Technical Review

☐ Implementation Plan

** Consent forms for staff collections should have been previously provided to quality if applicable.

RDAC project:

☐ RDAC Application Form (Copy only, original stored with Research Office)

☐ RDAC Final Report – if the project is funded (Copy only)

☐ Excel Sheet – with Names of Management Team for acknowledgment of project.

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The change management procedure utilises a three step process: the initial request (Step 1), minor change (Step 2) and project plan (Step 3). The utilisation of these steps is dependent on the type of change (administrative, IT/LIMS, minor, major and external) and on the progression of the change management process. Refer to Section 4 for details.

4 Actions

Prior to the preparation of any change management documentation it is recommended that ideas are discussed at the work unit level to determine the merit of each idea or proposal. If the process of change management is initiated it will need to follow the documentation requirements as listed in sections 4.1 to 4.9 and the workflow as shown in Appendix 1.

An exception is made for projects that are a mandatory requirement for the laboratory e.g. validation/verification of a new process or equipment item. In these cases it is possible to proceed directly to a full project plan (section 4.3).

For very large projects an overarching project number is allocated (by quality) to the work, and sub-projects may then be allocated “a letter” such that sections/parts of a project can be signed off separately. For example in validating an amplification kit a project number 1234 may be applied (for the overarching project), with sub-projects 1234a – referring the sensitivity testing, 1234b referring to concordance, 1234c referring to thresholds etc.

In cases where supplementary testing for a project is required (post-sign off), if the data is an extension of previous work - it may also be appropriate to allocate the supplementary work “a letter” ie. part b of the same work. If the supplementary work is substantially different in topic or content a new project number should be allocated.

Technical Review:
For major projects and for validations it is a requirement for the project to have a technical reviewer. The role of the technical reviewer is to 'peer view' critical technical aspects of the project (e.g. new instrument programs/settings, new analytical procedures) and/or to review data analysis with the project (e.g. Excel data transformations, formula's and calculations etc.). The technical reviewer/s are nominated by the team leader and/or management team as project proposal stage (section 4.3). The technical review is completed either during the project or at the completion of the laboratory work and data analysis - but prior to final report being presented to the management team. The technical review should provide to the Management Team as a written document that outlines the aspects of the project reviewed and general findings (Refer to Appendix 2 for template)

Communication:

- For large projects regular project updates should be given by the project leader (or delegate) to the management team. This will allow the management team to ensure that the project is meeting all requirements (NATA, internal needs etc), and that they have a full understanding of the project prior to final report preparation and sign off.
- When projects are complete - presentations should be made at team meetings so that all staff have an awareness of new processes and technology as it is released.
- Appropriate communications should be made at time of implementation (emails to applicable staff, additions to minor change registers, hardcopy records to quality etc).

4.1 Initial Request (Step 1)

Change requests can be initiated by any staff member within Forensic DNA Analysis, and are to be recorded on an **Initial Request Form** (QIS 31543). Submission of an initial request requires the following actions:

- Complete the **Initial Request Form** (QIS 31543). The initiator is required to complete the blue sections of the form only.
- Print the form and submit it to the Quality Team.
- Quality will allocate the request a proposal number, and then distribute it to the Line Manager of the person initiating the request. The Line Manager is to complete the red sections of the form.

The Line Manager will assess and sign the initial request recommending either:

- **Abandon process at Initial Request** (Refer to section 4.6)
- **Proceed to Step 2:**
  - **Minor Change** (Refer to section 4.2)
    or
  - **Project Proposal** (Refer to section 4.3)

  If the line manager wants to recommend proceeding to a full project proposal – they will need to seek Management Team approval.

If the initial request is abandon - no further action or documentation will be required.

All hardcopies of documents to be forwarded to Quality

4.2 Minor Change (Step 2)

The minor change form is used to document the purpose, method and date of change. If the Line Manager recommends that the change management is to proceed as a minor change, the project initiator must complete the blue sections of the **Minor Change Form**

(QIS 31548) and submit it to their line manager. In some circumstances a small amount of experimental data may be included within a minor change – where the date is used for decision making purposes.

The Line Manager must then complete to the following actions:

- **Add the change to the Minor Change Register** located in I:\Change Management
- Print the minor process change form 31548, sign it and submit it to the quality team.
- **Inform all stakeholders of the change** (e.g. SOPs, team meetings, emails).

All hardcopies of documents to be forwarded to Quality

4.3 Project Plan (Step 3)

If the Management Team recommends that a change management should proceed as a full proposal (administrative, IT/LIMS, major change or external project) the project leader is required to complete the following project documents:

1. **Project Plan Form** (QIS 22872): The level of detail entered into the project plan will depend on the size/importance of the project. This document includes the Risk Assessment for the project.

2. **Project Budget** (QIS 31052): A budget must be prepared and submitted to the Forensic DNA Analysis Management Team - with each project plan. A budget template is provided in QIS 31052. Additional resources for budgeting are located in G:\ForBiol\AAA Administration\Managing Scientist\Forensic DNA Analysis\Costing data\2013 HSSA Finance costings\1st cut

3. **Change Management Project Proposal Document**: In addition to the project plan form (QIS 22872), a project proposal will be required. The project proposal document should include an introduction to the project (including literature review), and detailed materials and methods sections - refer to QIS 23402 for writing guidelines and template for the project proposal (Template http://qheps.health.qld.gov.au/hsq-staff/comms/corporate-id/home.htm). These project proposals will essentially constitute the introduction and materials and methods section of the projects final project report.

   This project proposal must be prepared and submitted to the Forensic DNA Analysis Management Team with a Project Plan Form (QIS 22872) and a Project Budget (QIS 31052) for each change management proposal. This document should cover all aspects of what the project is proposing to do: purpose/background, methodology and experimental design (either laboratory experiments or data analysis as applicable).

4. **(Optional) Project Gantt Chart**: Preparation of a Gantt Chart is optional - it may be particularly useful for large projects. Refer to the Quality Team if Gantt Chart preparation is required.

After all three (or four) project documents have been prepared (as listed above); risk assessments (if applicable) and LIMS documentation completed (if applicable):

- Submit all documents to your Line Manager and to the Quality Team ([redacted]) by email. The Line Manager will submit the

documentation to the Forensic DNA Analysis Management Team for consideration (Refer the section 4.4).

The Line Manager should email the electronic copy of the documents to the Management Team a few days before the next scheduled Management Team meeting - to ensure there is time for pre-reading. A hardcopy of documentation is to be printed/supplied to the meeting – for signatures.

4.4 Forensic DNA Analysis Management Team – Consideration of Project Proposal

The Forensic DNA Analysis Management team will consider the change management project proposal documents as outlined in section 4.3. It is not necessary for all Management Team members to read and approve every proposal; however a quorum of the Management team must approve the proposal. The quorum must include the Managing Scientist, Team Leaders, Quality and Projects Senior Scientist, Senior Scientist that has Line Management of the staff/project and Senior Scientist/s of areas significantly affected by the project. For major projects and validations a technical reviewer submission should also be provided to the management team for consideration (Refer to section 4).

Consideration of the proposal should include:

1. *A determination of the impact of the proposed change on all stakeholders*
2. *Cost/Benefit Analysis of the project*
3. *Risk Assessment (Workplace Health & Safety and Business Risks)*
4. *A communication plan for all project participants and stakeholders*

The Forensic DNA Analysis Management Team will then make a recommendation as follows:

- **Implement proposal.** If the proposal is approved, the project plan documentation will be signed by the Management Team, and the project plan documents returned to the quality team and the project leader/appointed staff can initiate the project.
- **Implement proposal after change.** If the Management Team requires additions/edits to the project plan, the Management team will return the proposal to the project leader/appointed staff with feedback. The project documents will need to be edited and resubmitted (as per section 4.3.) before further consideration by the Management Team.
- **Abandon process.** Refer to Section 4.7 for details.

4.5 Implementation and Final Report (Step 3)

On completion of the change management project - a final report is required, this is usually written by the project leader (Refer to QIS 23402 for report preparation details). A Technical Review - if it is required (Appendix 2), and an Implementation Plan (Refer to Appendix 3) must also be prepared. The implementation plan will be a list of the steps required to be completed either before the change is implemented, or shortly after implementation. Although a proposal may not be implemented on completion, a basic implementation plan that can be refined closer to implementation should still be completed and submitted. On completion of the report, technical review and implementation plan, they are to be forwarded by email to your Line Manager. The Line Manager will submit the final report, technical review and implementation plan to the Forensic DNA Analysis Management Team for consideration/acceptance.

The Line Manager should email the electronic copy of the documents to the Management Team a few days before the next scheduled Management Team

meeting to ensure there is time for pre-reading. A hardcopy of documentation is to be printed/supplied to the meeting – for signatures.

If the final report is accepted by the Forensic DNA Analysis Management Team it will be signed and the project/change management process closed (hardcopy to be sent to the Quality Team). If the Management Team requires additions/edits to the final report, it will be returned to the project leader/appointed staff with feedback. The final report will need to be edited and resubmitted for consideration by the Management Team.

After acceptance of the final report the Forensic DNA Analysis Management team will recommend that the:

- **Change is implemented** into routine use (Refer to Appendix 3 for implementation plan for project leaders).
- **Change is accepted but will be implemented at a later date** (Refer to Appendix 3 for implementation plan for project leaders).
- **Change is abandoned** (Refer to Section 4.7 for details).

After completion of the project, all stakeholders must receive communications about the findings and outcomes of the project. This may include presentations at meetings, or the provision of final reports to stakeholders. For significant projects, a summary of the project is to be presented at team meetings.

All paperwork is to be submitted to quality on completion of the project for scanning and storing. Quality will also lock data files with a password on submission of final project report.

4.6 Responsibilities in Signing Documentation

When a project plan or report is submitted for review, it is the responsibility of the reviewer to ensure that all feedback is provided by the due date. Any feedback provided after the due date may not be considered (based on the merit of the feedback).

It is acceptable for a reviewer from the Forensic DNA Analysis Management Team to seek advice from other members of staff where it is deemed appropriate (e.g. where another person may have more experience in the subject of the report). In this instance, it is the responsibility of the person seeking the advice to provide the feedback to the project officer and to do so by the due date.

4.7 Abandoned/Cancellation

Should a change proposal not be approved, or if at any time the change is no longer required, the change management process may be abandoned/cancelled. This shall be recorded on the change management hard copy documents (to be forwarded to the Quality Team). If the project is abandon mid-way through a process an electronic file note can be created to detail the date and reason for project cessation.

It is possible to re-start abandon change management processes at a later date, and there are relevant sections in the change management forms to record a restarted process.

4.8 Recording Feedback

Project feedback, including feedback on project plans and reports, is to be tabulated and stored in the relevant change management folder.

All email communications regarding the project are also to be stored in the relevant change management folder.

5 Records

- All change management documentation (plans, reports, data etc.) are to be stored electronically in a network drive (e.g. I:Drive)
- Hardcopies of project documentation to be filed in Quality.
- On completion of projects all records (plans, reports, excel files etc) are to be stored in Forensic Register. To store records in FR:
    - Create new FR case Job Type=Research
    - Subject/Complainant=Project number and short title
    - Offence Class=Miscellaneous
    - Location=Forensic DNA Analysis Quality
    - Project documents loaded as an examination summary

6 Associated Documentation

QIS: 22872 Project Plan Form for Change Management in Forensic DNA Analysis
QIS: 23401 Forensic DNA Analysis Validation Guidelines
QIS: 23402 Writing Guidelines for Validation and Change Management Reports
QIS: 29100 Health & Safety Risk Assessment Form
QIS: 29106 FSS OHS Risk Assessment Procedure
QIS: 31052 Forensic DNA Analysis - Change Management Budget
QIS: 31543 Initial Request Form for Change Management in Forensic DNA Analysis
QIS: 31548 Minor Process Change Form for Change Management in Forensic DNA Analysis
QIS: 33017 FSS Research and Development short form
QIS: 33333 Participant Information and Consent Form (PICF) - Common Biological Samples
QIS: 33334 Participant Information and Consent Form (PICF) - Semen Samples
QIS: 33335 Participant Information and Consent Form (PICF) - Vaginal Samples

7 Amendment History

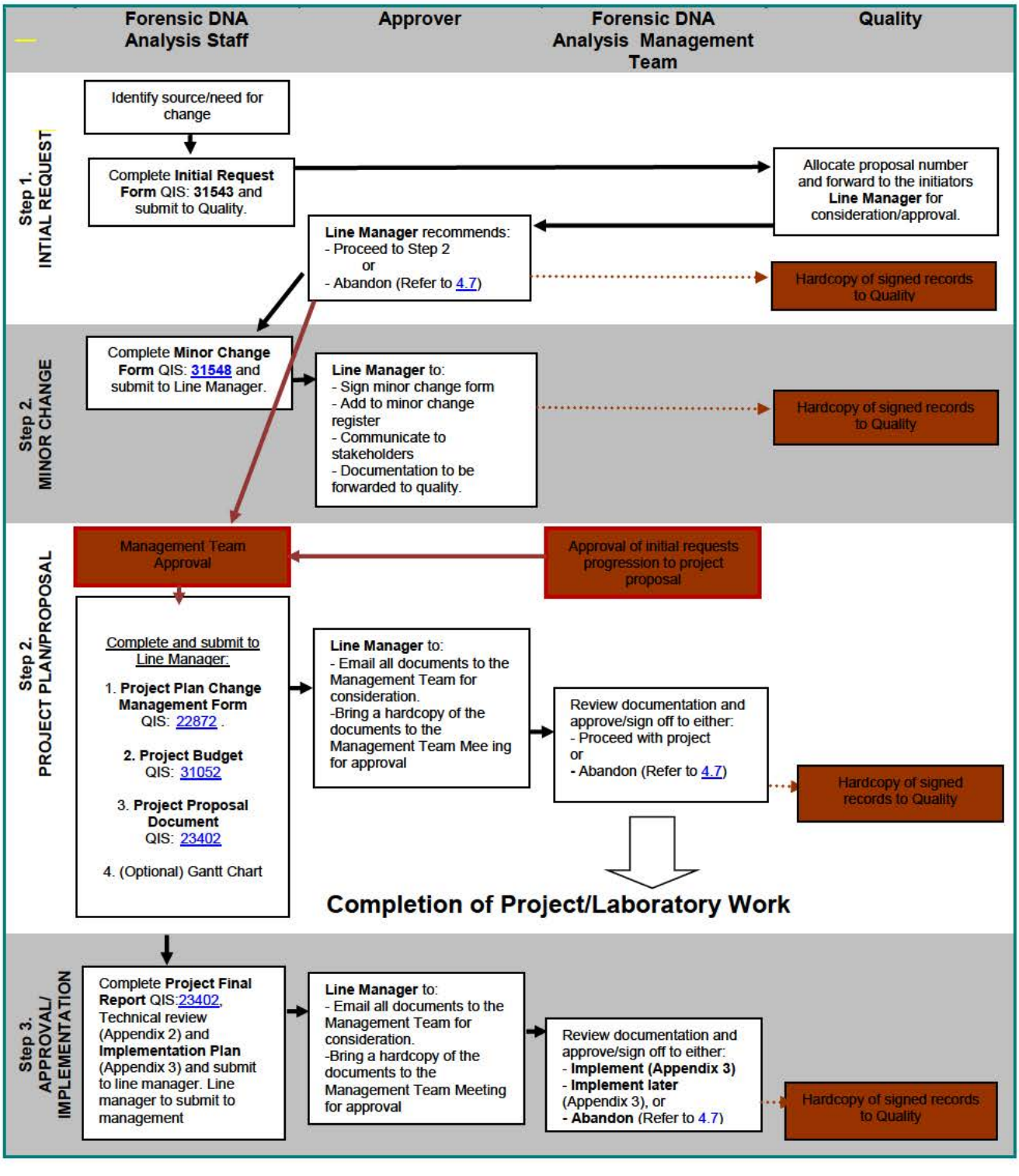
Version	Date	Author/s	Amendments
1	25 Aug 2005	Mary Gardam	First Issue
2	27 Feb 2007	Jane Olsson Mary Gardam Vanessa Ientile	Format Changed to include Project Management.
2	April 2008	QIS2 Migration Project	Headers and Footers changed to new CaSS format. Amended Business references from QHSS to FSS, QHPSS to CaSS and QHPS to Pathology Queensland
3	25 Sept 2008	Robyn Smith Crystal Revera	Formatting, Changes made to reflect new Laboratory name, Contact email addresses updated, SOP brought in line with changes made to template.
4	14 May 2012	Shannon Thompson Kirsten Scott	Major revision/re-write as the change management process changed.
5	21 Jan 2013	Kirsten Scott	Update QIS numbers for CM forms, update headers. Add records, additional associated documents and minor edits.
6	26 Mar 2013	Kirsten Scott	Clarify point 3 in section 4.4. Update hyperlinks

7	6 June 2014	Kirsten Scott	Remove Assessment Phase. Change in actions required by line managers for approving initial plan and minor change documents. Change content of appendix 2.
8	19 June 2015	Kerry-Anne Lancaster	Update to new template. Added reference to a milestone register and implementation plan. Changed content of appendix 2. Changed references to AUSLAB to LIMS. Defined project proposal document. Defined responsibilities of the reviewer. Added link to QIS 33017
9	21 Oct 2015	Kirsten Scott	Inclusion of consent forms in associated documents. Option for mandatory projects to proceed directly to project plan. Inclusion of RDAC processes into Change Management. Addition of Quality Checklist for project documentation
10	25 Nov 2015	Kirsten Scott	Inclusion of a technical review for major projects and validations – section 4, and minor text update in other section as a result of technical review
11	20 Sept 2016	Kirsten Scott	Specify implementation plan as mandatory, and add additional implementation examples. Section 4.5 and 5 add a note on locking of data files by quality. Section 3 clarify RDAC documentation requirements
12	1 June 2018	Kirsten Scott	Remove milestone register (section 4.3, 4.8). Add communication and project numbering to section 4. Addition of FR instructions section 5. Add technical review template as appendix 2. Minor text updates

8 Appendices

- APPENDIX 1: Change Management Process
- APPENDIX 2: Technical Review Template
- APPENDIX 3: Implementation Plan for project leaders
- APPENDIX 4: Checklist of documents required for a Change Management Project

8.1 APPENDIX 1: Change Management Process



8.2 APPENDIX 2: Technical Review Template

Technical review of Proposal #Project number
Project title

General project observations:

Experiment 1:

Program settings checked: Yes / No / Not Applicable. Comments:_____

Formulas checked: Yes / No / Not Applicable Comments:_____

Data transformations checked: Yes / No / Not Applicable Comments:_____

Calculations checked: Yes / No / Not Applicable Comments:_____

Experimental observations (design/results etc):

Experiment 2: (add additional experiments as required)

Program settings checked: Yes / No / Not Applicable. Comments:_____

Formulas checked: Yes / No / Not Applicable Comments:_____

Data transformations checked: Yes / No / Not Applicable Comments:_____

Calculations checked: Yes / No / Not Applicable Comments:_____

Experimental observations (design/results etc):

Technical Reviewer

Name	Position	Signature	Date

Project Manager

Name	Position	Signature	Date

8.3 APPENDIX 3: Implementation Plan for project leaders

Successful project implementation may require numerous tasks to be completed either prior to implementation, or shortly after the implementation date. Some of the considerations/tasks that may be required are listed below; however this is not intended to be a comprehensive list of tasks as each project will have different implementation requirements. Project leaders should devise and submit a comprehensive implementation plan for management review. Once complete, the checklist should be submitted to the quality team for filing with the signed project documents.

Task	Details	Date Completed
e.g. Create new procedures	New SOPs and training modules to be written and approved	
e.g. Update procedure/s	Existing SOPs and training modules to be revised and approved	
e.g. Staff training	Project members and relevant to staff to be issued with CTT statements as required	
	CTT staff to train relevant staff	
e.g. Software setup	Final version of software to be setup and reviewed on instrument	
	Check if Macro updates are required	
e.g. Equipment tasks	Add equipment to QIS	
	Add equipment to LIMS	
e.g. Consumable tasks	Add consumables to LIMS.	
	Addition of products to FAMMIS	
	Order new consumables	
e.g. Add to minor change register	Ensure that implementation has been added to the minor changes register	
e.g. Communication	Communicate to staff and other stakeholders – by meetings and emails.	

8.4 APPENDIX 4: Checklist of documents required for a Change Management Project

Minor Change:

☐ Initial Request Form (31543) (May not be required for mandatory projects)

☐ Minor Change Form (31548)

☐ Added to Minor Change Register

Major Project:

☐ Initial Request Form (31543) (May not be required for mandatory projects)

☐ Project Plan Form (22872)

☐ Project Budget (31052)

☐ Project Proposal Document

☐ Technical Review (for validations and major projects only)

☐ Risk Assessment (As applicable for new equipment and laboratory procedures 29100)

☐ (Optional) Gantt Chart

☐ Project Final Report

☐ Technical Review

☐ Implementation Plan

** Consent forms for staff collections should have been previously provided to quality if applicable.

RDAC project:

☐ RDAC Application Form (Copy only, original stored with Research Office)

☐ RDAC Final Report – if the project is funded (Copy only)

☐ Excel Sheet – with Names of Management Team for acknowledgment of project.

#184 KDS 06/08/2018

8.4 APPENDIX 4: Checklist of documents required for a Change Management Project

Minor Change:

N/A ☐ Initial Request Form (31543) (May not be required for mandatory projects)

N/A ☐ Minor Change Form (31548)

N/A ☐ Added to Minor Change Register

Major Project:

N/A ☐ Initial Request Form (31543) (May not be required for mandatory projects)

☑ Project Plan Form (22872)

N/A ☐ Project Budget (31052)

☑ Project Proposal Document

N/A ☐ Technical Review (for validations and major projects only)

N/A ☐ Risk Assessment (As applicable for new equipment and laboratory procedures 29100)

☒ (Optional) Gantt Chart

☐ Project Final Report
☐ Technical Review
☐ Implementation Plan

} Replaced with QPS Options paper. Implemented 12/02/2018 KDS 06/08/2018

** Consent forms for staff collections should have been previously provided to quality if applicable.

RDAC project:

N/A ☐ RDAC Application Form (Copy only, original stored with Research Office)

N/A ☐ RDAC Final Report – if the project is funded (Copy only)

N/A ☐ Excel Sheet – with Names of Management Team for acknowledgment of project.

Cathie Allen

From: Cathie Allen
Sent: Wednesday, 2 March 2022 12:29 PM
To: Troy O'Malley
Subject: RE: Request for Quote for Report

Thanks Troy.

I'll liaise with Justin regarding this and get back to you.

Cheers
Cathie

Cathie Allen **BSc, MSc (Forensic Science) (She/Her*)**
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

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

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*If you're wondering about the use of pronouns She/Her on this signature block, I encourage you to read some resources available here

From: Troy O'Malley <[redacted]
Sent: Wednesday, 2 March 2022 11:28 AM
To: Cathie Allen <[redacted]
Subject: RE: Request for Quote for Report

Cathie

Apologies for the delay we have been conducting an analysis of the data requested to gauge the effort needed to develop the report.

Please find attached a spreadsheet based on our analysis containing exhibits with a NDNAD and DIFP (No DNA Detected and DNA Insufficient for further processing) result and a subsequent PSTEXT (microcon) performed.

There are very few samples that met this criteria of the 35000+ samples reported as NDNAD and DIFP only ~600 samples have a PSTEXT (microcon) and we have provided a subset of the data you requested notably the pre and post Quant values identified.

Can I confirm this is the report that you would like created or have we misunderstood Justin's instructions?
This will give the barcodes with a result of these type and will contain all the NDNAD and DIFPs reported in that period. Further, we want to also see samples within this output if any had further Technique of PSTEXT, date of PSTEXT, Quant values (above) after PSTEXT, and the Process of RESULT and whatever result line/s that eventuated.

It was my understanding that FSS no longer routinely Microcon samples that are reported as NDNAD and DIFP. I infer from the previous analysis report and the comments Justin has made, that you are actually interested in ascertaining the success of obtaining useable profiles after PSTEXT (microcon) is performed?

We have estimated approximately two days of development and testing to provision a report (based on the aforementioned) allowing FSS to run the report for any arbitrary period, this equates to 80 hrs development time ($2,600 based on day rates for development services in the QITC FR Support Contract) which would include the analysis performed to date.

Happy to schedule a teams call with Justin and yourself to ensure the report we develop is fit for the intended purpose.

Troy

bdna
Troy O'Malley
Product Director (Forensic Software)
[redacted] [redacted] www.bdna.com.au

From: Cathie Allen <[redacted]
Sent: Tuesday, 1 March 2022 1:47 PM
To: Troy O'Malley <[redacted]
Subject: FW: Request for Quote for Report

Hi Troy

I was just wondering how the quote was coming along. We'd like to do some data interpretation to ensure that resources are being used efficiently and effectively.

Any update on this would be appreciated.

Cheers
Cathie

Cathie Allen **BSc, MSc (Forensic Science) (She/Her*)**
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

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

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From: Cathie Allen
Sent: Friday, 18 February 2022 11:15 AM
To: Troy O'Malley <[redacted]
Subject: Request for Quote for Report

Hi Troy

In 2018, Justin Howes compiled the attached as an Options Paper for the QPS to consider. Recently Insp Neville has raised that when samples that were not DNA profiled initially but underwent amplification, a DNA result was obtained. We would like to re-run this data review process and would like to obtain the data from the FR. It would be good if this report was available for us to run at any time (similar to the ACIC report that Dr Peter Culshaw uses within the FR).

Below are the parameters as set out by Justin.

Could you please review the below and provide a quote for cost of undertaking the work.

Please let me know if you have any queries.

Cheers
Cathie

Cathie Allen **BSc, MSc (Forensic Science) (She/Her*)**
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

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From: Justin Howes <[redacted]
Sent: Wednesday, 16 February 2022 4:09 PM
To: Cathie Allen <[redacted] Paula Brisotto <[redacted]
Subject: parameters for an FR report with quant values

Hi
I think we could request a report from the FR with the following:
- FR Number
- Barcode
- Date Received (01 July 2017 – 31 Dec 2021)
- Date of Process RESULT: Submitted- result pending (SRP)
- Description
- Category (eg. Trace DNA Kit)
- Quant Values: T.SA, T.IPC, T.LA, T.Y, T.SA (DI)
- Process type: RESULT
    - Result to be NDNAD and DIFP (No DNA Detected and DNA Insufficient for further processing)
    - Date of RESULT validation

This will give the barcodes with a result of these type and will contain all the NDNAD and DIFPs reported in that period. Further, we want to also see samples within this output if any had further Technique of PSTEXT, date of PSTEXT, Quant values (above) after PSTEXT, and the Process of RESULT and whatever result line/s that eventuated. The date for this final result validation would be requested too.

With all this, we will be able to see many things, including:
- Total no. of samples with this result in this period
- TAT for received to submitted, TAT for this initial final result (eg. NDNAD, DIFP), TAT to the final result after the PSTEXT
- When PSTEXT (microcon) was performed, the result outcome after this
- The difference between pre and post extraction quants

It will be a huge amount of data I would think, but will give something to drill down into with Excel. The multiple LRs will bulk up the results where pre-FR, non-contributions lines were reported with a grouping line.

Is there anything else that could be part of this data grab? Please let me know if you need any clarification as well.

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

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

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[redacted]

SRPDate	ident	NDNADDate
2018-02-19	NULL	NULL
2018-02-19	NULL	NULL
2018-02-19	NULL	NULL
2018-02-22	NULL	NULL
2018-03-13	NULL	NULL
2018-03-13	NULL	NULL
2018-04-04	NULL	NULL
2018-04-04	NULL	NULL
2018-04-04	683826	21:13.2
2018-04-04	683826	21:13.2
2018-04-04	688583	50:18.0
2018-04-05	NULL	NULL
2018-04-05	NULL	NULL
2018-04-05	NULL	NULL
2018-04-06	NULL	NULL
2018-04-06	688630	50:20.1
2018-04-09	NULL	NULL
2018-04-10	NULL	NULL
2018-04-10	NULL	NULL
2018-04-11	NULL	NULL
2018-04-17	NULL	NULL
2018-04-18	NULL	NULL
2018-04-20	NULL	NULL
2018-04-23	NULL	NULL
2018-04-23	NULL	NULL
2018-04-24	NULL	NULL
2018-04-24	NULL	NULL
2018-04-27	NULL	NULL
2018-05-15	NULL	NULL
2018-05-15	NULL	NULL
2018-05-15	NULL	NULL
2018-05-15	NULL	NULL
2018-05-15	NULL	NULL
2018-05-15	NULL	NULL
2018-05-21	NULL	NULL
2018-05-25	NULL	NULL
2018-06-01	NULL	NULL
2018-06-01	NULL	NULL
2018-06-01	NULL	NULL
2018-06-06	NULL	NULL
2018-06-11	NULL	NULL
2018-06-21	NULL	NULL
2018-06-21	NULL	NULL
2018-06-29	NULL	NULL
2018-07-02	NULL	NULL
2018-07-03	NULL	NULL
2018-07-03	NULL	NULL
2018-07-10	NULL	NULL
2018-07-11	NULL	NULL

[redacted]

2018-07-18	NULL	NULL	
2018-07-19	NULL	NULL	
2018-07-19	NULL	NULL	
2018-07-20	NULL	NULL	
2018-07-24	NULL	NULL	
2018-07-25	NULL	NULL	
2018-07-25	NULL	NULL	
2018-07-25	NULL	NULL	
2018-07-25	NULL	NULL	
2018-07-26	NULL	NULL	
2018-07-26	NULL	NULL	
2018-07-31	NULL	NULL	
2018-08-17	839758		31:46.6
2018-08-17	893477		04:22.7
2018-08-17	839758		31:46.6
2018-08-17	893477		04:22.7
2018-08-21	NULL	NULL	
2018-08-27	NULL	NULL	
2018-08-27	NULL	NULL	
2018-08-28	NULL	NULL	
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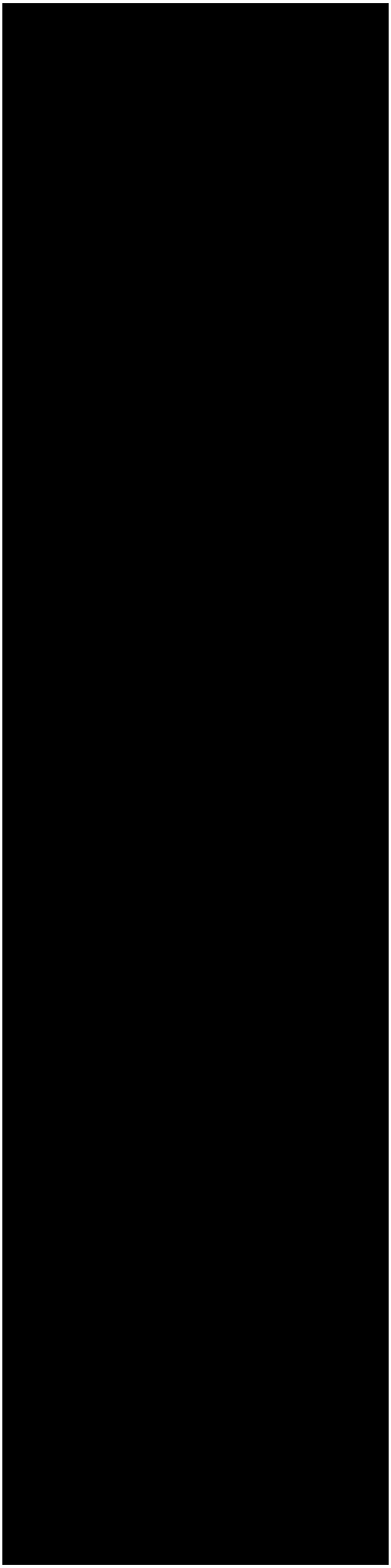

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2018-02-28		H9	0.004209	N	0.002931	0.00071
2018-03-26		E10	0.001451	N	5.76E-05	0.001112
2018-03-22		G10	0.00174	N	0.000815	0.000632
2018-04-10		A10	0.007863	N	0.001494	0.007232
2018-04-11		H6	0.001079	N	0.000131	0.000977
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2018-04-06		C3	0.006508	N	0.009263	0.010491
2018-04-17		D7	0.004241	N	0.003563	0.001855
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2018-06-15		C3	0.002416	N	0.001027	0.000141
2018-06-15		D3	0.003921	N	0.002172	0.000493
2018-04-17		H4	0.004566	N	0.00179	0.002359
2018-04-19		A9	0.003031	N	0.001692	0.003911
2018-04-26		G4	0.003079	N	0.001118	0.002803
2018-04-30		E10	0.001007	N	0.000522	0.000727
2018-04-30		C10	0.005102	N	0.003135	0.003391
2018-04-30		E3	0.001168	N	0.000152	0.001151
2018-05-03		D6	0.003147	N	0.002461	0.000712
2018-05-03		E6	0.00156	N	0.002054	0.00347
2018-05-04		F10	0.002496	N	0.000497	0.001647
2018-05-23		A9	0.002033	N	0.003242	0.004432
2018-05-21		H9	0.00682	N	0.00753	0.014195
2018-05-23		A4	0.005129	N	0.005464	0.004849
2018-09-03		D2	0.003107	N	0.002008	0.000869
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2018-09-03		D2	0.003107	N	0.002008	0.000869
2018-05-24		C11	0.00343	N	0.001684	0.003324
2018-05-28		F2	0.001122	N	0.000357	0.000791
2018-06-12		C12	0.005341	N	0.00293	0.004473
2018-06-06		C8	0.006848	N	0.002921	0.005205
2018-06-06		D8	0.004817	N	0.001619	0.003272
2018-06-11		E4	0.001258	N	0.001007	0.001307
2018-06-14		F7	0.003284	N	0.002373	0.004947
2018-06-26		C7	0.001055	N	NULL	0.001127
2018-06-26		H6	0.007625	N	0.004981	0.004826
2018-07-03		D3	0.00737	N	0.004191	0.007444
2018-07-13		D3	0.001259	N	0.000563	0.001139
2018-07-04		G2	0.004556	N	0.004957	0.003819
2018-07-04		A3	0.003413	N	0.001582	0.000844
2018-07-13		G12	0.002016	N	0.000756	0.0016
2018-07-17		D8	0.001085	N	0.000213	0.000586

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	2018-07-25		C12	0.001287	N	0.000966	0.00015
	2018-07-23		E8	0.001676	N	0.000294	0.000631
	2018-07-24		B11	0.008685	N	0.003902	0.008433
	2018-07-26		F2	0.006416	N	0.002732	0.006994
	2020-03-30		D2	0.001164	N	0.000162	0.001185
	2018-08-08		E3	0.001061	N	0.000126	0.000346
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	2018-07-30		F8	0.003767	N	0.0016	0.003536
	2018-07-30		A12	0.005341	N	0.00239	0.004925
	2018-08-02		D5	0.008067	N	0.004156	0.007374
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	2018-08-29		B6	0.008613	N	0.002299	0.012289
	2018-08-31		H11	0.002976	N	0.001501	0.002522
	2018-09-10		A9	0.001255	N	0.00044	0.000421
	2018-09-10		B9	0.002262	N	0.003075	0.001693
	2018-09-11		F3	0.008196	N	0.007484	0.007858
	2018-09-11		B4	0.002929	N	0.002092	0.000543
	2018-09-07		H2	0.001317	N	0.00079	0.000856
	2018-09-07		A3	0.004261	N	0.000231	0.002198
	2018-09-26		F10	0.00215	N	0.001009	0.001895
	2018-09-20		F2	0.003378	N	0.000857	0.002296
	2018-09-21		B8	0.001569	N	0.002862	0.000858
	2018-09-25		H3	0.001538	N	0.000912	0.001127
	2018-10-02		C7	0.001647	N	0.000551	0.000498
	2018-10-02		A9	0.006394	N	0.003375	0.006764
	2018-09-25		B7	0.007214	N	0.000825	0.005514
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	2018-09-27		B11	0.007458	N	0.00671	0.007988
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	2018-10-18		F5	0.007539	N	0.003208	0.006075
	2018-10-23		A8	0.003395	N	0.001206	0.002675
	2018-10-26		B3	0.002315	N	0.001461	0.000493
	2018-10-26		B3	0.001902	N	0.000893	NULL
	2018-10-30		B5	0.002228	N	0.001858	NULL
	2018-10-30		C6	0.002636	N	0.000766	0.002814
	2018-10-30		D6	0.003504	N	0.00228	0.00226
	2018-10-30		G6	0.002306	N	0.00066	0.000466
	2018-10-30		A7	0.008109	N	0.012011	0.000611
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	2018-11-02		E4	0.004859	N	0.001757	NULL

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	2018-11-02		F12	0.001671	N	0.000466	0.000508
	2018-11-02		G12	0.005297	N	0.002592	0.006292
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	2018-11-12		B8	0.001097	N	0.001391	0.002005
	2018-11-16		B7	0.002301	N	0.002741	NULL
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	2018-11-21		G12	0.00115	N	0.000239	0.001698
	2018-11-16		A3	0.007241	N	0.002627	0.00633
	2018-11-16		C3	0.002605	N	0.000171	0.00153
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	2018-11-21		A4	0.001393	N	0.000547	0.000946
	2018-11-21		C4	0.001184	N	0.00076	0.0009
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	2018-12-06		H10	0.001627	N	0.001095	0.000144
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	2019-01-11		G5	0.001361	N	0.000972	NULL
	2019-01-11		H5	0.00496	N	0.003122	0.000961
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	2019-02-11		B4	0.004435	N	0.002497	0.00139
	2019-02-11		C4	0.003405	N	0.001649	0.001604
	2019-03-08		D9	0.001744	N	0.000475	0.000682

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	2019-03-25		A10	0.001424	N	0.00089	0.000856
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	2019-03-28		D5	0.001134	N	0.000883	0.000391
	2019-04-09		E3	0.007573	N	0.006294	0.006959
	2019-04-09		F3	0.001091	N	0.000322	0.000633
	2019-04-17		B9	0.004223	N	0.001055	0.006709
	2019-05-08		E9	0.00331	N	0.002778	0.001707
	2019-05-14		H5	0.001113	N	0.001086	0.000421
	2019-05-14		C6	0.007173	N	0.002218	0.006793
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	2019-05-20		H5	0.006338	N	0.002882	0.005069
	2019-05-27		G9	0.003541	N	0.004857	0.006522
	2019-05-28		D4	0.00158	N	0.000542	0.002985
	2019-06-11		B10	0.002786	N	0.001337	0.00216
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	2019-06-14		C5	0.006384	N	0.000696	0.004126
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	2019-07-15		F6	0.002104	N	0.00192	0.002416
	2019-07-16		B6	0.003989	N	0.001635	0.003527
	2019-07-16		B8	0.003724	N	0.001615	0.002639
	2019-07-19		E6	0.004387	N	0.002403	0.005869
	2019-07-30		E3	0.004175	N	0.002435	0.00235
	2019-07-30		C4	0.005891	N	0.004268	0.004091
	2019-07-30		E6	0.003703	N	0.002476	0.002554
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	2019-08-21		G8	0.007973	N	0.001211	0.005062
	2019-08-20		F2	0.007067	N	0.00035	0.006412
	2019-08-20		E3	0.001757	N	0.000772	0.000152
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	2019-09-16		D10	0.007554	N	0.003231	0.007743
	2019-09-24		D7	0.006701	N	0.005339	0.006623
	2019-09-24		F7	0.002199	N	0.001814	0.002419
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	2019-09-24	[redacted]	D6	0.001133	N	0.001354	0.002577
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	2019-10-03		B9	0.001182	N	0.000572	0.002286
	2019-10-04		E3	0.008724	N	0.002172	0.009568
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	2019-11-01		C5	0.001636	N	0.001215	0.001473
	2019-11-01		C9	0.002976	N	0.002481	0.001254
	2019-11-06		A3	0.001786	N	0.001297	0.000297
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	2019-11-06		A4	0.001673	N	0.000567	0.000524
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	2019-11-07		F9	0.00306	N	0.002124	0.004473
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	2019-11-25		H7	0.004998	N	0.002165	0.002017
	2019-11-27		G11	0.001902	N	0.000597	0.001132
	2019-11-27		E10	0.005525	N	0.004219	0.003608
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	2019-11-27		A11	0.00152	N	0.001729	0.000586
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	2019-11-27		D7	0.001644	N	0.001993	0.001821
	2019-11-27		B11	0.008315	N	0.005541	0.003381
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	2019-12-10		H7	0.00207	N	0.000704	NULL
	2019-12-12		H3	0.003887	N	0.00152	0.003907
	2019-12-24		F12	0.001793	N	0.000411	NULL
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	2020-02-13		A11	0.005219	N	0.004908	0.00199
	2020-02-13		B11	0.002377	N	0.000806	0.000561
	2020-02-18		D10	0.001904	N	0.001327	0.001679
	2020-02-20		G10	0.005638	N	0.002384	0.007435
	2020-02-27		C9	0.001055	N	0.000165	0.000711
	2020-03-03		C6	0.001952	N	0.000769	0.000544
	2020-03-03		G7	0.001146	N	0.000603	0.000528
	2020-03-03		G5	0.008258	N	0.000414	0.00629
	2020-03-09		A4	0.008441	N	0.002966	0.007659
	2020-03-12		H5	0.002597	N	0.002323	0.000175
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	2020-03-31		G4	0.00495	N	0.007173	0.005992
	2020-03-31		H4	0.004708	N	0.004319	0.005307
	2020-03-31		A5	0.001785	N	0.001907	0.003303
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	2020-03-31		F6	0.002236	N	0.001524	0.000231
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	2020-04-30		G4	0.002376	N	0.000914	0.001723
	2020-04-30		H4	0.002251	N	0.000378	0.001373
	2020-05-01		B10	0.001669	N	0.000753	NULL
	2020-05-08		A7	0.002732	N	0.002718	0.003537
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	2020-05-29		D4	0.00742	N	0.004276	0.002099
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	2020-05-29		F10	0.004577	N	0.006529	0.000332
	2020-06-04		A3	0.002145	N	0.004105	0.001294
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	2020-06-29		C6	0.004809	N	0.003554	0.000638
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	2020-06-29		C12	0.003605	N	0.002422	0.002192
	2020-06-30		H4	0.005833	N	0.002959	0.006069
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	2020-08-05		G7	0.001065	N	NULL	NULL
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	2020-08-19		C5	0.005944	N	0.007492	0.006069
	2020-08-19		H5	0.005492	N	0.001864	0.004157
	2020-08-24		H2	0.002647	N	0.000725	0.001984
	2020-08-25		G11	0.002552	N	NULL	0.000413
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	2020-09-08		A10	0.003533	N	0.003209	0.001573
	2020-09-15		H11	0.006746	N	0.000295	0.006795
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	2020-10-16		D6	0.005644	N	0.005336	0.006934
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	2020-10-16		F6	0.002185	N	0.001616	0.001873
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	2020-10-20		F9	0.006441	N	0.001268	0.002473
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	2020-10-23		E4	0.002088	N	0.001144	0.002022
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	2020-10-23		C7	0.001005	N	0.000462	NULL
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	2020-10-29		B5	0.00173	N	0.00131	0.002548
	2020-11-02		F8	0.005396	N	0.003214	0.004833

	2020-11-03	[redacted]	E3	0.006157	N	0.0031	0.007909
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	2020-11-09		A6	0.007558	N	0.008056	0.00884
	2020-11-09		G6	0.007447	N	0.006482	0.005011
	2020-11-10		H7	0.0024	N	0.001025	0.001406
	2020-11-10		H7	0.00816	N	0.011473	0.00878
	2020-11-13		G2	0.001531	N	NULL	0.002534
	2020-11-19		B4	0.002199	N	0.001276	6.14E-05
	2020-11-19		G4	0.001	N	NULL	0.00052
	2020-11-17		C5	0.008762	N	0.007019	0.005658
	2020-11-17		H5	0.002382	N	0.00119	0.000222
	2020-11-17		B5	0.003021	N	0.001198	0.003111
	2020-11-19		D9	0.004143	N	0.002468	0.002459
	2020-12-07		G9	0.00138	N	NULL	0.001639
	2020-12-11		G2	0.00697	N	0.002615	0.004085
	2021-02-11		F12	0.008587	N	0.004595	0.00694
	2020-12-17		H6	0.006467	N	0.005052	0.005326
	2020-12-17		A8	0.002093	N	0.000946	0.001655
	2020-12-21		A6	0.004059	N	0.003763	NULL
	2020-12-21		A8	0.005558	N	0.004845	0.001642
	2020-12-24		B11	0.005426	N	0.002821	0.004976
	2021-01-07		F2	0.00217	N	0.002288	0.003462
	2021-01-07		G3	0.001952	N	0.002349	0.001565
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	2021-01-08		H8	0.001669	N	0.000745	NULL
	2021-01-09		H6	0.001995	N	0.000901	0.000762
	2021-01-14		E2	0.003504	N	0.00189	0.004006
	2021-01-12		D10	0.002256	N	0.001636	0.001506
	2021-01-15		E2	0.008031	N	0.009032	0.007315
	2021-01-15		C3	0.003103	N	0.001988	0.003426
	2021-01-15		B4	0.007137	N	0.005592	0.008189
	2021-01-15		C11	0.002798	N	0.001963	0.000897
	2021-01-18		F2	0.00208	N	0.000887	0.001236
	2021-01-15		F10	0.002618	N	0.002385	0.00072
	2021-01-15		D11	0.00633	N	0.004051	0.003385
	2021-01-19		F5	0.003687	N	0.002448	0.002162
	2021-01-19		B7	0.005881	N	0.004139	0.00459
	2021-01-19		F9	0.002626	N	0.001088	0.001524
	2021-01-19		H7	0.006043	N	0.005829	0.00213
	2021-01-19		E8	0.002197	N	0.002776	0.000467
	2021-01-19		B7	0.002382	N	0.001731	0.000557
	2021-01-27		H8	0.001612	N	0.00116	0.001719
	2021-01-27		A9	0.002497	N	0.000504	0.001323
	2021-01-27		F6	0.008447	N	0.00353	0.008117
	2021-02-02		G2	0.003331	N	0.002002	0.002109
	2021-02-08		D9	0.005873	N	0.00539	0.004502
	2021-02-05		E6	0.003036	N	0.000944	0.006213
	2021-02-08		E7	0.006999	N	0.001895	0.005811

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	2021-03-01		D6	0.006236	N	0.002302	0.007303
	2021-03-02		C6	0.005781	N	0.004899	0.005478
	2021-03-03		C10	0.001344	N	0.000255	0.001965
	2021-03-04		B4	0.005094	N	0.003106	0.003776
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	2021-03-09		B3	0.003197	N	0.001647	0.000427
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	2021-03-04		C11	0.001537	N	0.000383	0.000863
	2021-03-09		C3	0.003801	N	0.000768	0.003915
	2021-03-09		F3	0.003435	N	0.000586	0.002549
	2021-03-09		E6	0.005512	N	0.007727	0.006523
	2021-03-12		F3	0.003732	N	0.001453	NULL
	2021-03-12		H3	0.001011	N	0.000294	NULL
	2021-03-23		H3	0.001666	N	0.000699	0.000115
	2021-03-24		E9	0.00578	N	0.006246	0.005498
	2021-03-30		C11	0.005228	N	0.005292	NULL
	2021-03-30		B11	0.002192	N	0.001935	0.002709
	2021-03-31		H9	0.001472	N	0.000455	0.001115
	2021-03-31		H10	0.001507	N	0.000706	0.000755
	2021-03-31		C11	0.001858	N	0.000607	0.001499
	2021-03-31		D9	0.002229	N	0.000614	0.000733
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	2021-04-06		A4	0.006396	N	0.004675	0.001181
	2021-04-09		H8	0.001882	N	0.001437	0.000523
	2021-04-13		F5	0.005504	N	0.003468	0.003019
	2021-04-15		G3	0.002093	N	0.001742	0.000428
	2021-04-13		C4	0.001424	N	0.000328	0.001488
	2021-04-14		C9	0.003576	N	0.001195	0.00222
	2021-04-21		B5	0.00106	N	0.001033	0.001018
	2021-04-21		E6	0.003676	N	0.006546	0.007786
	2021-04-21		C5	0.003523	N	0.004415	0.006197
	2021-04-21		D5	0.003917	N	0.005262	0.004116
	2021-04-21		B6	0.004471	N	0.008299	0.008475
	2021-04-21		F6	0.006564	N	0.011458	0.008737
	2021-04-19		C4	0.002983	N	0.002221	0.001963
	2021-04-20		F4	0.007097	N	NULL	0.006695

	2021-04-20	[redacted]	C10	0.001599	N	0.00034	0.000409
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	2021-05-19		B9	0.00681	N	0.009266	0.006732
	2021-05-19		C9	0.00475	N	0.004883	0.004149
	2021-05-19		D9	0.004882	N	0.005317	0.001922
	2021-05-19		E9	0.004426	N	0.002156	0.002265
	2021-05-19		F9	0.007229	N	0.007597	0.006078
	2021-05-19		G9	0.005404	N	0.005964	0.003714
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	2021-06-07		D7	0.001325	N	0.000512	0.001502
	2021-06-07		A8	0.001335	N	0.000728	0.002816
	2021-06-09		C4	0.005186	N	0.003212	0.001957
	2021-06-23		E2	0.002738	N	0.00097	0.000485
	2021-06-23		D2	0.002323	N	0.00146	0.001011
	2021-07-01		E2	0.004319	N	0.00611	0.004321
	2021-07-01		D2	0.001121	N	0.000881	0.000217
	2021-07-01		C5	0.006362	N	0.006844	NULL
	2021-06-29		C3	0.001092	N	0.0004	0.001183
	2021-07-06		E6	0.002171	N	0.003547	NULL
	2021-07-06		F6	0.004635	N	0.005583	0.00329
	2021-07-06		G6	0.007282	N	0.007495	0.00334
	2021-07-06		H6	0.00392	N	0.008258	0.002693
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	2021-07-13		H3	0.003504	N	0.001025	0.004191
	2021-07-13		F8	0.001687	N	0.001858	0.001641
	2021-07-20		H4	0.003128	N	0.002002	0.003631
	2021-07-20		B5	0.00145	N	0.000462	0.001045
	2021-07-22		C5	0.007846	N	0.00495	0.008482
	2021-07-23		F6	0.001475	N	0.000452	0.000638
	2021-07-23		C5	0.007099	N	0.003315	0.0039
	2021-07-26		F2	0.002399	N	0.001877	0.001672
	2021-07-27		G9	0.003294	N	0.00279	0.00178
	2021-07-28		B6	0.002505	N	0.001361	0.001295
	2021-07-28		H6	0.00458	N	0.002031	0.002417
	2021-07-28		E7	0.0039	N	0.001553	0.001422
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	2021-08-04		C7	0.004221	N	0.003822	0.007589
	2021-08-04		H7	0.001404	N	0.001584	0.001991
	2021-08-04		G9	0.005067	N	0.003562	0.005363
	2021-08-04		H9	0.00341	N	0.002458	0.003419
	2021-08-06		C4	0.004466	N	0.000199	0.001765
	2021-08-06		D4	0.00347	N	0.004263	0.003351
	2021-08-06		E4	0.005092	N	0.004319	0.004503
	2021-08-06		E6	0.00691	N	0.008772	0.005498
	2021-08-12		G7	0.004022	N	0.006001	0.003011
	2021-08-12		C8	0.004229	N	0.004928	0.003387
	2021-08-16		F3	0.002868	N	0.000804	0.00257
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	2021-08-26		F5	0.005317	N	0.004114	0.002493
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	2021-09-06		D4	0.004944	N	0.001845	0.002637	
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	2021-09-09		E10	0.003369	N	0.004191	0.003883	
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	2021-09-14		C3	0.004711	N	0.002482	0.004986	
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	2021-09-15		H5	0.001968	N	0.000692	0.000394	
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	2021-09-15		F8	0.004006	N	0.001353	0.004732	
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	2021-09-15		C11	0.00252	N	0.001074	NULL	
	2021-09-16		G2	0.002079	N	0.000785	0.00066	
	2021-09-17		F2	0.001708	N	0.001678	0.001389	
	2021-09-17		H2	0.003726	N	0.00336	0.002173	
	2021-09-17		C3	0.003002	N	0.003441	0.001207	
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	2021-09-22		D2	0.008731	N	0.006851	0.002786	
	2021-09-22		G2	0.003307	N	0.002962	0.003619	
	2021-09-22		H2	0.00417	N	0.004665	0.003159	
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	2021-09-24		D3	0.001222	N	0.000935	0.001124	
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	2021-09-28		G2	0.001282	N	0.000141	NULL	

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2021-11-09		H7	0.004394	N	0.004894	0.003389
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0.012247	0.015405	0.013516
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0.011105	0.01452	0.016125
0.004182	0.001401	0.009321
0.003233	0.010064	0.008769
0.004247	0.007529	0.010797
0.000406	0.00323	0.003587
0.014015	0.008971	0.008843
0.007309	0.014319	0.013967
0.008273	0.006144	0.010466
0.001725	0.000396	0.002371
0.007272	NULL	0.00594
0.014796	0.003048	0.017435
0.007345	0.013528	0.013051
0.007024	0.006494	0.007257
0.004865	0.001831	0.004023
0.002007	0.001482	0.000913
0.001689	0.009509	0.012926
0.020855	0.014244	0.015115
0.001094	NULL	0.002785
0.001987	0.002001	0.005543
0.003984	0.00401	0.005443
0.001476	0.003334	0.004075
0.00978	0.008987	0.010217
0.00265	0.003732	0.004087
0.002744	0.004803	0.004451
0.002578	0.001684	0.00716
0.002794	0.002292	0.004571
0.001989	0.001585	0.004673
0.003388	0.004542	0.009165
0.004884	0.006206	0.008027
0.009105	0.011623	0.017073
0.003981	0.002907	0.00379
0.009707	0.004292	0.012116
0.006456	0.00468	0.007915
0.003316	0.000565	0.00538
0.003016	0.006113	0.00605
0.002326	0.007488	0.00918
0.023929	0.027059	0.028634
0.001855	0.006058	0.003133
0.014379	0.020225	0.018375
0.00184	0.011508	0.010041
0.002153	0.023738	0.020001

0.014085	0.01325	0.012385
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NULL	NULL	NULL
NULL	NULL	NULL
NULL	NULL	NULL
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NULL	NULL	NULL
NULL	NULL	NULL
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0.000765	0.003712	0.002606
0.009296	0.018404	0.019872
0.011265	0.01188	0.011932
0.000449	0.00269	0.002563
0.003884	0.004656	0.007631
0.000482	0.002009	0.003793
0.001138	0.000879	0.004335
0.00235	0.003851	0.014454
4.58E-05	0.001257	0.003713
0.000864	0.004808	0.006649
0.000784	0.002784	0.006034
0.009679	0.012747	0.01452
0.005696	0.000369	0.014259
0.000187	0.000421	0.001563
0.000633	0.000499	0.000612
0.01562	0.018194	0.022267
0.011258	0.000803	0.01513
0.002993	0.003625	0.002705
0.000946	0.000973	0.002068
0.001291	0.002077	0.004275
0.001087	0.001477	0.001632
0.00114	0.001509	0.003062
0.002915	0.001831	0.003825
0.019118	0.005343	0.027895
0.004061	0.002766	0.008955
0.002842	0.00108	0.00338
0.002579	0.000338	0.003953
0.000837	0.002062	0.003546
0.00395	0.003659	0.008938
0.00098	0.001849	0.001339
0.005917	0.00665	0.006364
0.003878	0.006812	0.004737
0.003715	0.005763	0.005196
0.004956	0.006146	0.003857
0.015363	0.012686	0.013406
0.004244	0.006771	0.007523
0.000306	0.026697	0.022321

0.001882	0.003291	0.002417
0.001796	0.0042	0.00636
NULL	NULL	NULL
NULL	NULL	NULL
NULL	NULL	NULL
NULL	NULL	NULL
NULL	0.000085	NULL
NULL	NULL	NULL
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NULL	NULL	NULL
NULL	NULL	NULL
NULL	NULL	NULL
NULL	NULL	NULL
0.008381	0.003582	0.008718
0.012077	0.003476	0.024292
0.010664	0.014136	0.016678
0.010845	0.011175	0.01458
0.01352	0.009848	0.014528
0.016892	0.013618	0.022021
0.017849	0.018148	0.020808
0.011382	0.006566	0.014404
0.003582	0.00458	0.014189
NULL	NULL	NULL
0.002193	0.002869	0.003808
0.007922	0.007539	0.012724
0.003261	0.000185	0.002245
0.00308	0.002876	0.003186
0.001125	0.00356	0.003367
0.006607	0.00799	0.010238
0.003155	0.001773	0.003784
0.002824	0.001183	0.002675
0.013271	0.008495	0.011369
0.001695	0.001105	0.001466
0.014814	0.000169	0.016859
0.001676	0.004639	0.004714
0.001163	0.000167	0.001488
0.004324	0.000383	0.002082
0.008328	0.003565	0.009866
0.012109	0.004131	0.008735
0.004289	0.004066	0.003599
0.000556	0.002833	0.002259

0.006617	0.013948	0.015538
0.014796	0.006793	0.01347
0.001136	0.001995	0.003025
0.00014	0.000989	0.002184
0.002315	0.003777	0.005956
0.003414	0.003964	0.005943
0.00509	0.004384	0.006973
0.001499	0.004882	0.004026
0.010541	0.024176	0.023532
0.001314	0.002314	0.003014
0.007564	0.010789	0.014918
0.003337	0.002547	0.002941
0.009686	0.003024	0.009047
0.001742	0.004789	0.008099
0.002997	0.007101	0.014393
0.004837	0.005679	0.010751
0.020023	NULL	0.023144
0.000307	NULL	0.000194
0.005569	0.002764	0.005102
0.005642	0.005571	0.005041
0.009379	0.010817	0.011439
0.002623	0.00475	0.005598
0.008586	0.009255	0.013212
0.003318	0.005959	0.007791
0.000145	0.00579	0.007954
0.008013	0.007861	0.007276
0.011336	0.012381	0.011028
0.018228	0.014601	0.014639
0.002902	0.002019	0.003914
0.002174	0.002225	0.002966
0.005019	0.008154	0.00898
0.002111	0.001465	0.002767
0.002968	0.006582	0.006274
8.88E-05	NULL	NULL
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0.005952	0.006823	0.0117
0.002538	0.002718	0.004883
0.009397	0.006752	0.010992
0.004039	0.004313	0.006602
0.011684	0.014318	0.013703
0.005247	0.004847	0.007703
0.002077	0.001592	0.002442
0.012149	0.016649	0.011144
0.009112	0.020669	0.019579
0.010015	0.01112	0.011412
0.002489	0.00453	0.004691
0.00238	0.004978	0.002944
0.008923	0.008586	0.008001
0.001398	0.000454	0.001693
0.001326	0.000458	0.002635

0.000655	0.000858	0.000908
0.020735	0.006258	0.0195
0.001579	0.004236	0.005054
0.00143	0.003478	0.003937
0.001712	0.000685	0.002272
0.005275	0.006189	0.009827
0.003135	0.001698	0.004303
0.006592	0.003407	0.006443
0.001491	0.000511	0.008867
0.002981	0.003873	0.002612
0.000906	0.001216	0.001445
0.003117	0.008072	0.012465
0.003636	0.006202	0.009413
0.001533	0.003955	0.005139
0.00305	0.008432	0.010481
0.001758	0.004841	0.005887
0.002692	0.012589	0.018194
0.005187	0.008848	0.010571
0.011639	0.005532	0.015305
0.002264	0.006623	0.007806
NULL	0.001669	0.002095
0.002887	0.00809	0.009255
0.009452	0.004196	0.012134
0.001678	NULL	0.003883
0.002627	NULL	0.005207
0.002067	0.003226	0.004746
0.003132	0.004457	0.006893
0.001712	0.00265	0.005641
0.008494	0.000663	0.008569
0.015267	0.005491	0.018098
0.004161	0.004407	0.004094
0.018773	0.013217	0.012177
0.000951	0.000914	0.001791
0.001266	0.003495	0.002918
0.00276	0.002511	0.004335
0.004088	0.004413	0.007446
0.000095	0.00054	0.003637
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0.000333	0.002488	0.004723
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NULL	0.000722	0.005434
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0.005041	0.004003	0.007111
0.011493	0.010145	0.008609
0.009436	0.001549	0.016641
0.001546	0.000158	0.005939
0.001175	0.001615	0.004098
0.000603	0.000931	0.002661
NULL	0.00104	0.001067
0.000684	0.00054	0.002235

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0.001401	0.002524	0.002707
0.007837	0.0013	0.008396
0.006465	NULL	0.003655
0.008731	0.001217	0.006315
0.005796	0.007166	0.005134
0.007349	0.013645	0.010014
0.016807	0.019621	0.016592
0.004167	0.00371	0.004975
0.007162	0.005724	0.008972
0.001812	0.004538	0.00536
0.00147	0.001683	0.002001
0.001873	0.000172	0.003332
0.011536	0.009145	0.007474
0.005516	0.003207	0.004104
0.008601	NULL	0.006782
0.003855	0.003613	0.012707
0.004288	0.00736	0.008511
0.011724	0.005017	0.017666
0.004691	0.008857	0.006977
0.00714	0.004388	0.009544
0.002442	0.000539	0.002726
0.014395	0.022253	0.021681
0.000567	0.000908	0.00194
0.004786	0.004776	0.00384
0.008594	0.006564	0.008129
0.010568	0.018811	0.017089
0.001405	0.002782	0.002681
0.000612	0.001799	0.001474
0.005262	NULL	0.015413
0.003209	0.002454	0.003359
0.025121	0.022734	0.021589
0.020622	0.019444	0.016728
0.003441	0.002915	0.00244
0.002913	0.002462	0.002844
0.009637	0.010179	0.010307
0.008138	0.005354	0.010282
0.002962	0.003716	0.002963
0.006403	0.00618	0.008461
0.004611	0.010243	0.011627
0.001634	0.001074	0.003427
0.002472	0.028609	0.024657
0.015181	0.027297	0.030572
0.010178	0.01138	0.01584
0.007121	0.010106	0.011494
0.005965	0.007939	0.016447
0.004427	0.004168	0.007448
0.000287	0.000974	0.001632
0.001336	0.002354	0.002665
0.002545	0.01767	0.01655

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0.005394	0.003962	0.006459
0.009353	0.009484	0.008984
0.00938	0.005153	0.004381
0.002652	0.002353	0.001265
0.004028	0.00036	0.005816
0.001818	0.001393	0.002941
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0.004758	0.009266	0.0065
0.012535	0.009936	0.013286
0.000443	NULL	0.000969
0.000637	0.001872	0.003657
0.013401	0.013413	0.017016
0.004268	0.005155	0.003387
0.019555	0.01597	0.015707
0.003661	0.005262	0.005838
0.002724	0.002308	0.002713
0.005307	0.007751	0.009379
0.000714	0.002168	0.002602
0.002047	0.00661	0.005857
0.001883	0.004427	0.006765
0.0002	0.003564	0.005011
0.001407	0.003492	0.004964
0.005167	0.007277	0.009587
0.008094	0.009235	0.014218
0.006321	0.006984	0.00908
0.000824	0.003833	0.005839
0.017827	0.027095	0.03707
0.002496	0.007828	0.013381
0.01059	0.013955	0.018393
0.009478	0.016809	0.01491
0.008301	0.009656	0.007666
0.00089	0.000895	0.000797
0.006148	0.004866	0.00583
0.004093	0.004762	0.00429
0.013983	0.011883	0.016076
0.00066	0.000212	0.002226
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0.004184	0.0102	0.01126
0.013848	0.021303	0.018445
0.004717	0.005164	0.00646
0.010627	0.012186	0.010798
0.003394	0.005565	0.004479
0.014212	0.013462	0.015002
0.01152	0.011848	0.011776
0.003157	0.004268	0.008219
0.003096	0.004716	0.008797
0.007802	0.008214	0.021322
0.007625	0.015204	0.018363
0.008469	0.003914	0.008083

0.003485	0.003211	0.004086
0.001154	0.003417	0.003443
0.00587	0.005139	0.00611
0.012159	0.012784	0.013419

Cathie Allen

From: Cathie Allen
Sent: Wednesday, 2 March 2022 12:12 PM
To: Justin Howes
Subject: FW: Request for Quote for Report
Attachments: NDNAD_DIFP.xlsx

Hi Justin

We've just received the data back from bdna – they're unsure that they've collected the correct data. Can you please review and advise me?

Cheers
Cathie

Cathie Allen **BSc, MSc (Forensic Science) (She/Her*)**
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

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

p 07 [redacted] **m** [redacted]
a 39 Kessels Road, Coopers Plains, QLD 4108
e [redacted] **w** www.health.qld.gov.au/fss

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

*If you're wondering about the use of pronouns She/Her on this signature block, I encourage you to read some resources available here

From: Troy O'Malley <[redacted]
Sent: Wednesday, 2 March 2022 11:28 AM
To: Cathie Allen <[redacted]
Subject: RE: Request for Quote for Report

Cathie

Apologies for the delay we have been conducting an analysis of the data requested to gauge the effort needed to develop the report.

Please find attached a spreadsheet based on our analysis containing exhibits with a NDNAD and DIFP (No DNA Detected and DNA Insufficient for further processing) result and a subsequent PSTEXT (microcon) performed.

There are very few samples that met this criteria of the 35000+ samples reported as NDNAD and DIFP only ~600 samples have a PSTEXT (microcon) and we have provided a subset of the data you requested notably the pre and post Quant values identified.

Can I confirm this is the report that you would like created or have we misunderstood Justin's instructions?
This will give the barcodes with a result of these type and will contain all the NDNAD and DIFPs reported in that period. Further, we want to also see samples within this output if any had further Technique of PSTEXT, date of PSTEXT, Quant values (above) after PSTEXT, and the Process of RESULT and whatever result line/s that eventuated.

It was my understanding that FSS no longer routinely Microcon samples that are reported as NDNAD and DIFP. I infer from the previous analysis report and the comments Justin has made, that you are actually interested in ascertaining the success of obtaining useable profiles after PSTEXT (microcon) is performed?

We have estimated approximately two days of development and testing to provision a report (based on the aforementioned) allowing FSS to run the report for any arbitrary period, this equates to 80 hrs development time ($2,600 based on day rates for development services in the QITC FR Support Contract) which would include the analysis performed to date.

Happy to schedule a teams call with Justin and yourself to ensure the report we develop is fit for the intended purpose.

Troy

bdna

Troy O'Malley
Product Director (Forensic Software)
[redacted] [redacted] www.bdna.com.au

From: Cathie Allen
Sent: Friday, 18 February 2022 11:15 AM
To: Troy O'Malley <[redacted]
Subject: Request for Quote for Report

Hi Troy

In 2018, Justin Howes compiled the attached as an Options Paper for the QPS to consider. Recently Insp Neville has raised that when samples that were not DNA profiled initially but underwent amplification, a DNA result was obtained. We would like to re-run this data review process and would like to obtain the data from the FR. It would be good if this report was available for us to run at any time (similar to the ACIC report that Dr Peter Culshaw uses within the FR).

Below are the parameters as set out by Justin.

Could you please review the below and provide a quote for cost of undertaking the work.

Please let me know if you have any queries.

Cheers
Cathie

Cathie Allen **BSc, MSc (Forensic Science) (She/Her*)**
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

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

p 07 [redacted] **m** [redacted]
a 39 Kessels Road, Coopers Plains, QLD 4108
e [redacted] **w** www.health.qld.gov.au/fss

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From: Justin Howes <[redacted]
Sent: Wednesday, 16 February 2022 4:09 PM
To: Cathie Allen <[redacted] Paula Brisotto <[redacted]
Subject: parameters for an FR report with quant values

Hi
I think we could request a report from the FR with the following:
- FR Number
- Barcode
- Date Received (01 July 2017 – 31 Dec 2021)
- Date of Process RESULT: Submitted- result pending (SRP)
- Description
- Category (eg. Trace DNA Kit)
- Quant Values: T.SA, T.IPC, T.LA, T.Y, T.SA (DI)
- Process type: RESULT
    - Result to be NDNAD and DIFP (No DNA Detected and DNA Insufficient for further processing)
    - Date of RESULT validation

This will give the barcodes with a result of these type and will contain all the NDNAD and DIFPs reported in that period. Further, we want to also see samples within this output if any had further Technique of PSTEXT, date of PSTEXT, Quant values (above) after PSTEXT, and the Process of RESULT and whatever result line/s that eventuated. The date for this final result validation would be requested too.

With all this, we will be able to see many things, including:
- Total no. of samples with this result in this period

- TAT for received to submitted, TAT for this initial final result (eg. NDNAD, DIFP), TAT to the final result after the PSTEXT
- When PSTEXT (microcon) was performed, the result outcome after this
- The difference between pre and post extraction quants

It will be a huge amount of data I would think, but will give something to drill down into with Excel. The multiple LRs will bulk up the results where pre-FR, non-contributions lines were reported with a grouping line.

Is there anything else that could be part of this data grab? Please let me know if you need any clarification as well.

Thanks
Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

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

p (07) [redacted] **m** [redacted]
a 39 Kessels Road, Coopers Plains, QLD 4108
e [redacted] **w** **www.health.qld.gov.au/fss**

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.

****

****

Cathie Allen

From: Troy O'Malley <[redacted]
Sent: Wednesday, 2 March 2022 1:21 PM
To: Cathie Allen
Subject: RE: Request for Quote for Report

Cathie

I'm available 4pm today or 11am tomorrow are my earliest opportunities.

Troy

From: Cathie Allen <[redacted]
Sent: Wednesday, 2 March 2022 1:16 PM
To: Troy O'Malley <[redacted]
Subject: RE: Request for Quote for Report

Hi Troy

Justin's looked at data and I think it would be best if we had a Teams meeting to ensure all 3 of us are on the same page.

Are you able to advise when you might be available for a chat please?

Cheers
Cathie

Cathie Allen **BSc, MSc (Forensic Science) (She/Her*)**
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

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

p 07[redacted] **m** [redacted]
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Sent: Wednesday, 2 March 2022 11:28 AM
To: Cathie Allen <[redacted]
Subject: RE: Request for Quote for Report

Cathie

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Happy to schedule a teams call with Justin and yourself to ensure the report we develop is fit for the intended purpose.

Troy

bdna
Troy O'Malley
Product Director (Forensic Software)
[redacted] [redacted] www.bdna.com.au

From: Cathie Allen <[redacted]
Sent: Tuesday, 1 March 2022 1:47 PM
To: Troy O'Malley <[redacted]
Subject: FW: Request for Quote for Report

Hi Troy

I was just wondering how the quote was coming along. We'd like to do some data interpretation to ensure that resources are being used efficiently and effectively.

Any update on this would be appreciated.

Cheers
Cathie

Cathie Allen **BSc, MSc (Forensic Science) (She/Her*)**
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

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

p 07 [redacted] **m** [redacted]
a 39 Kessels Road, Coopers Plains, QLD 4108
e [redacted] **w** www.health.qld.gov.au/fss

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

*If you're wondering about the use of pronouns She/Her on this signature block, I encourage you to read some resources available here

From: Cathie Allen
Sent: Friday, 18 February 2022 11:15 AM
To: Troy O'Malley <[redacted]
Subject: Request for Quote for Report

Hi Troy

In 2018, Justin Howes compiled the attached as an Options Paper for the QPS to consider. Recently Insp Neville has raised that when samples that were not DNA profiled initially but underwent amplification, a DNA result was obtained. We would like to re-run this data review process and would like to obtain the data from the FR. It would be good if this report was available for us to run at any time (similar to the ACIC report that Dr Peter Culshaw uses within the FR).

Below are the parameters as set out by Justin.

Could you please review the below and provide a quote for cost of undertaking the work.

Please let me know if you have any queries.

Cheers
Cathie

Cathie Allen **BSc, MSc (Forensic Science) (She/Her*)**
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

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From: Justin Howes <[redacted]
Sent: Wednesday, 16 February 2022 4:09 PM
To: Cathie Allen <[redacted] Paula Brisotto <[redacted]
Subject: parameters for an FR report with quant values

Hi
I think we could request a report from the FR with the following:
- FR Number
- Barcode
- Date Received (01 July 2017 – 31 Dec 2021)
- Date of Process RESULT: Submitted- result pending (SRP)
- Description
- Category (eg. Trace DNA Kit)
- Quant Values: T.SA, T.IPC, T.LA, T.Y, T.SA (DI)
- Process type: RESULT
    - Result to be NDNAD and DIFP (No DNA Detected and DNA Insufficient for further processing)
    - Date of RESULT validation

This will give the barcodes with a result of these type and will contain all the NDNAD and DIFPs reported in that period. Further, we want to also see samples within this output if any had further Technique of PSTEXT, date of PSTEXT, Quant values (above) after PSTEXT, and the Process of RESULT and whatever result line/s that eventuated. The date for this final result validation would be requested too.

With all this, we will be able to see many things, including:

- Total no. of samples with this result in this period
- TAT for received to submitted, TAT for this initial final result (eg. NDNAD, DIFP), TAT to the final result after the PSTEXT
- When PSTEXT (microcon) was performed, the result outcome after this
- The difference between pre and post extraction quants

It will be a huge amount of data I would think, but will give something to drill down into with Excel. The multiple LRs will bulk up the results where pre-FR, non-contributions lines were reported with a grouping line.

Is there anything else that could be part of this data grab? Please let me know if you need any clarification as well.

Thanks
Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

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

p (07) [redacted] **m** [redacted]
a 39 Kessels Road, Coopers Plains, QLD 4108
e [redacted] **w** **www.health.qld.gov.au/fss**

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

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Cathie Allen

Subject:	FR data
Location:	Microsoft Teams Meeting
Start:	Wed 2/03/2022 4:00 PM
End:	Wed 2/03/2022 4:30 PM
Recurrence:	(none)
Meeting Status:	Meeting organizer
Organizer:	Cathie Allen
Required Attendees:	Troy O'Malley; Justin Howes

Let's have a quick chat regarding FR data.

Microsoft Teams meeting

[redacted]

Queensland Government

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SRP YEAR	Priority	ResultEXRMnemonic	Exhibits
2017	1	NDNAD	68
2017	2	DIFP	15
2017	2	NDNAD	1407
2017	3	NDNAD	357
2018	1	DIFP	37
2018	1	NDNAD	40
2018	2	DIFP	1649
2018	2	NDNAD	3246
2018	3	DIFP	2928
2018	3	NDNAD	2115
2019	1	NDNAD	15
2019	2	DIFP	1632
2019	2	NDNAD	3126
2019	3	DIFP	2632
2019	3	NDNAD	1621
2020	1	NDNAD	8
2020	2	DIFP	1714
2020	2	NDNAD	3168
2020	3	DIFP	2347
2020	3	NDNAD	1461
2021	1	NDNAD	10
2021	2	DIFP	1891
2021	2	NDNAD	2938
2021	3	DIFP	2436
2021	3	NDNAD	1536

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B7	0.0008720784	N	0.0000781387	0.0002654322	11.1606483459
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B4	NULL	N	NULL	0.0001976733	NULL	
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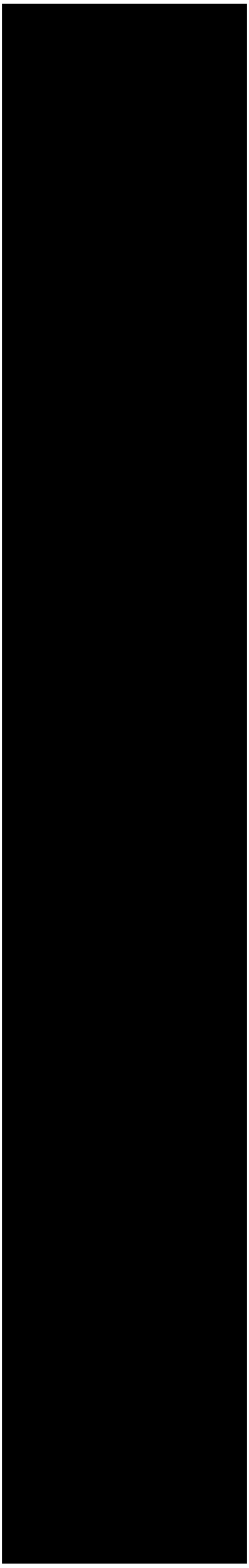

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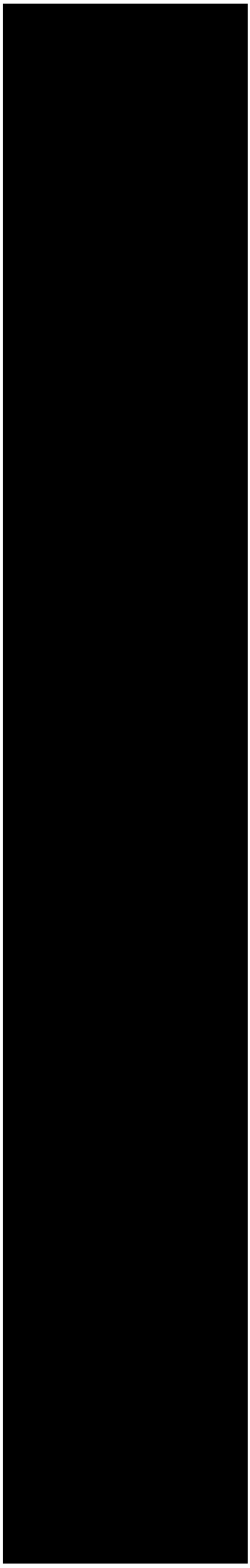

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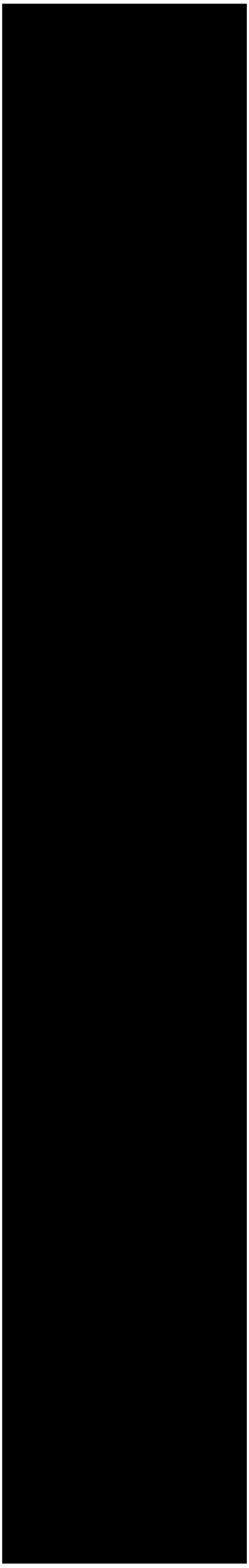

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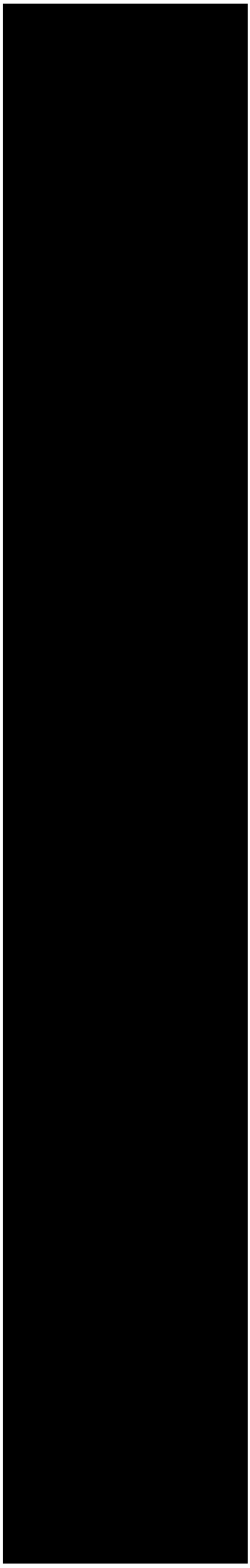

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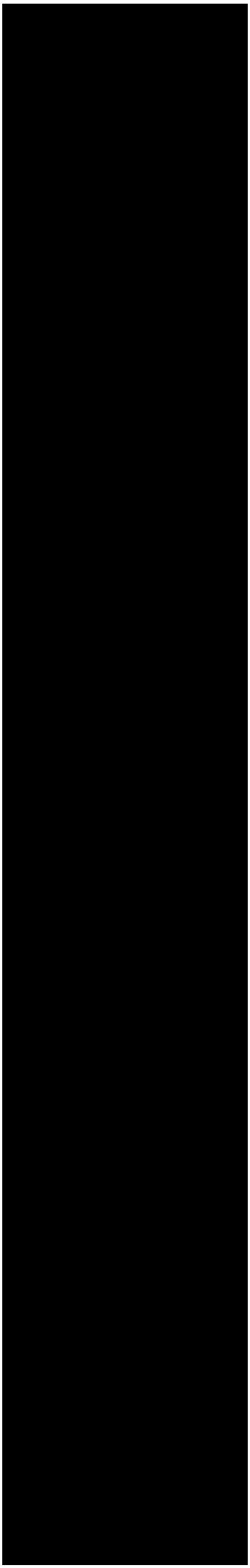

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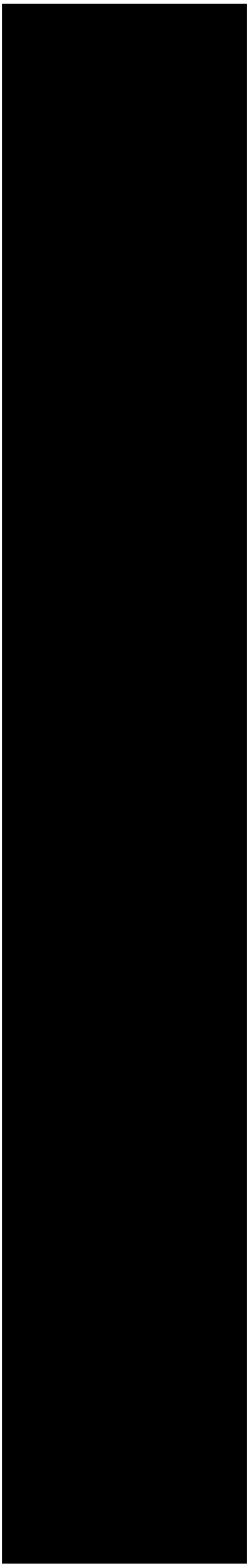

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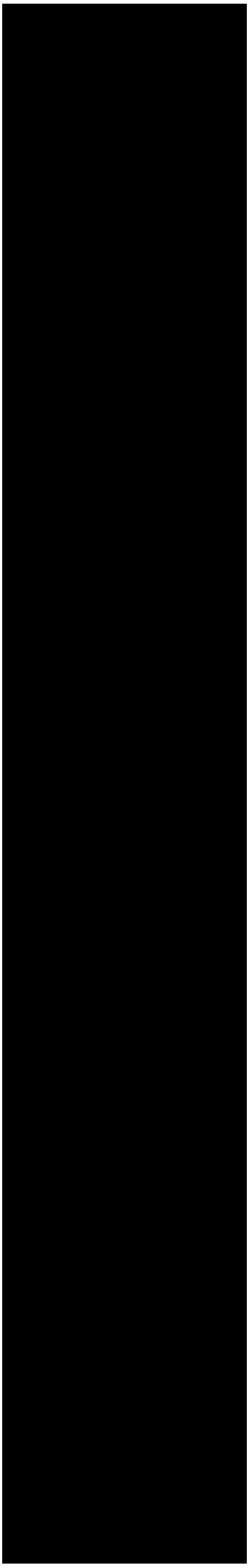

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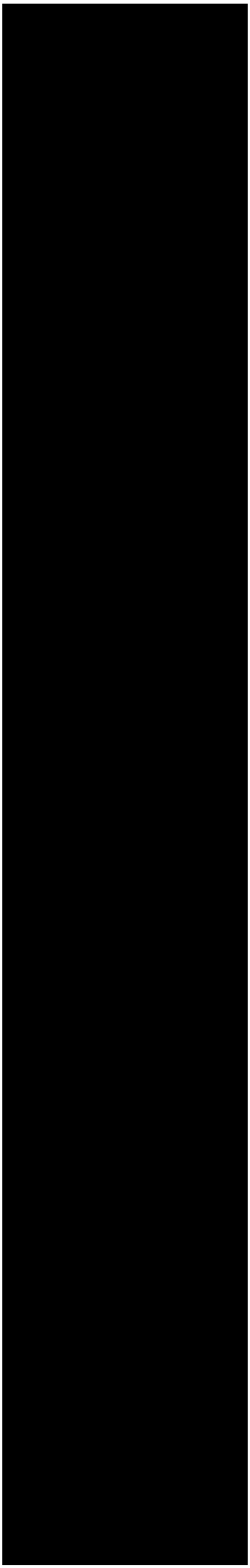

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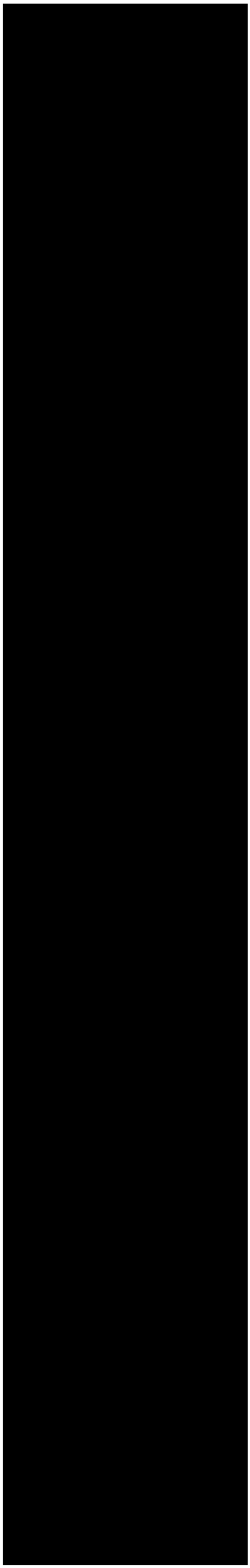

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0.0041893162	0.0065251626	1.6899218559	Y	2021/12/02	
0.0031456195	0.0017829944	0.7296130061	Y	2022/02/02	
0.0122567946	0.0108948816	0.5604596138	N	2022/01/28	
0.0012525771	0.0033828090	3.7386896610	Y	2021/12/14	
0.0026363300	0.0008576957	0.8715062737	Y	2021/12/14	
0.0039118789	0.0034135892	1.0798026323	Y	2021/12/14	
0.0000957560	0.0008775559	15.2930822372	Y	2021/12/14	
0.0016973040	0.0032671236	1.4402536154	Y	2021/12/14	
0.0013292376	0.0011172123	1.8877668381	Y	2021/12/14	
0.0002070340	0.0015465412	8.8465642929	Y	2021/12/14	
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0.0027853532	0.0028467264	1.6218565702	Y	2021/12/14	
0.0061032292	0.0034053563	1.0458309650	Y	2021/12/14	
0.0016020415	0.0011123247	1.9280198812	Y	2021/12/14	
0.0004154335	0.0011322504	5.9928159714	Y	2021/12/14	
0.0054121874	0.0046703410	1.5101574659	Y	2021/12/24	
0.0015305486	0.0017706705	2.5493757725	Y	2021/12/24	
0.0050425404	0.0087494031	1.6505299807	N	2021/12/10	
0.0036997080	0.0072633703	1.5573291779	Y	2021/12/23	
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0.0043365029	0.0045683403	0.6441115141	Y	2022/01/19	
0.0017194536	0.0024442163	0.8371385932	Y	2022/01/19	
0.0065686903	0.0068944516	0.9987673759	N	2022/01/19	
0.0007210767	0.0008829626	3.4841954708	Y	2022/01/25	
0.0040030223	0.0060184579	1.0117315054	Y	2022/01/17	
0.0024070044	0.0049873665	1.9627355337	Y	2022/01/17	
0.0051505733	0.0075780717	1.5650767088	N	2022/01/17	
0.0025075625	0.0016946994	1.0329371691	Y	2022/01/18	
0.0051854248	0.0040297592	0.6454242468	Y	2022/01/18	
0.0013032451	0.0027534072	2.1147954464	Y	2022/01/17	

0.0054468084	0.0029159326	0.8362866640	Y	2022/02/04
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0.0012580671	0.0011998266	1.6334064007	Y	2022/01/17
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0.0076527712	0.0050870772	1.1450566053	N	2022/02/16
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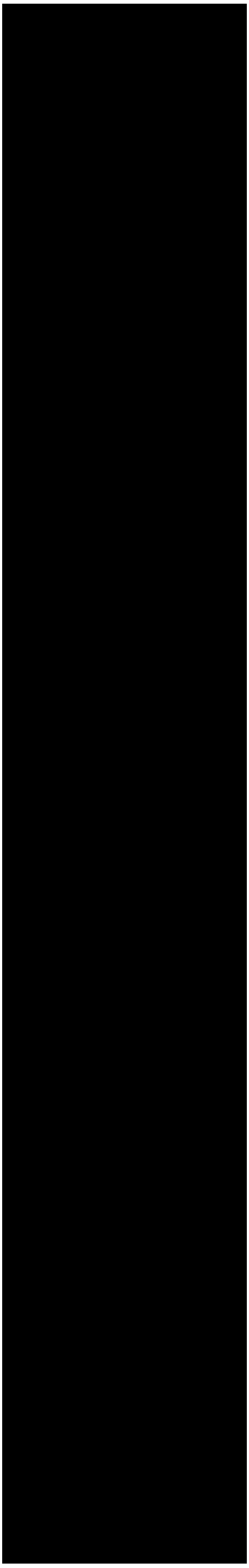
0.0004471786	0.0006126653	2.7584733963	Y	2022/02/02
0.0017194195	0.0031960236	1.4818549156	Y	2022/02/02
0.0016570536	0.0054857619	1.8455127478	Y	2022/02/16



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C12	0.0051325904	N	0.0006374772	0.0034700711	8.0514097214
C6	0.0086124772	N	0.0013246631	0.0050237444	6.5016360283
E2	0.0262499284	N	0.0102579109	0.0032645122	2.5589935780
H10	0.0019571474	N	0.0005609918	0.0006552009	3.4887270927
A11	0.0026048445	N	0.0010386632	0.0036305850	2.5078818798
F10	0.0199379865	N	0.0053065899	0.0238894727	3.7572126389
E10	0.0022156460	N	0.0004255497	0.0016417867	5.2065501213
B7	0.0032057608	N	0.0007599812	0.0008677779	4.2182106972
B7	0.0032057608	N	0.0007599812	0.0008677779	4.2182106972
C7	0.0028362975	N	0.0010471726	0.0003966234	2.7085292339
E6	0.0028838308	N	0.0015665875	0.0050703851	1.8408361673
D6	0.0086874310	N	0.0127825104	0.0111084115	0.6796341538
E2	0.0135157527	N	0.0122474907	0.0154053513	1.1035528183
D7	0.0090944227	N	0.0091602579	0.0022568030	0.9928129315
E7	0.0023651102	N	0.0023208207	0.0015284910	1.0190834999
F7	0.0027600504	N	0.0009939902	0.0001509778	2.7767379284
B11	0.0027407764	N	0.0006016147	0.0003448239	4.5557007790
A12	0.0031636932	N	0.0012882012	0.0005237493	2.4558999538
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F6	0.0045381705	N	0.0022515883	0.0049635167	2.0155417919
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G5	0.0047047040	N	0.0021479588	0.0008472783	2.1903138161
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F2	0.0031725143	N	0.0003782556	0.0019278241	8.3872241974
G10	0.0038003726	N	0.0033605241	0.0025575084	1.1308869123
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A9	0.0051786145	N	0.0026661465	0.0034465841	1.9423593283
A9	0.0051786145	N	0.0026661465	0.0034465841	1.9423593283
A9	0.0051786145	N	0.0026661465	0.0034465841	1.9423593283
A9	0.0051786145	N	0.0026661465	0.0034465841	1.9423593283
A7	0.0028960982	N	0.0017376714	0.0033659390	1.6666547060
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B4	0.0032299021	N	0.0000752325	0.0022476905	42.9322509766
G12	0.0135583859	N	0.0064134980	0.0091435779	2.1140391827
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H11	0.0059545995	N	0.0014513824	0.0010129883	4.1027088165
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B11	0.0048152665	N	0.0010639511	0.0045761843	4.5258345604
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E2	0.0025539638	N	0.0006031492	0.0018895183	4.2343816757
E2	0.0025539638	N	0.0006031492	0.0018895183	4.2343816757
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C9	0.0001934525	N	NULL	NULL	NULL
C9	0.0001934525	N	NULL	NULL	NULL
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H2	0.0214786734	N	0.0028608483	0.0097288247	7.5077986717
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F6	0.0079143336	N	0.0084815305	0.0070346436	0.9331256747
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A7	0.0052672252	N	0.0026517105	0.0048422529	1.9863499403
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F3	0.0058949869	N	0.0022702487	0.0018448605	2.5966260433
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D6	0.0072038951	N	0.0074219028	0.0062581780	0.9706264138
G9	0.0026926883	N	0.0004386270	0.0019978173	6.1389017105
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C9	0.0006251804	N	0.0001043420	NULL	5.9916434288
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A7	0.0117835123	N	0.0113005014	0.0127487723	1.0427423716
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A5	0.0015542391	N	0.0005224670	0.0014991674	2.9748084545
C5	0.0165572315	N	0.0023220174	0.0112176631	7.1305370331
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C8	0.0173189845	N	0.0192235447	0.0089624710	0.9009256363
F6	0.0035835369	N	0.0007431798	0.0003608452	4.8218979836
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H2	0.0026124655	N	0.0003918803	0.0017865436	6.6664886475
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F2	0.0075050835	N	0.0069984533	0.0015100682	1.0723917484
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D9	0.0066962517	N	0.0044702096	0.0056574834	1.4979726076
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E11	0.0077471752	N	0.0065272287	0.0020080230	1.1869010925
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C8	0.0114615764	N	0.0175683163	0.0109468140	0.6524003744
F3	0.0109419459	N	0.0113680447	0.0113919564	0.9625178576
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D7	0.0059396825	N	0.0072717317	NULL	0.8168181777
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H3	0.0055427263	N	0.0019866177	0.0020013617	2.7900316715
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A12	0.0198717192	N	0.0092961593	0.0184044037	2.1376268864
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F10	0.0013391901	N	0.0009798565	0.0018492695	1.3667206764
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G6	0.0144041581	N	0.0113819120	0.0065659764	1.2655305862
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A5	0.0113692563	N	0.0132709090	0.0084947739	0.8567051888
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A6	0.0056407782	N	0.0017118262	0.0026499506	3.2951817513
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C7	0.0184451360	N	0.0138477879	0.0213027168	1.3319915533
D9	0.0064597386	N	0.0047174734	0.0051643034	1.3693217039
C9	0.0107975630	N	0.0106267771	0.0121862674	1.0160713196
G6	0.0044790548	N	0.0033935953	0.0055648279	1.3198553324

A6	0.0150021072	N	0.0142115951	0.0134622529	1.0556244850
B6	0.0117757171	N	0.0115198307	0.0118480120	1.0222127438
D6	0.0082185073	N	0.0031566387	0.0042678677	2.6035628319
C6	0.0087967729	N	0.0030958643	0.0047158552	2.8414595127
E6	0.0213215556	N	0.0078020641	0.0082144532	2.7328095436
F6	0.0183625426	N	0.0076253866	0.0152042406	2.4080803394
H4	0.0080825742	N	0.0084690861	0.0039141444	0.9543620348
B5	0.0040859459	N	0.0034852908	0.0032109942	1.1723400354
C10	0.0034433457	N	0.0011540471	0.0034165182	2.9837133884
B10	0.0061098118	N	0.0058704033	0.0051388354	1.0407823324
C4	0.0134186856	N	0.0121590160	0.0127838077	1.1035996675

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Results

SRP,SEMND,MNS,NDNAD,NWQPS
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SRP,DIFP,QFIH,QCFRQ

SRP,DIFP,CMPU
SRP,DIFP,CMPU
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SRP,DIFP,CMPU
SRP,DIFP,CMPU
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SRP,DIFP,SUFP,CMPU
SRP,DIFP,CMPU
SRP,DIFP,PPUCP
SRP,DIFP,CMPU
SRP,DIFP,CMPU
SRP,DIFP,CMPU
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SRP,DIFP,SUFP,CMPU
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SRP,DIFP,SUFP,CMPU
SRP,SPPDNA,DIFP,SUFP,CMPU
SRP,DIFP,CMPU
SRP,DIFP,1S9L10
SRP,SPPDNA,DIFP,3MX,3MXNC,3MXNC,SCSNC,SCSC4,SCSNC,SCSC7,3MXNC,3MX4,3MXNC,3MXNC,3MX7
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SRP,SPPDNA,DIFP,CMPU
SRP,DIFP,CMPU
SRP,DIFP,CMPU
SRP,DIFP,CMPU
SRP,DIFP,CMPU
SRP,DIFP,CMPU
SRP,DIFP,CMPU
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SRP,DIFP,CMPU
SRP,DIFP,CMPU
SRP,DIFP,CMPU
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SRP,LDIS,DIFP,2MX,2MX7,2MXNC
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SRP,DIFP,SUFP,CMPU
SRP,DIFP
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SRP,DIFP
SRP,DIFP
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SRP,NDNAD,SUFP,CMPU
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SRP,DIFP,TRQ,CMPU
SRP,LDIS,DIFP,TRQ,CMPU,SUFP

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SRP,DIFP,TRQ,CMPU
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(NC

EVDEXC,3MXR7,EVDEXC,EVDEXC,SCANM,SCANM,SCANM,SCANM,SCANM,SCANM,SCANM,EVDEXC,SUFV

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C,2MXNC,2MXNC,2MXNC,2MXNC,SCSNC,SCSNC,SCSNC,SCSNC

N,SCSNC,SCSNC,3MXNC

*N*C,3MXCON,SCANM,SCANM,EVDEXC

Cathie Allen

From: Troy O'Malley <[redacted]
Sent: Thursday, 3 March 2022 4:06 PM
To: Cathie Allen
Subject: FW: Request for Quote for Report
Attachments: NDNAD_DIFP_DATA.xlsx

Cathie

Based on the discussions yesterday, please find attached the updated data extract for NDNAD and DIFP samples:

- TAB 1 - total exhibits broken down by year, priority and result;
- TAB 2 - extracted data where a subsequent PSTEXT (microcon) was performed (including results reported for each sample)

It will take approximately 60 hrs of development and testing to provision the report (equivalent to the extract provided) allowing FSS to run the report for any arbitrary period. The 60 hrs development time equates to $1,950 based on day rates for development services in the QITC FR Support Contract (this will be inclusive of the analysis and extracts performed to date).

Will we invoice for this work or will it be drawn from the development hours included in the FR IP Commercialisation agreement?

Troy

bdna
Troy O'Malley
Product Director (Forensic Software)
[redacted] [redacted] www.bdna.com.au

From: Cathie Allen <[redacted]
Sent: Tuesday, 1 March 2022 1:47 PM
To: Troy O'Malley <[redacted]
Subject: FW: Request for Quote for Report

Hi Troy

I was just wondering how the quote was coming along. We'd like to do some data interpretation to ensure that resources are being used efficiently and effectively.

Any update on this would be appreciated.

Cheers
Cathie

Cathie Allen **BSc, MSc (Forensic Science) (She/Her*)**
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

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

p 07 [redacted] **m** [redacted]
a 39 Kessels Road, Coopers Plains, QLD 4108
e [redacted] **w** www.health.qld.gov.au/fss

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

*If you're wondering about the use of pronouns She/Her on this signature block, I encourage you to read some resources available here

From: Cathie Allen
Sent: Friday, 18 February 2022 11:15 AM
To: Troy O'Malley <[redacted]
Subject: Request for Quote for Report

Hi Troy

In 2018, Justin Howes compiled the attached as an Options Paper for the QPS to consider. Recently Insp Neville has raised that when samples that were not DNA profiled initially but underwent amplification, a DNA result was obtained. We would like to re-run this data review process and would like to obtain the data from the FR. It would be good if this report was available for us to run at any time (similar to the ACIC report that Dr Peter Culshaw uses within the FR).

Below are the parameters as set out by Justin.

Could you please review the below and provide a quote for cost of undertaking the work.

Please let me know if you have any queries.

Cheers
Cathie

Cathie Allen **BSc, MSc (Forensic Science) (She/Her*)**
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the

Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

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

p 07 [redacted] **m** [redacted]
a 39 Kessels Road, Coopers Plains, QLD 4108
e [redacted] **w** www.health.qld.gov.au/fss

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*If you're wondering about the use of pronouns She/Her on this signature block, I encourage you to read some resources available here

From: Justin Howes <[redacted]
Sent: Wednesday, 16 February 2022 4:09 PM
To: Cathie Allen <[redacted] Paula Brisotto <[redacted]
Subject: parameters for an FR report with quant values

Hi
I think we could request a report from the FR with the following:
- FR Number
- Barcode
- Date Received (01 July 2017 – 31 Dec 2021)
- Date of Process RESULT: Submitted- result pending (SRP)
- Description
- Category (eg. Trace DNA Kit)
- Quant Values: T.SA, T.IPC, T.LA, T.Y, T.SA (DI)
- Process type: RESULT
    - Result to be NDNAD and DIFP (No DNA Detected and DNA Insufficient for further processing)
    - Date of RESULT validation

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Is there anything else that could be part of this data grab? Please let me know if you need any clarification as well.

Thanks

Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

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

p (07) [redacted] **m** [redacted]
a 39 Kessels Road, Coopers Plains, QLD 4108
e [redacted] **w** www.health.qld.gov.au/fss

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

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****

Cathie Allen

From: Lara Keller
Sent: Friday, 4 March 2022 11:57 AM
To: Cathie Allen
Subject: RE: Request for Quote for Report

Thanks Cathie
If you consider the data to be valuable and that the report will assist you, I am happy to support.
Thanks and kind regards
Lara

Lara Keller, B App Sc (MLS), Grad Cert Health Mgt, MAIMS, CMgr FIML
A/Executive Director

Forensic and Scientific Services
Prevention Division, Queensland Health

m [redacted]
a Administration, 39 Kessels Road, Coopers Plains
e [redacted] **w** **www.health.qld.gov.au/fss**

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From: Cathie Allen <[redacted]
Sent: Friday, 4 March 2022 9:44 AM
To: Lara Keller <[redacted]
Subject: FW: Request for Quote for Report

Hi Lara

bdna have provided the data and Justin's currently reviewing it. They've also advised that it would 12 hours to develop the report within the new version of the FR.

Do we want to proceed with the quote and pay for the development or do we want to ask about using development hours for this? There are 750 development hours per year in the agreement. I believe the agreement is from October to October each year (as that's when the agreement was signed).

Cheers
Cathie

Cathie Allen **BSc, MSc (Forensic Science) (She/Her*)**
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
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Prevention Division, Queensland Health

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From: Troy O'Malley <[redacted]
Sent: Friday, 4 March 2022 9:40 AM
To: Cathie Allen <[redacted]
Subject: FW: Request for Quote for Report

Cathie

Based on the discussions yesterday, please find attached the updated data extract for NDNAD and DIFP samples:

- TAB 1 - total exhibits broken down by year, priority and result;
- TAB 2 - extracted data where a subsequent PSTEXT (microcon) was performed (including results reported for each sample)

It will take approximately 12 hrs of development and testing to provision the report (equivalent to the extract provided) allowing FSS to run the report for any arbitrary period. The development time equates to $1,950 based on day rates for development services in the QITC FR Support Contract (this will be inclusive of the analysis and extracts performed to date).

Will we invoice for this work or will it be drawn from the development hours included in the FR IP Commercialisation agreement?

Troy

bdna
Troy O'Malley
Product Director (Forensic Software)
[redacted] [redacted] www.bdna.com.au

Cathie Allen

From: Cathie Allen
Sent: Friday, 4 March 2022 9:44 AM
To: Troy O'Malley
Subject: RE: Request for Quote for Report

Thanks Troy. Justin reviewing the data now, and I'll get back to you regarding the quote.

Cheers
Cathie

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Troy

bdna | **Troy O'Malley**
Product Director (Forensic Software)
[redacted] [redacted] www.bdna.com.au

From: Cathie Allen <[redacted]
Sent: Tuesday, 1 March 2022 1:47 PM
To: Troy O'Malley <[redacted]
Subject: FW: Request for Quote for Report

Hi Troy

I was just wondering how the quote was coming along. We'd like to do some data interpretation to ensure that resources are being used efficiently and effectively.

Any update on this would be appreciated.

Cheers
Cathie

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From: Cathie Allen
Sent: Friday, 18 February 2022 11:15 AM
To: Troy O'Malley <[redacted]
Subject: Request for Quote for Report

Hi Troy

In 2018, Justin Howes compiled the attached as an Options Paper for the QPS to consider. Recently Insp Neville has raised that when samples that were not DNA profiled initially but underwent amplification, a DNA result was obtained. We would like to re-run this data review process and would like to obtain the data from the FR. It would be good if this report was available for us to run at any time (similar to the ACIC report that Dr Peter Culshaw uses within the FR).

Below are the parameters as set out by Justin.

Could you please review the below and provide a quote for cost of undertaking the work.

Please let me know if you have any queries.

Cheers
Cathie

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From: Justin Howes <[redacted]
Sent: Wednesday, 16 February 2022 4:09 PM
To: Cathie Allen <[redacted] Paula Brisotto <[redacted]
Subject: parameters for an FR report with quant values

Hi
I think we could request a report from the FR with the following:
- FR Number
- Barcode
- Date Received (01 July 2017 – 31 Dec 2021)
- Date of Process RESULT: Submitted- result pending (SRP)
- Description
- Category (eg. Trace DNA Kit)
- Quant Values: T.SA, T.IPC, T.LA, T.Y, T.SA (DI)
- Process type: RESULT
    - Result to be NDNAD and DIFP (No DNA Detected and DNA Insufficient for further processing)
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It will be a huge amount of data I would think, but will give something to drill down into with Excel. The multiple LRs will bulk up the results where pre-FR, non-contributions lines were reported with a grouping line.

Is there anything else that could be part of this data grab? Please let me know if you need any clarification as well.

Thanks
Justin

Justin Howes
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Cathie Allen

From: Cathie Allen
Sent: Wednesday, 9 March 2022 12:06 PM
To: Troy O'Malley
Subject: RE: Request for Quote for Report

Hi Troy

As this is relatively easy, could you do a new extract with the Priority column added please?

Cheers
Cathie

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From: Troy O'Malley <[redacted]
Sent: Wednesday, 9 March 2022 12:02 PM
To: Cathie Allen <[redacted]
Subject: RE: Request for Quote for Report

Cathie

The priority can be added to samples listed in TAB 2 relatively easily without a change to the estimate provided.

Do you require a new export of data now or when we provision the report?

Troy

From: Cathie Allen <[redacted]
Sent: Wednesday, 9 March 2022 10:22 AM
To: Troy O'Malley <[redacted]
Subject: RE: Request for Quote for Report

Hi Troy

Justin has reviewed the data and done some interpretation. We were wondering how easy or hard it would be to have the Priority listed in a column for Tab 2 (rather than just the total, we could separate the raw data into priorities). Are you able to let me know if this is easy to do for this lot of data.

Cheers
Cathie

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Sent: Thursday, 3 March 2022 4:06 PM
To: Cathie Allen <[redacted]
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It will take approximately 60 hrs of development and testing to provision the report (equivalent to the extract provided) allowing FSS to run the report for any arbitrary period. The 60 hrs development time equates to $1,950 based on day rates for development services in the QITC FR Support Contract (this will be inclusive of the analysis and extracts performed to date).

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[redacted]

RPDate	AnalyticalPriority	NDNADDate
2017/07/20	2	2017/08/02
2018/02/19	1	NULL
2018/02/19	1	NULL
2018/02/19	1	NULL
2018/02/22	2	NULL
2018/03/13	3	NULL
2018/03/13	3	NULL
2018/04/04	3	NULL
2018/04/04	3	NULL
2018/04/04	2	2018/04/12
2018/04/04	2	2018/04/12
2018/04/04	2	2018/04/17
2018/04/05	1	NULL
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2018/06/21	2	NULL
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[redacted]

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2019/09/06	2	NULL
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2019/09/20	2	NULL
2019/09/20	2	NULL

[redacted]

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2019/10/02	3	NULL
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2019/11/25	2	NULL
2019/11/25	2	NULL
2019/12/05	2	NULL
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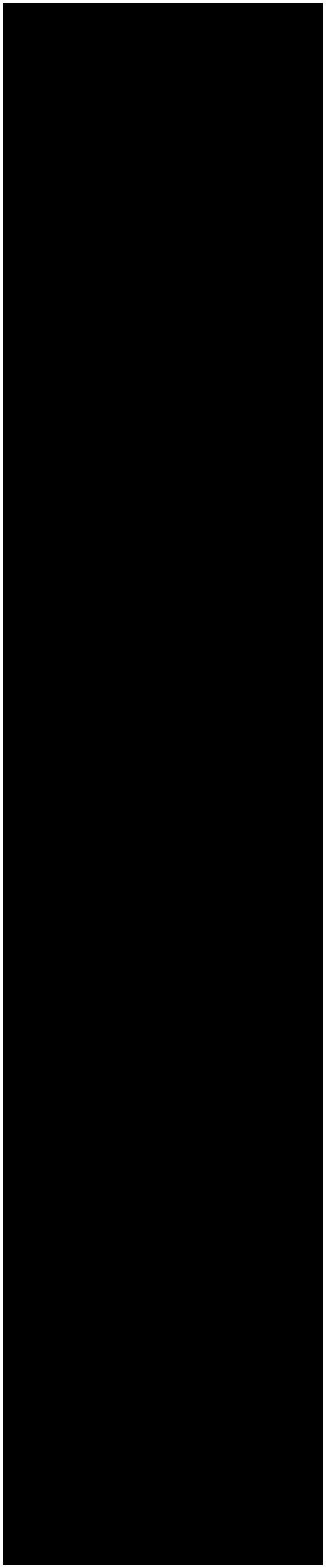

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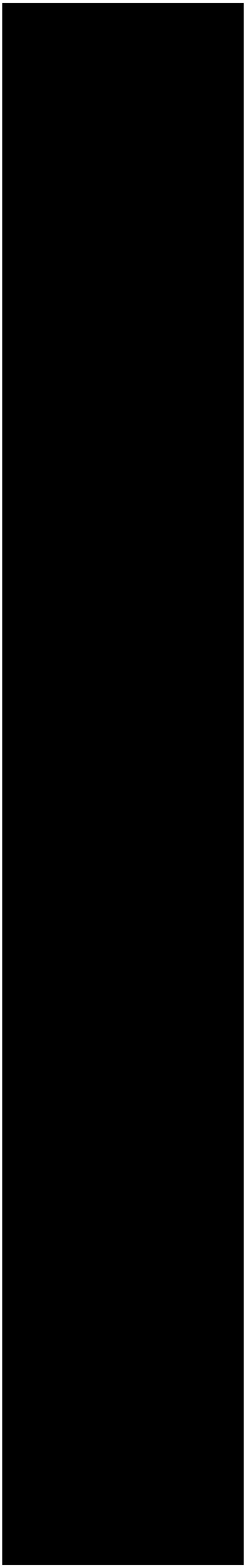

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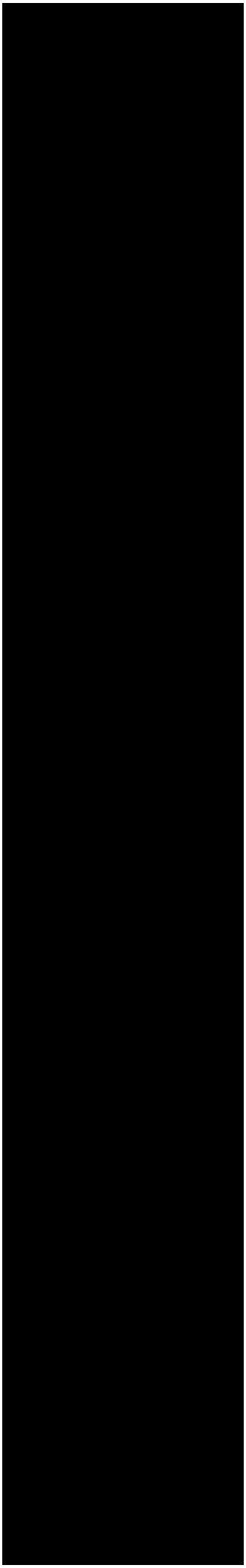

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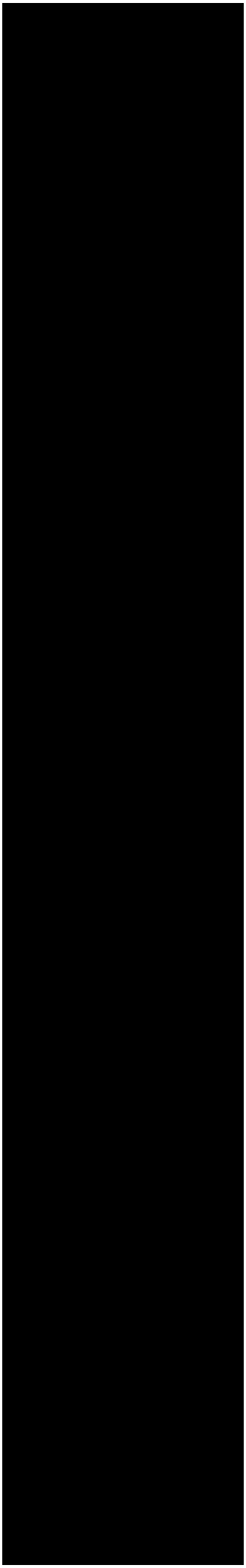

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0.0042085671	N	0.0029311019	0.0007097430	1.4358310699	Y
0.0014509142	N	0.0000576474	0.0011122335	25.1687602997	Y
0.0017401137	N	0.0008154355	0.0006320904	2.1339683533	Y
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0.0010791066	N	0.0001307414	0.0009768333	8.2537450790	Y
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0.0012994426	N	0.0002697635	NULL	4.8169703484	Y
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0.0065081790	N	0.0092630405	0.0104913153	0.7025964260	N
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0.0039211079	N	0.0021719630	0.0004925879	1.8053290844	Y
0.0045658373	N	0.0017904467	0.0023588603	2.5501108170	N
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0.0030790539	N	0.0011178841	0.0028030523	2.7543590069	N
0.0010068675	N	0.0005215699	0.0007270714	1.9304556847	Y
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0.0015600380	N	0.0020538419	0.0034700485	0.7595705986	N
0.0024960237	N	0.0004973973	0.0016472776	5.0181694031	Y
0.0020327291	N	0.0032420591	0.0044317292	0.6269870400	N
0.0068200794	N	0.0075299414	0.0141947744	0.9057281017	N
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0.0012592088	N	0.0005634392	0.0011393136	2.2348620892	Y
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0.0012260207	N	0.0005636811	0.0010690175	2.1750254631	Y
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0.0053408309	N	0.0023902939	0.0049250741	2.2343826294	N
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0.0060314517	N	0.0020041463	0.0020981100	3.0094866753	N
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0.0024076027	N	0.0006954789	0.0022872814	3.4617912769	Y
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0.0011496816	N	0.0002392012	0.0016983348	4.8063383102	Y
0.0072412486	N	0.0026274673	0.0063301669	2.7559804916	N
0.0026053020	N	0.0001707802	0.0015303165	15.2552928925	Y
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0.0028976088	N	0.0025254458	0.0010760659	1.1473653316	N
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0.0010910699	N	0.0003219737	0.0006332264	3.3886928558	Y
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0.0071725990	N	0.0022179652	0.0067927330	3.2338645458	Y
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0.0032545500	N	0.0011416136	0.0038853299	2.8508334160	Y
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0.0011432983	N	0.0020728698	0.0017901780	0.5515533686	Y
0.0011468530	N	0.0001008322	0.0018412833	11.3738765717	Y
0.0021035164	N	0.0019196563	0.0024157097	1.0957776308	Y
0.0039890916	N	0.0016348450	0.0035267395	2.4400427341	Y
0.0037237380	N	0.0016150682	0.0026390916	2.3056228161	Y
0.0043871724	N	0.0024034104	0.0058686566	1.8253946304	Y
0.0041746832	N	0.0024352300	0.0023504044	1.7142870426	Y
0.0058908979	N	0.0042682765	0.0040913504	1.3801584244	Y
0.0037031486	N	0.0024755260	0.0025544323	1.4959037304	Y
0.0056396797	N	0.0038637014	0.0068440670	1.4596573114	Y
0.0036322731	N	0.0012878835	0.0028716750	2.8203427792	Y
0.0049665114	N	0.0021155493	0.0049408483	2.3476226330	Y
0.0079731001	N	0.0012106020	0.0050615100	6.5860619545	Y
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0.0033927388	N	0.0044296151	NULL	0.7659217715	Y
0.0060626077	N	0.0053346264	0.0014544211	1.1364634037	Y
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0.0067011523	N	0.0053388914	0.0066230008	1.2551580667	N
0.0021988212	N	0.0018135130	0.0024191539	1.2124650478	Y

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0.0017133780	N	0.0015318013	0.0011663103	1.1185380220	Y
0.0033922526	N	0.0027645654	0.0042251716	1.2270473242	Y
0.0011817815	N	0.0005717396	0.0022858887	2.0669927597	Y
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0.0014153575	N	0.0009765354	0.0014492813	1.4493663311	Y
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0.0065114619	N	0.0044391737	0.0003014832	1.4668184519	Y
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0.0019039247	N	0.0013273961	0.0016794552	1.4343304634	Y
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0.0010552390	N	0.0001654663	0.0007106513	6.3773646355	Y
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0.0084406454	N	0.0029659336	0.0076588858	2.8458645344	Y
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0.0049495045	N	0.0071733738	0.0059915711	0.6899827719	Y
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0.0017850955	N	0.0019065439	0.0033028268	0.9362992048	Y
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0.0022356103	N	0.0015236202	0.0002313897	1.4673014879	Y
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0.0083392439	N	0.0091714710	0.0079844138	0.9092591405	N
0.0069852429	N	0.0108056553	0.0067564216	0.6464432478	N
0.0042327135	N	0.0007402981	0.0025932502	5.7175798416	Y
0.0023002329	N	0.0018227807	0.0020135371	1.2619361877	Y
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0.0056444542	N	0.0053359657	0.0069335382	1.0578130484	N
0.0019374803	N	0.0021002532	0.0019055082	0.9224984050	Y
0.0021854762	N	0.0016158489	0.0018731795	1.3525251150	Y
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0.0061565479	N	0.0031000366	0.0079089208	1.9859597683	Y
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0.0024001442	N	0.0010252225	0.0014058907	2.3410959244	Y
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0.0019952729	N	0.0009013168	0.0007619681	2.2137310505	Y
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0.0022562081	N	0.0016359848	0.0015057785	1.3791131973	Y
0.0080306921	N	0.0090320911	0.0073149987	0.8891288042	N
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0.0021965143	N	0.0027760705	0.0004666634	0.7912314534	Y
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0.0046349429	N	0.0055827531	0.0032900432	0.8302252889	Y
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0.0014043751	N	0.0015837287	0.0019907395	0.8867523074	Y
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0.0060644126	N	0.0066952477	0.0039658183	0.9057787061	Y
0.0020549349	N	0.0012580671	0.0011998266	1.6334064007	Y
0.0034534079	N	0.0003560927	0.0007177105	9.6980590820	Y
0.0075952802	N	0.0023849842	0.0023981798	3.1846249104	Y
0.0066053164	N	0.0023140840	0.0032327182	2.8543977737	Y
0.0087628560	N	0.0076527712	0.0050870772	1.1450566053	N
0.0023882836	N	0.0024911629	0.0026227648	0.9587023258	Y
0.0012335301	N	0.0004471786	0.0006126653	2.7584733963	Y
0.0025479302	N	0.0017194195	0.0031960236	1.4818549156	Y
0.0015494593	N	0.0010720657	0.0029448930	1.4453026056	Y
0.0030581136	N	0.0016570536	0.0054857619	1.8455127478	Y

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2018/11/22		C12	0.0051325904	N	0.0006374772
2018/11/23		C6	0.0086124772	N	0.0013246631
2018/03/27		E2	0.0262499284	N	0.0102579109
2018/06/06		H10	0.0019571474	N	0.0005609918
2018/06/06		A11	0.0026048445	N	0.0010386632
2018/06/06		F10	0.0199379865	N	0.0053065899
2018/06/06		E10	0.0022156460	N	0.0004255497
2018/04/20		B7	0.0032057608	N	0.0007599812
2018/04/20		B7	0.0032057608	N	0.0007599812
2018/04/20		C7	0.0028362975	N	0.0010471726
2018/04/27		E6	0.0028838308	N	0.0015665875
2018/04/27		D6	0.0086874310	N	0.0127825104
2018/04/27		E2	0.0135157527	N	0.0122474907
2018/04/20		D7	0.0090944227	N	0.0091602579
2018/04/20		E7	0.0023651102	N	0.0023208207
2018/04/20		F7	0.0027600504	N	0.0009939902
2018/11/22		B11	0.0027407764	N	0.0006016147
2018/11/22		A12	0.0031636932	N	0.0012882012
2018/06/11		C5	0.0071296664	N	0.0037473142
2018/06/06		F6	0.0045381705	N	0.0022515883
2018/09/28		G3	0.0059592305	N	0.0017121197
2018/05/30		G2	0.0035065021	N	0.0006194481
2018/05/30		D2	0.0097787194	N	0.0069753421
2018/05/30		E2	0.0038524522	N	0.0003713430
2019/07/31		G5	0.0047047040	N	0.0021479588
2019/07/31		H5	0.0024941417	N	0.0025653022
2018/05/30		F2	0.0031725143	N	0.0003782556
2018/06/06		G10	0.0038003726	N	0.0033605241
2018/10/26		E2	0.0070884181	N	0.0054412750
2018/09/05		A9	0.0051786145	N	0.0026661465
2018/09/05		A9	0.0051786145	N	0.0026661465
2018/09/05		A9	0.0051786145	N	0.0026661465
2018/09/05		A9	0.0051786145	N	0.0026661465
2018/06/06		A7	0.0028960982	N	0.0017376714
2018/06/29		C11	0.0010256594	N	0.0005683876
2018/06/21		G8	0.0086324755	N	0.0084831594
2018/07/05		A4	0.0152310543	N	0.0055392790
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2018/07/05		B4	0.0032299021	N	0.0000752325
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2020/03/30		A11	0.0037577513	N	0.0026221422

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2020/03/31		F2	0.0026078804 N	NULL
2018/11/22		G9	0.0221445002 N	0.0120148575
2018/11/20		B3	0.0174718797 N	0.0065401844
2020/03/31		E2	0.0025539638 N	0.0006031492
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2018/11/28		G2	0.0209282134 N	0.0034854489
2018/09/05		C12	0.0047643567 N	0.0013235862
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2018/12/06		D8	0.0033330724 N	0.0044280509
2018/12/06		G8	0.0108984560 N	0.0084586749
2018/12/06		E8	0.0015556378 N	0.0007091914
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2018/11/20		G2	0.0089645041 N	0.0007527759
2018/11/29		A4	0.0023387922 N	0.0010597761
2018/11/20		E2	0.0036315226 N	0.0016284438
2018/11/29		G3	0.0019071884 N	0.0009350959
2018/10/08		C5	0.0060020755 N	0.0041702017
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2018/12/13		C12	0.0100487862 N	0.0016904217
2018/11/28		D3	0.0159141216 N	0.0024088738
2018/10/26		D12	0.0022894598 N	0.0000576712
2018/12/13		E12	0.0087323636 N	0.0037218607
2018/11/07		A12	0.0018580039 N	0.0001698314
2019/01/03		C12	0.0124275163 N	0.0055846511
2018/11/28		B3	0.0207037404 N	0.0057798349
2019/12/19		F3	0.0101824487 N	0.0030895672
2018/11/16		A10	0.0030895660 N	0.0011700960
2018/10/30		E2	0.0038881127 N	0.0028045247
2018/11/05		E11	0.0060203020 N	0.0031638353
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2018/11/13		D4	0.0092917383	N	0.0061779632
2018/11/15		G4	0.0104418639	N	0.0151479254
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2018/11/13		G2	0.0017450707	Y	NULL
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2018/11/28		E3	0.0020231595	N	0.0022406229
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2018/11/16		E2	0.0110985329	N	0.0020799569
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2018/11/16		H2	0.0055913338	N	0.0029952687
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2019/02/15		G2	0.0082019418	N	0.0041024056
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2019/05/30		E2	0.0221285690	N	0.0123434616
2019/06/06		G2	0.0028254809	N	0.0018680778
2019/06/26		A8	0.0045616068	N	0.0023727771
2019/06/26		H7	0.0115121054	N	0.0070530362
2020/03/25		H2	0.0214786734	N	0.0028608483
2019/09/19		E5	0.0010261066	N	0.0005807465
2019/09/19		F5	0.0086264051	N	0.0063400352
2020/06/29		H2	0.0073631518	N	0.0035189611
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2019/10/24		A12	0.0071638334	N	0.0025581040
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2019/11/18		H6	0.0078180442	N	0.0073250034
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2020/11/12		C8	0.0173189845	N	0.0192235447
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2021/10/01		B8	0.0014833984 N	0.0001954614
2021/10/01		H7	0.0071110143 N	0.0050412556
2021/10/01		G7	0.0086085694 N	0.0114930961
2021/10/01		F7	0.0166408215 N	0.0094361873
2021/10/06		D5	0.0059387260 N	0.0015464609

2021/10/01	[redacted]	A8	0.0040982170 N	0.0011745500
2021/10/06		H5	0.0026611020 N	0.0006029406
2021/10/14		H3	0.0010668167 N	NULL
2021/10/14		A4	0.0022352696 N	0.0006841241
2021/10/14		B4	0.0014766080 N	0.0012505861
2021/10/14		C4	0.0027071401 N	0.0014012984
2021/10/14		D4	0.0083961664 N	0.0078370050
2021/10/19		E5	0.0036554600 N	0.0064654914
2021/10/19		F5	0.0063147661 N	0.0087311091
2021/10/08		C10	0.0051341075 N	0.0057964129
2021/10/19		A6	0.0100139482 N	0.0073489025
2021/10/08		B10	0.0165915284 N	0.0168071669
2021/10/08		A10	0.0049754544 N	0.0041672233
2021/10/14		E4	0.0089717191 N	0.0071619428
2021/10/21		F10	0.0053601055 N	0.0018120273
2021/11/30		D4	0.0020012048 N	0.0014695449
2021/12/02		F6	0.0033317145 N	0.0018727721
2021/10/19		B6	0.0074742115 N	0.0115361055
2021/10/19		C6	0.0041036657 N	0.0055155358
2021/12/01		F10	0.0067820037 N	0.0086009428
2021/10/21		A11	0.0127073070 N	0.0038552352
2021/10/21		H10	0.0085105449 N	0.0042880271
2021/11/26		C3	0.0176655687 N	0.0117241051
2021/10/26		E9	0.0069772108 N	0.0046907212
2021/12/02		G6	0.0095436526 N	0.0071401699
2021/12/02		H6	0.0027262249 N	0.0024421769
2021/11/09		B9	0.0216813646 N	0.0143952081
2021/11/19		H11	0.0019403410 N	0.0005673316
2021/11/01		G7	0.0038399608 N	0.0047856336
2021/11/01		H7	0.0081286244 N	0.0085942699
2021/12/10		C6	0.0170885175 N	0.0105680237
2021/12/10		B6	0.0026811117 N	0.0014050694
2021/11/02		F2	0.0014741275 N	0.0006116744
2021/11/02		F3	0.0154130692 N	0.0052623395
2021/11/02		C3	0.0033594018 N	0.0032091849
2021/11/02		D3	0.0215889104 N	0.0251213536
2021/11/02		E3	0.0167276524 N	0.0206215177
2021/11/02		G3	0.0024403196 N	0.0034411773
2021/12/17		B3	0.0028436829 N	0.0029132452
2021/12/17		A3	0.0103066936 N	0.0096372431
2021/12/17		C3	0.0102823824 N	0.0081379320
2021/11/18		A9	0.0029626309 N	0.0029624037
2021/11/18		H8	0.0084606959 N	0.0064027281
2021/11/12		E3	0.0116270725 N	0.0046108002
2021/11/26		E3	0.0034268573 N	0.0016341443
2022/03/01		G9	0.0036415684 N	0.0013478937
2022/03/01		F9	0.0029801333 N	0.0009788017
2022/03/01		E9	0.0073866118 N	0.0027921314
2022/03/01		H9	0.0045564119 N	0.0021847242
2021/11/12		F3	0.0246566329 N	0.0024722635

2021/11/12	[redacted]	E2	0.0305721574	N	0.0151814027
2021/11/12		G3	0.0158397313	N	0.0101777278
2021/12/01		A9	0.0114944717	N	0.0071212291
2021/11/18		F9	0.0164469462	N	0.0059648701
2021/11/18		E9	0.0074483790	N	0.0044271951
2021/11/18		B9	0.0016324678	N	0.0002866763
2021/11/18		C9	0.0026646762	N	0.0013359908
2021/12/08		H2	0.0165497325	N	0.0025452727
2021/11/18		D9	0.0021837212	N	0.0012177886
2021/12/01		B9	0.0064589959	N	0.0053939167
2022/03/01		D9	0.0052170502	N	0.0025994808
2021/11/30		E4	0.0089844409	N	0.0093529820
2022/02/02		E9	0.0043810885	N	0.0093799587
2022/02/02		F9	0.0012652935	N	0.0026516260
2021/11/26		F3	0.0058156056	N	0.0040280651
2021/12/01		C9	0.0029409607	N	0.0018182035
2021/12/14		A7	0.0174170397	N	0.0112930518
2021/12/14		F7	0.0064997491	N	0.0047576083
2021/12/14		D7	0.0132861808	N	0.0125348782
2021/12/01		H10	0.0009691101	N	0.0004427599
2021/12/02		D6	0.0036567755	N	0.0006366727
2021/12/02		E6	0.0170160364	N	0.0134007847
2022/02/02		A10	0.0033867657	N	0.0042682681
2022/01/28		A4	0.0157071371	N	0.0195551533
2021/12/14		D8	0.0058378745	N	0.0036612174
2021/12/14		E8	0.0027133801	N	0.0027240401
2021/12/14		G8	0.0093788030	N	0.0053073377
2021/12/14		H8	0.0026021800	N	0.0007135301
2021/12/14		F8	0.0058574849	N	0.0020472039
2021/12/14		H6	0.0067654690	N	0.0018833645
2021/12/14		G6	0.0050110193	N	0.0001997452
2021/12/14		B7	0.0049636159	N	0.0014070191
2021/12/14		C7	0.0095873792	N	0.0051669781
2021/12/14		B9	0.0142182410	N	0.0080936849
2021/12/14		A9	0.0090801436	N	0.0063212714
2021/12/14		E7	0.0058389874	N	0.0008243521
2021/12/24		G5	0.0370696373	N	0.0178268794
2021/12/24		H5	0.0133808050	N	0.0024962078
2022/03/07		C6	0.0057228184	N	0.0067967367
2021/12/10		H6	0.0183929913	N	0.0105904173
2021/12/23		F6	0.0149096604	N	0.0094778230
2022/01/19		B5	0.0076655783	N	0.0083005223
2022/01/19		D5	0.0007966777	N	0.0008904721
2022/01/19		C5	0.0058301659	N	0.0061477376
2022/01/19		A5	0.0042903782	N	0.0040928801
2022/01/19		H4	0.0160759706	N	0.0139832599
2022/01/25		C3	0.0022261019	N	0.0006596518
2022/01/17		A7	0.0174183846	N	0.0122206453
2022/01/17		H6	0.0112599367	N	0.0041844202
2022/01/17		C7	0.0184451360	N	0.0138477879

2022/01/18	[redacted]	D9	0.0064597386	N	0.0047174734
2022/01/18		C9	0.0107975630	N	0.0106267771
2022/01/17		G6	0.0044790548	N	0.0033935953
2022/02/04		A6	0.0150021072	N	0.0142115951
2022/02/04		B6	0.0117757171	N	0.0115198307
2022/01/17		D6	0.0082185073	N	0.0031566387
2022/01/17		C6	0.0087967729	N	0.0030958643
2022/01/17		E6	0.0213215556	N	0.0078020641
2022/01/17		F6	0.0183625426	N	0.0076253866
2022/02/16		H4	0.0080825742	N	0.0084690861
2022/02/16		B5	0.0040859459	N	0.0034852908
2022/02/02		C10	0.0034433457	N	0.0011540471
2022/02/02		B10	0.0061098118	N	0.0058704033
2022/03/07		H12	0.0108174300	N	0.0039403574
2022/02/16		C4	0.0134186856	N	0.0121590160

TYQty	TSADegIndex	TSALOWQT	Results
NULL	0.4522636235	Y	SRP,SEMND,MNS,NDNAD,NWQPS
0.0036167365	5.1694979668	Y	SRP,DIFP,SUFP,CMPU
0.0034700711	8.0514097214	Y	SRP,DIFP,SUFP,CMPU
0.0050237444	6.5016360283	N	SRP,DIFP,SUFP,CMPU
0.0032645122	2.5589935780	N	SRP,LDIS,DIFP,CMPU
0.0006552009	3.4887270927	Y	SRP,DIFP,CMPU
0.0036305850	2.5078818798	N	SRP,DIFP,CMPU
0.0238894727	3.7572126389	N	SRP,DIFP,CMPU
0.0016417867	5.2065501213	Y	SRP,DIFP,CMPU
0.0008677779	4.2182106972	Y	SRP,LDIS,PSTP,NDNAD,DIFP,CMPU
0.0008677779	4.2182106972	Y	SRP,LDIS,PSTP,NDNAD,DIFP,CMPU
0.0003966234	2.7085292339	Y	SRP,PSTN,NDNAD,CMPU
0.0050703851	1.8408361673	N	SRP,DIFP,CMPU
0.0111084115	0.6796341538	N	SRP,DIFP,SUFP,1SS20L
0.0154053513	1.1035528183	N	SRP,DIFP,SUFP,1SS20L
0.0022568030	0.9928129315	N	SRP,PSTP,DIFP,CMPU
0.0015284910	1.0190834999	N	SRP,PSTP,NDNAD,CMPU
0.0001509778	2.7767379284	Y	SRP,PSTP,DIFP,CMPU
0.0003448239	4.5557007790	Y	SOHAA,SRP,DIFP,PSTN,CMPU,SUFP
0.0005237493	2.4558999538	Y	SOHAA,SRP,DIFP,PSTN,CMPU,SUFP
0.0041384399	1.9026070833	N	SRP,DIFP,3MX,3MXCON,3MXRNC
0.0049635167	2.0155417919	N	SRP,DIFP,CMPU
0.0032771307	3.4806156158	N	SRP,DIFP,SPPDNA,SUFP,1SS,PSTI
0.0044553187	5.6606869698	Y	SRP,DIFP,CMPU
0.0092485771	1.4018981457	N	SRP,DIFP,1SS20L
0.0035533821	10.3743782043	Y	SRP,DIFP,1S9L10
0.0008472783	2.1903138161	Y	SRP,DIFP,CMPU
0.0034250210	0.9722603559	Y	SRP,DIFP,1SS,1SSNCD,1SS20L
0.0019278241	8.3872241974	Y	SRP,DIFP,SUFP,CMPU
0.0025575084	1.1308869123	N	SRP,DIFP,SCANM,SUFP,1SS,1SSNCD
0.0091506783	1.3027126789	N	SRP,DIFP,1SS20L
0.0034465841	1.9423593283	N	SRP,DIFP,DIFP,SUFP,1S9L10
0.0034465841	1.9423593283	N	SRP,DIFP,DIFP,SUFP,1S9L10
0.0034465841	1.9423593283	N	SRP,DIFP,DIFP,SUFP,1S9L10
0.0034465841	1.9423593283	N	SRP,DIFP,DIFP,SUFP,1S9L10
0.0033659390	1.6666547060	N	SRP,DIFP,CMPU
0.0006850999	1.8045068979	Y	SRP,DIFP,PPUCP
0.0127005531	1.0176014900	N	SRP,DIFP,2MX,NSIP
0.0189690981	2.7496457100	N	SRP,DIFP,CMPU
0.0104192272	3.2196588516	N	SRP,DIFP,CMPU
0.0009538942	1.4264765978	Y	SRP,DIFP,CMPU
0.0068780435	1.5920803547	N	SOHAA,SRP,DIFP,CMPU
0.0022476905	42.9322509766	Y	SRP,DIFP,CMPU
0.0091435779	2.1140391827	N	SRP,DIFP,CMPU,SUFP
0.0110325404	2.3529982567	N	SRP,DIFP,SUFP,1SS9L7,1SSNCD
0.0025839359	5.7798180580	Y	SRP,DIFP,CMPU
0.0030142018	0.8220859766	N	SRP,DIFP,SUFP,CMPU
0.0010129883	4.1027088165	N	SRP,DIFP,CMPU,SUFP
0.0045006284	1.4330844879	Y	SRP,DIFP,CMPU

0.0022906996	2.2120542526	N	SRP,DIFP,CMPU
0.0045761843	4.5258345604	N	SRP,DIFP,CMPU
0.0002574672	1.1968764067	Y	SRP,DIFP,CMPU
0.0019580042	NULL	Y	SRP,DIFP,NDPPTP
0.0173595604	1.8430930376	N	SRP,DIFP,3MX,2MXIND,3MX7,EVDEXC,SCANM
0.0227520540	2.6714658737	N	SRP,DIFP,1S9L10,SUFP
0.0018895183	4.2343816757	Y	SOHAA,SRP,DIFP,DIFP,NDPPTP
0.0018895183	4.2343816757	Y	SOHAA,SRP,DIFP,DIFP,NDPPTP
0.0018895183	4.2343816757	Y	SOHAA,SRP,DIFP,DIFP,NDPPTP
0.0018895183	4.2343816757	Y	SOHAA,SRP,DIFP,DIFP,NDPPTP
0.0102935052	4.0146694183	N	SRP,DIFP,CMPU
0.0091818608	3.4651262760	N	SRP,DIFP,CMPU
0.0114315813	1.5246996880	N	SRP,DIFP,CMPU
NULL	NULL	Y	SRP,NDNAD,NDNAD,NDPPTP
NULL	NULL	Y	SRP,NDNAD,NDNAD,NDPPTP
NULL	NULL	Y	SRP,NDNAD,NDNAD,NDPPTP
NULL	NULL	Y	SRP,NDNAD,NDNAD,NDPPTP
0.0039250231	2.3052420616	N	SRP,DIFP,1SS
0.0054608309	3.5694527626	N	SRP,DIFP,SUFP,CMPU
0.0221741255	6.0044527054	N	SRP,DIFP,SUFP,CMPU
0.0047689383	3.5995817184	N	SRP,DIFP,CMPU
0.0016062384	1.5433949232	Y	SRP,DIFP,SUFP,CMPU
0.0044764099	0.7527177334	N	SRP,DIFP,SUFP,CMPU
0.0086535048	1.2884353399	N	SRP,DIFP,1SS,1SSNCD,SUFP,PSTI
0.0005759294	2.1935374737	Y	SRP,DIFP,SUFP,CMPU
0.0021353026	6.2003893852	Y	SRP,DIFP,CMPU,SUFP
0.0076961522	11.9085960388	Y	SRP,DIFP,CMPU,SUFP
0.0018820872	2.2068738937	N	SRP,EXREV,DIFP,SUFP,CMPU
0.0027869567	2.2300570011	N	SRP,DIFP,CMPU,SUFP
0.0016672387	2.0395643711	Y	SRP,DIFP,SUFP,CMPU
0.0053610951	1.4392770529	N	SRP,DIFP,2MX,NSIP
0.0011338793	1.7927206755	Y	SRP,DIFP,SUFP,CMPU
0.0081207789	5.9445438385	N	SRP,DIFP,CMPU
0.0170869399	6.6064572334	N	SRP,DIFP,SUFP,CMPU
0.0028735728	39.6984710693	Y	SRP,DIFP,CMPU
0.0081363311	2.3462359905	N	SRP,DIFP,SUFP,CMPU
0.0009662507	10.9402818680	Y	SRP,NDNAD,SPPDNA,SUFP,CMPU
0.0004025676	2.2252986431	Y	SRP,DIFP,1SSAKN,SUFP
0.0143973958	3.5820643902	N	SRP,DIFP,SUFP,CMPU
0.0059463866	3.2957525253	Y	SRP,DIFP,SUFP,CMPU
0.0011667211	2.6404380798	N	SRP,DIFP,CMPU,SUFP
NULL	1.3863713741	N	SRP,DIFP,SUFP,1SS20L,PSTI
NULL	1.9028493166	N	SRP,DIFP,SUFP,PPUCP
0.0049078716	2.7343130112	N	SRP,DIFP,SUFP,CMPU
0.0059927246	2.9702188969	N	SRP,DIFP,SUFP,CMPU
0.0004894045	2.9319839478	Y	SRP,DIFP,CMPU
0.0027447969	1.1088703871	N	SRP,DIFP,SUFP,2MX,EVDEXC,EVDEXC,EVDEXC,EVDEXC
0.0009191571	3.1026029587	Y	SRP,DIFP,SUFP,CMPU
NULL	1.0322605371	N	SRP,DIFP,SUFP,1SSAKN
NULL	2.2526128292	N	SRP,DIFP,SUFP,CMPU

0.0000952165	2.4490029812	Y	SRP,DIFP,SUFP,CMPU
NULL	NULL	N	SRP,DIFP,SUFP,1S9L10
0.0016002782	2.7306239605	N	SRP,DIFP,SUFP,CMPU
0.0035026560	0.7853648663	N	SRP,DIFP,SUFP,CMPU,NWQPS
0.0025432704	2.9913098812	Y	SRP,DIFP,SUFP,CMPU
0.0025883599	3.9447031021	Y	SRP,DIFP,SUFP,CMPU
0.0045741485	3.0031864643	Y	SRP,DIFP,SUFP,CMPU
0.0055213482	1.8481179476	N	SRP,DIFP,SUFP,CMPU
0.0003996538	1.8122659922	Y	SRP,DIFP,SUFP,CMPU
0.0035203302	2.3710095882	Y	SRP,DIFP,SUFP,CMPU
0.0023715564	2.3718764782	Y	SRP,DIFP,SUFP,CMPU
0.0118319280	1.7331019640	N	SRP,DIFP,SUFP,2MX,2MX7,2MXNC,2MXNC,EVDEXC,EV
0.0074637653	1.5040131807	N	SRP,DIFP
0.0025559643	0.6893263459	N	SRP,DIFP,SEMND,MNS,SUFP,2MX,EVDEXC,EVDEXC,EV
0.0001597713	30.0004425049	Y	SRP,DIFP,SUFP,PPUCP
NULL	NULL	N	SRP,DIFP,SEMND,MNS,SUFP,NDPPTP
0.0009705891	NULL	Y	SRP,DIFP,SEMND,MNS,SUFP,NDPPTP
0.0063866582	1.7092798948	N	SRP,DIFP,1SS,1SSNCD,1S9L10
NULL	0.9029451609	N	SRP,DIFP,SEMND,MNS,SUFP,1SS,1SSAKN
0.0052608130	19.1210079193	Y	SOHAA,SRP,DIFP,1SSLND,SUFP,CPU
0.0007909101	1.4978586435	Y	SRP,DIFP,PPUCP
0.0125944391	5.3359436989	N	SRP,DIFP,SUFP,CMPU
0.0025559014	7.2132811546	Y	SRP,DIFP,SUFP,CMPU
0.0083526038	2.9550809860	N	SRP,DIFP,CMPU,SUFP
0.0019570533	1.8667219877	N	SRP,DIFP,CMPU,SUFP
0.0072343079	4.3867664337	Y	SRP,DIFP,SUFP,2MX,2MX7,2MXNC,2MXNC,2MXNC,2M
0.0105583966	1.9764720201	N	SRP,DIFP,SUFP,CMPU
0.0023563763	1.7949123383	N	SRP,DIFP,SUFP,CMPU
0.0011303322	1.1945794821	N	SRP,DIFP,SUFP,CMPU
0.0009461247	2.5467429161	Y	SRP,DIFP,SUFP,CMPU
0.0009001379	1.5586851835	Y	SRP,DIFP,SUFP,CMPU
0.0003697862	2.0525367260	Y	SRP,DIFP,SUFP,PPUCP
NULL	1.3952053785	N	SRP,DIFP,SUFP,PPUCP
0.0001741644	2.8986558914	Y	SRP,DIFP,SUFP,PPUCP
0.0003100244	2.5682845116	Y	SRP,DIFP,SUFP,PPUCP
NULL	0.9908994436	N	SRP,DIFP,SUFP,PPUCP
NULL	1.4272005558	N	SRP,DIFP,SUFP,PPUCP
NULL	2.3477776051	N	SRP,DIFP,SUFP,PPUCP
0.0001390304	31.4785671234	Y	SRP,DIFP,CMPU
0.0024761800	2.3053431511	Y	SRP,DIFP,CMPU
0.0044140671	2.4388349056	Y	SRP,DIFP,CMPU
0.0038836244	1.9993005991	Y	SRP,DIFP,CMPU
0.0022662722	0.8728674650	Y	SRP,DIFP,CMPU
0.0047549712	2.7898957729	Y	SRP,DIFP,CMPU
0.0001127937	0.9564587474	Y	SRP,LDIS,NDNAD,NOPROF,PSTI
NULL	NULL	N	SRP,LDIS,NDNAD,NOPROF
0.0050671669	6.1944565773	N	SRP,DIFP,CMPU
0.0309709348	35.7303771973	N	SRP,DIFP,NDPPTP
0.0041662399	1.2540707588	Y	SRP,DIFP,PSTP,CMPU
0.0021015417	0.8664543629	Y	SRP,DIFP,PSTP,CMPU

0.0057059485	1.7904280424	Y	SRP,DIFP,CMPU
0.0090034306	9.7473030090	Y	SRP,LDIS,DIFP,CMPU
0.0113866683	9.0067672729	Y	SRP,LDIS,DIFP,1SS,1SSNCD
0.0041366136	33.8762397766	Y	SRP,DIFP,CMPU
0.0041276431	7.8523597717	Y	SRP,DIFP,TRQ,CMPU
0.0098588346	1.8942433596	N	SRP,DIFP,TRQ,CMPU
0.0002567828	3.4155194759	Y	SRP,DIFP,CMPU
0.0187547132	0.6146094203	N	SRP,DIFP,3MX,3MX7,3MXNC,2MXIND
0.0047040316	1.9611697197	Y	SRP,DIFP,CMPU
0.0084479768	4.8029966354	Y	SRP,DIFP,2MX,2MXIND,2MXIND,2MX7
0.0046463376	1.3496620655	Y	SRP,DIFP,CMPU
0.0030240472	3.4680564404	Y	SRP,DIFP,SUFP,CMPU
0.0169865526	3.9881982803	Y	SRP,DIFP,SUFP,CMPU
0.0035557961	1.3557294607	Y	SRP,DIFP,CMPU
0.0117098046	1.1560624838	N	SRP,DIFP,SUFP,CMPU
0.0196910817	1.7927360535	N	SRP,DIFP,QFIH,QCFRQ
0.0042941626	1.5125070810	Y	SRP,DIFP,CMPU
0.0042357189	1.9224759340	Y	SRP,DIFP,CMPU
0.0120708095	1.6322197914	N	SRP,DIFP,CMPU
0.0097288247	7.5077986717	Y	SRP,DIFP,CMPU
0.0010858757	1.7668752670	Y	SRP,NDNAD,SUFP,PPUCP
0.0003024600	1.3606241941	Y	SRP,DIFP,SUFP,CMPU
NULL	2.0924220085	Y	SRP,SRMI,DIFP,TRQ,1SS9L6,SUFP
0.0015749845	1.0902168751	Y	SRP,DIFP,SPPDNA,CMPU
0.0008062188	1.1965860128	Y	SRP,DIFP,SPPDNA,CMPU
0.0024759911	1.0625935793	Y	SRP,DIFP,CMPU
0.0068920613	2.2996432781	Y	SRP,DIFP,SUFP1,CMPU
0.0045868633	2.8004465103	Y	SRP,DIFP,SUFP,CMPU
0.0168215092	1.6821583509	N	SRP,DIFP,3MX,NSIP,SCSNC
0.0016590279	1.0196273327	Y	SRP,DIFP,CMPU
0.0059801117	1.3817957640	N	SRP,DIFP,CMPU
0.0046339333	1.5353362560	Y	SRP,DIFP,CMPU
0.0021392689	6.5740375519	Y	SRP,DIFP,SPPDNA,CMPU
0.0058095199	2.7215614319	Y	SRP,DIFP,SUFP,CMPU
0.0099205775	2.9079437256	N	SRP,DIFP,TRQ,2MX,2MXIND
0.0144470837	7.4240980148	Y	SRP,DIFP,TRQ,CMPU,SUFP
0.0215618089	27.5945930481	Y	SRP,DIFP,TRQ,1SS
0.0019447664	4.8387393951	Y	SRP,DIFP,SUFP,CMPU
NULL	1.2637492418	Y	SRP,DIFP,SEMND,MNS,SUFP,1SSAKN
NULL	1.2310563326	Y	SRP,DIFP,SEMND,MNS,SUFP,1SSAKN
0.0032805917	1.8280030489	Y	SRP,DIFP,PSTN,CMPU
0.0061908085	1.7255668640	N	SRP,DIFP,PSTN,2MX,2MXCON,2MXR5,EVDEXC,SUFP
0.0042464528	5.4155874252	Y	SRP,DIFP,SUFP,CMPU
0.0051354985	3.7033262253	Y	SRP,NDNAD,CMPU,SUFP
0.0260917973	4.9271650314	N	SRP,DIFP,1S9L10,SUFP
0.0039235959	4.1841492653	Y	SRP,DIFP,TRQ,3MX,3MX7,SCSNC,SCSNC,SCSNC,SCSNC
0.0121811712	2.4130673409	N	SRP,DIFP,CMPU
0.0169923827	2.0596575737	N	SRP,DIFP,SUFP,CMPU
0.0070346436	0.9331256747	N	SRP,DIFP,CMPU,SUFP
0.0045592031	2.0950300694	Y	SRP,DIFP,SUFP,CMPU

0.0060161701	1.6129927635	N	SRP,DIFP,CMPU
0.0007270810	3.5065169334	Y	SRP,DIFP,SUFP,1SSAKN
0.0032428419	1.2077600956	Y	SRP,DIFP,SUFP,CMPU
0.0118233087	1.5312043428	N	SRP,DIFP,CMPU
0.0014314373	1.6529251337	Y	SRP,DIFP,CMPU
0.0241230689	4.7836842537	Y	SRP,DIFP,SUFP,CMPU
0.0065553784	1.2022901773	N	SRP,DIFP,CMPU
0.0073521072	1.8123368025	Y	SRP,DIFP,SUFP,CMPU
0.0042838603	1.0673092604	Y	SRP,DIFP,SUFP,CMPU
0.0100385472	0.9516028762	N	SRP,DIFP,SUFP,CMPU
0.0134151187	2.3324878216	Y	SRP,DIFP,SUFP,CMPU
0.0048422529	1.9863499403	Y	SRP,DIFP,SUFP,CMPU
0.0025758697	1.6164497137	Y	SRP,DIFP,SUFP,CMPU
0.0031654167	0.9676534534	Y	SRP,DIFP,SUFP,CMPU,SPP
0.0018448605	2.5966260433	Y	SRP,DIFP,SUFP,CMPU,SPP
0.0035924891	1.0154004097	Y	SRP,DIFP,CMPU,SUFP
0.0062581780	0.9706264138	N	SRP,DIFP,CMPU
0.0019978173	6.1389017105	Y	SRP,DIFP,SUFP,NOPROF,PSTI
0.0036837962	1.2408006191	Y	SRP,DIFP,MNS,1SS9L8,1SS9L8
0.0094937934	2.0195174217	N	SRP,DIFP,SUFP,1SS
0.0023654816	2.5538976192	Y	SRP,DIFP,SUFP,CMPU
0.0073127476	16.0110969543	Y	SRP,DIFP,SUFP,CMPU
0.0117946658	4.4020752907	Y	SRP,DIFP,SUFP,CMPU
0.0094237328	1.4762128592	N	SRP,DIFP,SUFP,CMPU
0.0033398326	1.6439037323	Y	SRP,DIFP,CMPU
0.0087912893	1.6764305830	N	SRP,DIFP,TRQ,CMPU
0.0011213403	1.7135008574	Y	SRP,DIFP,CMPU
0.0085198823	1.2610312700	N	SRP,DIFP,CMPU,SUFP
0.0026856358	5.9261035919	Y	SRP,DIFP,CMPU
0.0026478129	1.3123688698	Y	SRP,DIFP,CMPU
0.0017804444	0.7058219910	Y	SRP,DIFP,CMPU
0.0052937344	1.0174205303	N	SRP,DIFP,CMPU
0.0090947840	1.3239817619	N	SRP,DIFP,CMPU
0.0016891058	3.8573546410	Y	SRP,DIFP,CMPU
0.0010614785	4.0283646584	Y	SRP,LDIS,DIFP,PPUCP
0.0016100738	4.8200902939	Y	SRP,DIFP,PPUCP
0.0108383661	1.8535716534	N	SRP,PSTP,DIFP,TRQ,SUFP,CMPU
NULL	2.3310754299	Y	SRP,DIFP,TRQ,CMPU
0.0073807300	1.2808547020	N	SRP,DIFP,CMPU
0.0001388971	1.5813380480	Y	SRP,DIFP,PSTP,SUFP,CMPU
0.0002526837	1.3325439692	Y	SRP,DIFP,PSTP,SUFP,CMPU
NULL	NULL	N	SRP,NDNAD,SUFP,NOPROF
0.0171658713	1.0827237368	N	SRP,DIFP,SUFP,1SS,1S9L10
0.0081620179	1.1298524141	N	SRP,DIFP,1SS,1SSNCD
0.0092315134	2.1657149792	N	SRP,DIFP,CMPU
NULL	NULL	N	SRP,NDNAD,QCF
0.0098490883	1.2153011560	N	SRP,DIFP,SUFP,CMPU
0.0001410862	NULL	Y	SRP,DIFP,SUFP,NDPPTP
0.0055778278	2.1219563484	N	SRP,DIFP,CMPU
0.0022791482	2.3672051430	Y	SRP,DIFP,SUFP,CMPU

0.0023747894	3.6778755188	Y	SRP,DIFP,CMPU
0.0145832999	1.9099849463	N	SRP,DIFP,CMPU,SUFP
0.0067845262	2.2530121803	N	SRP,DIFP,CMPU
0.0055873767	1.7711852789	N	SRP,DIFP,SUFP,CMPU
0.0024887484	1.7999211550	Y	SRP,DIFP,CMPU,SUFP
0.0027253700	2.1788573265	Y	SRP,DIFP,SUFP,CMPU
0.0085424874	4.0223765373	Y	SRP,DIFP,SUFP1,CMPU
0.0034119843	9.3646869659	Y	SRP,DIFP,SUFP,CMPU
0.0002943121	3.8684101105	Y	SRP,DIFP,CMPU
0.0014019043	1.6105279922	Y	SRP,DIFP,CMPU
0.0110452026	100.5477828979	Y	SRP,DIFP,1SS,1SSNCD
0.0155258961	2.0525238514	N	SRP,LDIS,DIFP,SUFP,CMPU
0.0009879419	1.2170048952	Y	SRP,DIFP,CMPU
0.0344916098	1.4449703693	N	SRP,DIFP,2MX,2MXIND,2MXIND,2MX7
0.0018159362	24.0376720428	Y	SRP,DIFP
0.0027452274	54.2650337219	Y	SRP,DIFP
0.0010544664	34.5676116943	Y	SRP,DIFP
NULL	5.9916434288	Y	SRP,NDNAD
0.0061027166	9.8967895508	Y	SRP,DIFP
0.0009584469	1.6467996836	Y	SRP,DIFP,CMPU
0.0127487723	1.0427423716	N	SRP,DIFP,CMPU
0.0173670463	5.2402138710	N	SRP,DIFP,SUFP,CMPU
0.0115359686	1.3303166628	N	SRP,DIFP,SUFP,CMPU
0.0083431387	2.1746680737	Y	SRP,DIFP,SUFP,CMPU
0.0009305771	3.0317935944	Y	SRP,DIFP,SUFP,CMPU
0.0054736841	2.1008269787	Y	SRP,DIFP,SUFP,CMPU
0.0144373523	1.2992665768	N	SRP,LDIS,DIFP,SUFP,CMPU
0.0070453263	2.1651694775	N	SRP,DIFP,SUFP,2MX,2MXIND,2MXNC
0.0014991674	2.9748084545	Y	SRP,DIFP,PPUCP
0.0112176631	7.1305370331	Y	SRP,DIFP,CMPU
0.0072985026	1.7545756102	N	SRP,DIFP,SUFP,CMPU
0.0091298372	0.9150779247	N	SRP,DIFP,CMPU
0.0089624710	0.9009256363	N	SRP,DIFP,3MX,3MXCON,3MXR7
0.0003608452	4.8218979836	Y	SRP,DIFP,PSTP,CMPU
0.0394050293	2.1367263794	N	SRP,DIFP,CMPU
0.0144638866	2.6339187622	N	SRP,DIFP,CMPU
0.0085325064	2.0708966255	Y	SRP,DIFP,CMPU
0.0022246805	1.2638399601	Y	SRP,DIFP,CMPU
NULL	1.9178608656	Y	SOHAA,SRP,DIFP,SUFP,1SSAKN
0.0076759965	1.2071433067	N	SRP,DIFP,CMPU
0.0073516639	1.5952640772	N	SRP,DIFP,CMPU
0.0111953011	3.0230903625	Y	SRP,DIFP,CMPU
0.0096435649	1.3131537437	N	SRP,DIFP,SUFP,2MX,2MXIND
0.0038710260	1.6238999367	Y	SRP,DIFP,SUFP,1SS9L3
0.0069840518	1.4253133535	Y	SRP,DIFP,SUFP,CMPU
0.0017865436	6.6664886475	Y	SRP,DIFP,CMPU
0.0021573778	1.4575476646	Y	SRP,DIFP,CMPU
0.0060416609	1.3287863731	N	SRP,DIFP,SUFP,CMPU
NULL	1.0684057474	N	SRP,DIFP,1SSAKN,SUFP
0.0042975629	2.0339627266	Y	SRP,DIFP,SUFP,CMPU

0.0024393492	3.2961633205	Y	SRP,DIFP,CMPU
0.0027222938	2.0917775631	Y	SRP,DIFP,TRQ,CMPU
0.0056376555	1.5825895071	N	SRP,DIFP,SUFP,CMPU
0.0064187637	1.9632594585	N	SRP,DIFP,CMPU
0.0088166799	1.5564900637	N	SRP,DIFP,CMPU,SUFP
0.0015100682	1.0723917484	Y	SRP,DIFP,PSTN,SUFP,CMPU
0.0069177509	3.8755433559	Y	SRP,DIFP,SUFP,1SS9L9
0.0049528773	2.0599706173	Y	SRP,DIFP,SUFP,CMPU
0.0175236147	3.4298050404	N	SRP,DIFP,3MX,3MX7
0.0230592713	1.3452038765	N	SRP,DIFP,CMPU
0.0204995442	4.9888887405	N	SRP,DIFP,CMPU,SUFP
0.0025002693	3.7702693939	Y	SRP,DIFP,SUFP,CMPU
0.0017585796	1.6455402374	Y	SRP,DIFP,SUFP,CMPU
0.0015423783	1.7432241440	Y	SRP,DIFP,QFIH,QCFRQ
0.0004365220	4.3251228333	Y	SRP,DIFP,SUFP,CMPU
0.0007712270	2.5252478123	Y	SRP,NDNAD,SUFP,CMPU
0.0002815792	1.0982240438	Y	SRP,NDNAD,SUFP,CMPU
0.0050855414	3.0715653896	Y	SRP,DIFP,CMPU
0.0035001223	1.9649608135	Y	SRP,DIFP,CMPU
NULL	1.0251991749	N	SRP,DIFP,SUFP,1SS,1SSNCD
NULL	NULL	Y	SRP,DIFP,TRQ,NWQPSR
NULL	NULL	N	SOHAA,SRP,DIFP,TRQ,NWQPSR
NULL	16.9475574493	Y	SOHAA,SRP,DIFP,TRQ,NWQPSR
0.0111337584	1.3190218210	N	SRP,DIFP,SUFP,3MX,2MXNCD
0.0077613685	3.1231923103	Y	SRP,DIFP,SUFP,CMPU
0.0056574834	1.4979726076	Y	SRP,DIFP,SUFP,CMPU
0.0024083804	1.4926993847	Y	SRP,DIFP,CMPU
0.0127357990	0.8673720956	N	SRP,DIFP,QFIH,QCFRQ
0.0020080230	1.1869010925	Y	SRP,DIFP,SUFP,CMPU
0.0402182676	5.3926773071	N	SRP,DIFP,1SS,1SSNCD,1S9L10
0.0109468140	0.6524003744	N	SRP,DIFP,CMPU
0.0113919564	0.9625178576	N	SRP,SPPDNA,DIFP,1SS,SUFP,1SS20L
0.0057375780	2.8672003746	Y	SRP,DIFP,SUFP,CMPU
0.0044649751	2.6040620804	Y	SRP,DIFP,SUFP,CMPU
0.0034560622	1.4669758081	Y	SRP,DIFP,QFIH,QCFRQ,CMPU
0.0097074825	1.6901222467	N	SRP,DIFP,QFIH,3MXR7,3MXCI,SCANM,SCANM,SCANM
0.0041593006	1.4339356422	Y	SRP,DIFP,QFIH,QCFRQ,PSTI,SUFP,1SSAKN
0.0040163021	2.3508217335	Y	SRP,DIFP,QFIH,QCFRQ,1SSAKN
0.0009566759	5.1507978439	Y	SRP,DIFP,QFIH,QCFRQ,CMPU
0.0061938507	3.4807674885	Y	SRP,DIFP,SPP
0.0054083038	5.3629732132	Y	SRP,DIFP,SPP
0.0037007981	1.3933880329	Y	SRP,LDIS,DIFP,CMPU
0.0077008945	1.2667487860	Y	SRP,DIFP,1SS,1SSNCD,PSTI,1S9L10
0.0001857124	2.1473181248	Y	SRP,DIFP,CMPU
0.0029787340	1.7134433985	Y	SRP,DIFP,CMPU
0.0126217287	1.9642810822	N	SRP,DIFP,CMPU
0.0192475803	1.8713032007	N	SRP,DIFP,3MX,3MX7,3MXNC,3MXNC
0.0024336856	2.0364167690	Y	SRP,DIFP,CMPU
0.0006918954	0.8975879550	Y	SRP,DIFP,SPPDNA,CMPU
0.0048979558	20.3960189819	Y	SRP,DIFP,QFIH,QCFRQ

0.0093681719	2.3113930225	N	SRP,DIFP,CMPU
0.0006985691	2.7547364235	Y	SRP,DIFP,CMPU
0.0147869792	0.5185821056	N	SRP,DIFP,SPPDNA,1SS20L,1SSNCD
0.0199979134	1.3597422838	N	SRP,DIFP,CMPU
0.0141447829	1.6074830294	N	SRP,DIFP,CMPU
0.0037748788	1.3764290810	Y	SRP,DIFP,CMPU
0.0196295455	0.8821307421	N	SRP,DIFP,3MX,2MXIND,3MX7,SUFWC,3MXCON,3MXR
0.0035154279	9.6366596222	Y	SRP,DIFP,SUFP,CMPU
0.0027617700	1.8365758657	Y	SRP,DIFP,CMPU
0.0013959570	3.5500938892	Y	SRP,DIFP,PPUCP
0.0145200659	1.4520239830	N	SRP,DIFP,CMPU
0.0014010991	2.2289454937	Y	SRP,DIFP,CMPU
0.0100641260	2.7124595642	Y	SRP,DIFP,CMPU
0.0075293928	2.5423700809	Y	SRP,DIFP,CMPU,SUFP
0.0032297398	8.8303642273	Y	SRP,DIFP,SUFP,CMPU
0.0089711165	0.6309356093	N	SRP,SPPDNA,DIFP,SUFP,1SS20L,PSTI
0.0143186087	1.9110749960	N	SRP,LDIS,DIFP,1SS,1SSNCD
0.0061444286	1.2650063038	N	SRP,DIFP,SUFP,CMPU
0.0003955616	1.3747020960	Y	SRP,DIFP,SUFP,CMPU
NULL	0.8168181777	N	SRP,SPPDNA,DIFP,SUFP,CMPU
0.0030482844	1.1783796549	Y	SRP,DIFP,CMPU
0.0135283452	1.7768861055	N	SRP,DIFP,1S9L10
0.0064942241	1.0331685543	N	SRP,SPPDNA,DIFP,3MX,3MXNC,3MXNC,SCSNC,SCSC4,
0.0018305448	0.8268681765	Y	SRP,SPPDNA,DIFP,3MX,3MXLOW,3MXNC,3MXNC,SCS
0.0014822255	0.4548309445	Y	SRP,SPPDNA,NDNAD,CMPU
0.0095091909	7.6509480476	Y	SRP,DIFP,CMPU
0.0142435329	0.7247920632	N	SRP,DIFP,CMPU
NULL	2.5456953049	Y	SRP,DIFP,CMPU
0.0020013617	2.7900316715	Y	SRP,DIFP,CMPU
0.0040098242	1.3661491871	Y	SRP,SPPDNA,DIFP,1SS20L
0.0033343905	2.7607266903	Y	SRP,DIFP,SUFP,CMPU
0.0089870878	1.0446051359	N	SRP,SPPDNA,DIFP,1SSAKN,PSTI
0.0037320808	1.5426019430	Y	SRP,SPPDNA,DIFP,CMPU
0.0048031486	1.6220139265	Y	SRP,SPPDNA,DIFP,CMPU
0.0016836936	2.7770111561	Y	SRP,DIFP,CMPU
0.0022918913	1.6361830235	Y	SRP,DIFP,CMPU
0.0015850974	2.3499228954	Y	SRP,DIFP,CMPU
0.0045416243	2.7052273750	Y	SRP,DIFP,CMPU
0.0062063723	1.6436409950	Y	SRP,DIFP,CMPU
0.0116229281	1.8751932383	N	SRP,DIFP,CMPU
0.0029074897	0.9519373178	Y	SRP,DIFP,CMPU
0.0042920774	1.2480745316	Y	SRP,DIFP,CMPU
0.0046804412	1.2259775400	Y	SRP,DIFP,CMPU
0.0005652494	1.6223951578	Y	SRP,DIFP,CMPU
0.0061129597	2.0063529015	Y	SRP,DIFP,CMPU
0.0074883047	3.9463624954	Y	SRP,DIFP,CMPU
0.0270589646	1.1966321468	N	SRP,DIFP,CMPU
0.0060582967	1.6890845299	Y	SRP,DIFP,CMPU
0.0202248394	1.2779257298	N	SRP,DIFP,CMPU
0.0115079423	5.4561786652	Y	SRP,DIFP,SEMND,MNS,INT,CMPU

0.0237384886	9.2894315720	Y	SRP,DIFP,CMPU
0.0132495603	0.8793163300	N	SRP,DIFP,SUFP,3MX,3MXNC,3MX7
NULL	NULL	N	SRP,NDNAD,SUFP,PPUCP
NULL	NULL	N	SRP,NDNAD,SUFP,NOPROF
NULL	NULL	N	SRP,NDNAD,SUFP,NOPROF
NULL	NULL	N	SRP,NDNAD,SUFP,NOPROF
0.0009227932	3.0217833519	Y	SRP,NDNAD,SUFP,CMPU
NULL	NULL	N	SRP,NDNAD,SUFP,NDPPTP
NULL	NULL	N	SRP,NDNAD,SUFP,NOPROF
NULL	NULL	N	SRP,NDNAD,SUFP,PPUCP
NULL	NULL	N	SRP,NDNAD,SUFP,PPUCP
NULL	NULL	N	SRP,NDNAD,SUFP,NOPROF
NULL	NULL	N	SRP,NDNAD,SUFP,NDPPTP
0.0052724844	2.1717741489	N	SRP,DIFP,MNS,SUFP,1SSAKN
0.0037119740	3.4064996243	Y	SRP,DIFP,TRQ,CMPU
0.0184044037	2.1376268864	N	SRP,DIFP,2MX,2MXIND,2MXNC,2MXNC
0.0118803065	1.0591909885	N	SRP,LDIS,DIFP,2MX,2MX7,2MXNC
0.0026899462	5.7034268379	Y	SRP,DIFP,CMPU
0.0046564438	1.9649497271	Y	SRP,DIFP,SUFP,CMPU
0.0020087804	7.8690271378	Y	SRP,DIFP
0.0008792094	3.8095021248	Y	SRP,DIFP,PSTP,SUFP,CMPU
0.0038505550	6.1495695114	Y	SRP,DIFP,TRQ,TRQ,SUFP,CMPU
0.0012574632	81.0595169067	Y	SRP,DIFP
0.0048077432	7.6956872940	Y	SRP,DIFP
0.0027836324	7.6927280426	Y	SRP,DIFP
0.0127466070	1.5001522303	N	SRP,DIFP,3MX,3MXNC,3MXNC
0.0003686691	2.5033044815	Y	SRP,DIFP,1SS,1SSNCD,SUFP
0.0004209187	8.3509931564	Y	SRP,DIFP,PPUCP
0.0004990918	0.9667839408	Y	SRP,SPPDNA,DIFP,CMPU
0.0061283726	21.3157978058	Y	SRP,DIFP
0.0181936193	1.4255456924	N	SRP,DIFP,3MX,2MXIND,3MX7,2MXIND
0.0008029562	1.3439836502	Y	SRP,DIFP,TRQ,2MX,2MXIND
0.0036248497	0.9038219452	Y	SRP,DIFP,TRQ,CMPU
0.0009730507	2.1863520145	Y	SRP,DIFP,TRQ,CMPU
0.0020767879	3.3116447926	Y	SRP,DIFP,CMPU
0.0014768388	1.5016183853	Y	SRP,DIFP,CMPU,SUFP
0.0015094507	2.6867859364	Y	SRP,DIFP,TRQ,CMPU
0.0018311541	1.3120911121	Y	SRP,DIFP,TRQ,CMPU
0.0053427424	1.4591095448	N	SRP,DIFP,CMPU,SUFP
0.0027658765	2.2052483559	Y	SRP,DIFP,SUFP,CMPU
0.0010799702	1.1891745329	Y	SRP,SPPDNA,DIFP,SUFP,CMPU
0.0003378206	1.5327463150	Y	SRP,PAPPRP,MNS,DIFP,SUFP,CMPU
0.0020622793	4.2380609512	Y	SRP,DIFP,SUFP,PPUCP
0.0036593103	2.2627604008	Y	SRP,DIFP,CMPU
0.0018492695	1.3667206764	Y	SRP,SPPDNA,DIFP,TRQ,1S9L10,SUFP
0.0066502392	1.0755969286	N	SRP,SPPDNA,DIFP,TRQ,1SS20L,SUFP
0.0068121995	1.2214629650	Y	SRP,SPPDNA,DIFP,TRQ,1SS20L,SUFP
0.0057632346	1.3985838890	Y	SRP,SPPDNA,DIFP,TRQ,1S9L10,SUFP
0.0061459476	0.7782562971	Y	SRP,SPPDNA,DIFP,TRQ,2MX,2MXCON,2MXR7,SUFP
0.0126860915	0.8726479411	N	SRP,SPPDNA,DIFP,TRQ,3MX,3MXCON,3MXR7,SUFP

0.0067710336	1.7725459337	Y	SRP,DIFP,CMPU
0.0266973451	73.0524978638	Y	SRP,DIFP,2MX,2MXCON,2MXUNS
0.0032906840	1.2844862938	Y	SRP,DIFP,TRQ,CMPU
0.0041997847	3.5416753292	Y	SRP,DIFP,CMPU
NULL	NULL	N	SRP,NDNAD,SUFP,NDNAD
NULL	NULL	N	SRP,NDNAD,SUFP,NDNAD
NULL	NULL	N	SRP,NDNAD,SUFP,NDNAD
NULL	NULL	N	SRP,NDNAD,SUFP,NDNAD
0.0000850172	NULL	Y	SRP,NDNAD,SUFP,NOPROF
NULL	NULL	N	SRP,NDNAD,SUFP,NDNAD
NULL	NULL	N	SRP,NDNAD,SUFP,NDNAD
NULL	NULL	N	SRP,NDNAD,SUFP,NDNAD
NULL	NULL	N	SRP,NDNAD,SUFP,NDNAD
NULL	NULL	N	SRP,NDNAD,SUFP,NDNAD
NULL	NULL	N	SRP,NDNAD,SUFP,NDNAD
NULL	NULL	N	SRP,NDNAD,SUFP,NDNAD
NULL	NULL	N	SRP,NDNAD,SUFP,NDNAD
NULL	NULL	N	SRP,NDNAD,SUFP,NOPROF
NULL	NULL	N	SRP,NDNAD,SUFP,NOPROF
NULL	NULL	N	SRP,NDNAD,SUFP,NOPROF
NULL	NULL	N	SRP,NDNAD,SUFP,NOPROF
NULL	NULL	N	SRP,NDNAD,SUFP,NOPROF
NULL	NULL	N	SRP,NDNAD,SUFP,NOPROF
NULL	NULL	N	SRP,NDNAD,TRQ,NOPROF,SUFP
0.0035824953	1.0401151180	Y	SRP,SPPDNA,DIFP,TRQ,2MX,2MXCON,2MXRND,EVDE
0.0034762742	2.0113823414	Y	SRP,DIFP,SUFP,MIX,MIX1,MIX4,MIX5,MIX1,MIX3,MIX
0.0141363721	1.5640481710	N	SRP,DIFP,TRQ,3MX,3MXCON,3MXR7
0.0111746332	1.3444615602	N	SRP,DIFP,TRQ,2MX,2MXCON,2MXR1
0.0098475637	1.0745538473	N	SRP,DIFP,TRQ,3MX,3MXCON,3MXR7
0.0136181172	1.3036249876	N	SRP,DIFP,TRQ,3MX,3MXCON,3MXR7,2MXCND
0.0181476343	1.1657758951	N	SRP,DIFP,TRQ,3MX,3MXCON,3MXR6
0.0065659764	1.2655305862	N	SRP,DIFP,TRQ,3MX,3MXCON,3MXR7
0.0045803026	3.9611794949	Y	SRP,DIFP,TRQ,SUFP,CMPU
NULL	NULL	N	SRP,SPPDNA,NDNAD,TRQ,SUFP,NOPROF
0.0028694815	1.7368589640	Y	SRP,SPPDNA,DIFP,2MX,2MXCON,2MXR7,2MXRND
0.0075387564	1.6062511206	N	SRP,PAPPRP,MNS,DIFP,3MX,3MXCON,3MXR7
0.0001852628	0.6882459521	Y	SRP,SPPDNA,DIFP,CMPU,SUFP
0.0028758487	1.0340943336	Y	SRP,DIFP,CMPU
0.0035600376	2.9938468933	Y	SRP,DIFP,CMPU
0.0079903519	1.5495198965	N	SRP,DIFP,TRQ,CMPU
0.0017732756	1.1993095875	Y	SRP,SPPDNA,DIFP,TRQ,3MX,3MXCON,3MXRNC
0.0011834407	0.9471157789	Y	SRP,SPPDNA,DIFP,TRQ,3MX,3MXCON,3MXRNC
0.0084947739	0.8567051888	N	SRP,SPPDNA,DIFP,TRQ,3MX,3MXCON,3MXRNC
0.0011045318	0.8653721213	Y	SRP,SPPDNA,DIFP,TRQ,2MX,2MXNC,2MXNC
0.0001692447	1.1380225420	Y	SRP,SPPDNA,DIFP,TRQ,2MX,2MXCON
0.0046393466	2.8123881817	Y	SRP,DIFP,CMPU
0.0001670418	1.2793520689	Y	SRP,SPPDNA,DIFP,SUFP,CMPU
0.0003826410	0.4816587269	Y	SRP,SPPDNA,DIFP,SUFP,CMPU
0.0035646171	1.1846809387	Y	SRP,SPPDNA,DIFP,SUFP
0.0041310345	0.7213240862	Y	SRP,SPPDNA,DIFP,SUFP,2MX,2MXCON,2MXR7,EVDEX

0.0040659225	0.8390615582	Y	SRP,SPPDNA,DIFP,SUFP,CMPU
0.0028329829	4.0621051788	Y	SRP,NDNAD,CMPU,TRQ
0.0139479917	2.3481750488	N	SRP,DIFP,TRQ,CMPU
0.0067926026	0.9103733301	N	SRP,SPPDNA,DIFP,TRQ,3MX,3MXCON,3MXR7,3MXRN
0.0019950694	2.6632766724	Y	SRP,DIFP,CMPU
0.0009886757	15.5882997513	Y	SRP,DIFP,CMPU
0.0037770907	2.5722634792	Y	SRP,DIFP,TRQ,SUFP,CMPU
0.0039641201	1.7407031059	Y	SRP,DIFP,CMPU
0.0043838802	1.3699994087	Y	SRP,DIFP,TRQ,CMPU
0.0048823133	2.6868038177	Y	SRP,DIFP,TRQ,CMPU
0.0241755713	2.2323317528	N	SRP,DIFP,TRQ,CMPU
0.0023135522	2.2946064472	Y	SRP,DIFP,TRQ,CMPU
0.0107891560	1.9722062349	N	SRP,DIFP,TRQ,CMPU
0.0025466555	0.8813955784	Y	SRP,SPPDNA,DIFP,TRQ,3MX,3MXCON,3MXR7,3MXRN
0.0030238433	0.9340040684	Y	SRP,DIFP,TRQ,3MX,NSIP
0.0047889319	4.6491866112	Y	SRP,DIFP,TRQ,CMPU
0.0071014231	4.8028120995	Y	SRP,DIFP,TRQ,CMPU
0.0056787808	2.2227470875	Y	SRP,DIFP,TRQ,CMPU
NULL	1.1558653116	N	SRP,PAPPRP,MNS,DIFP,TRQ,2MX,2MXNC,2MXNC,2M
NULL	0.6305838227	Y	SRP,SPPDNA,NDNAD,TRQ,1SS,1SSAKN
0.0145866154	1.8246830702	N	SRP,DIFP,TRQ,CMPU
0.0027636068	0.9161416292	Y	SRP,DIFP,TRQ,CMPU
0.0055706692	0.8935137987	N	SRP,DIFP,TRQ,CMPU,SUFP
0.0108168954	1.2196669579	N	SRP,DIFP,SUFP,CMPU
0.0047497670	2.1341190338	Y	SRP,DIFP,TRQ,CMPU
0.0092551233	1.5388008356	N	SRP,DIFP,TRQ,MIX,MIX8,MIX3,MIX5,MIX1,PRNCID,MI
0.0059594968	2.3481724262	Y	SRP,DIFP,TRQ,CMPU
0.0057904930	54.7790756226	Y	SRP,DIFP,SUFP1,CMPU,SUFP
0.0078608580	0.9079577923	N	SRP,DIFP,TRQ,CMPU
0.0123805786	0.9728748202	N	SRP,DIFP,TRQ,CMPU
0.0146006895	0.8030964732	N	SRP,DIFP,TRQ,CMPU
0.0020194387	1.3486430645	Y	SRP,SPPDNA,DIFP,SUFP,3MX,3MXCON,3MXR7
0.0022245201	1.3641989231	Y	SRP,SPPDNA,DIFP,SUFP,1SS20L,PSTI
0.0081535801	1.7890001535	N	SRP,DIFP,TRQ,CMPU,SUFP
0.0014653892	1.3106725216	Y	SOHAA,SRP,DIFP,TRQ,CMPU
0.0065824217	2.1138153076	Y	SOHAA,SRP,LDIS,MISSTL,EXREV,DIFP,SUFP,CMPU
NULL	NULL	Y	SRP,NDNAD,TRQ,PPUCP,SUFP
0.0027655459	1.6254750490	Y	SRP,DIFP,TRQ,3MX,3MX7,3MXNC,3MX2,3MXLOW,3M
0.0068229577	1.9658401012	N	SRP,DIFP,TRQ,CMPU
0.0027181413	1.9235461950	Y	SRP,DIFP,TRQ,CMPU
0.0067515369	1.1697273254	N	SRP,DIFP,TRQ,CMPU
0.0043134531	1.6345840693	Y	SRP,DIFP,TRQ,3MX,3MX7,EVDEXC,3MXNC,3MXLOW,3
0.0143177127	1.1728167534	N	SRP,DIFP,SUFP,3MX,2MXIND,3MX7,3MXNC,3MXNC,3
0.0048473491	1.4679962397	Y	SRP,DIFP,TRQ,CMPU
0.0015920082	1.1757926941	Y	SRP,DIFP,TRQ,CMPU
0.0166494530	0.9172980189	N	SRP,DIFP,SUFP,3MX,2MXIND
0.0206689648	2.1486682892	N	SRP,NDNAD,SUFP,CMPU
0.0111200828	1.1394035816	N	SRP,DIFP,SUFP,3MX,3MX7
0.0045303386	1.8843837976	Y	SRP,DIFP,TRQ,CMPU
0.0049776686	1.2368178368	Y	SRP,DIFP,TRQ,CMPU

0.0085861739	0.8966888785	N	SRP,LDIS,DIFP,TRQ,CMPU,SUFP
0.0004543406	1.2112828493	Y	SRP,SPPDNA,NDNAD,SUFP,CMPU
0.0004579119	1.9866119623	Y	SRP,PAPPRP,MNS,DIFP,TRQ,SUFP,CMPU
0.0008581177	1.3852586746	Y	SRP,SPPDNA,NDNAD,CMPU
0.0062578158	0.9404332638	N	SRP,SPPDNA,DIFP,TRQ,SUFP,3MX,NSIP
0.0042364760	3.2003915310	Y	SRP,DIFP,TRQ,CMPU
0.0034779976	2.7530467510	Y	SRP,DIFP,SPP
0.0006848032	1.3271278143	Y	SRP,DIFP,SPP
0.0061894450	1.8630715609	N	SRP,DIFP,SPP
0.0016979651	1.3725368977	Y	SRP,DIFP,SPP
0.0034069060	0.9774087667	Y	SRP,SPPDNA,DIFP,SUFP,3MX,3MXCON
0.0005108460	5.9451856613	Y	SRP,DIFP,CMPU
0.0038728535	0.8760741353	Y	SRP,SPPDNA,DIFP,TRQ,3MX,3MXCON,3MXR7,3MXRN
0.0012162079	1.5944784880	Y	SRP,SPPDNA,DIFP,TRQ,2MX,2MXCON,2MXR7,EVDEXC
0.0099237626	0.9740239978	N	SRP,SPPDNA,DIFP
0.0080718659	3.9991011620	Y	SRP,DIFP,TRQ,2MX,2MX7,2MXNC,EVDEXC
0.0062022507	2.5885860920	Y	SRP,DIFP,CMPU
0.0039548767	3.3518633842	Y	SRP,DIFP,CMPU
0.0084315222	3.4361686707	Y	SRP,DIFP,CMPU
0.0048408806	3.3482680321	Y	SRP,DIFP,CMPU
0.0125892125	6.7581787109	Y	SRP,DIFP,CMPU
0.0088481735	2.0380585194	N	SRP,DIFP,CMPU
0.0055315164	1.3150104284	N	SRP,DIFP,MIX,MIX1,MIX2,MIX5,MIX5,MIX1,MIX5,MIX
0.0066231936	3.4481317997	Y	SRP,DIFP,CMPU
0.0016687488	NULL	Y	SRP,DIFP,CMPU
0.0080904989	3.2052707672	Y	SRP,DIFP,CMPU
0.0041956427	1.2837600708	Y	SRP,DIFP,3MX,3MXCON,3MXR5,3MXR1,3MXRL,3MXR
NULL	2.3142309189	Y	SRP,DIFP,CMPU
NULL	1.9817150831	Y	SRP,DIFP,1SSAKN
0.0032261480	2.2960031033	Y	SRP,DIFP,TRQ,CMPU
0.0044570956	2.2010343075	Y	SRP,DIFP,TRQ,CMPU,SUFP
0.0026499506	3.2951817513	Y	SRP,DIFP,TRQ,CMPU,SUFP
0.0006633830	1.0088655949	Y	SRP,SPPDNA,DIFP,SUFP,2MX,2MXCON,2MXRNC,EVDE
0.0054912423	1.1854630709	N	SRP,SPPDNA,DIFP,TRQ,3MX,3MXCON,3MXR1,3MXR7
0.0044074534	0.9840205908	Y	SRP,SPPDNA,DIFP,TRQ,1SS20L
0.0132172611	0.6486325264	N	SRP,SPPDNA,DIFP,TRQ,1SS20L
0.0009138867	1.8838733435	Y	SRP,DIFP,TRQ,CMPU
0.0034950578	2.3053753376	Y	SRP,DIFP,TRQ,CMPU
0.0025110340	1.5706377029	Y	SRP,DIFP,TRQ,CMPU
0.0044128909	1.8216276169	Y	SRP,DIFP,TRQ,CMPU
0.0005401015	38.2796440125	Y	SRP,DIFP,CMPU
0.0011218546	2.5363559723	Y	SRP,DIFP,CMPU
0.0024881673	14.1674985886	Y	SRP,DIFP,CMPU
0.0008339597	3.7359006405	Y	SRP,DIFP,CMPU
0.0007220027	NULL	Y	SRP,DIFP,CMPU
0.0011609909	7.5892124176	Y	SRP,DIFP,CMPU
0.0040028510	1.4105641842	Y	SRP,DIFP,CMPU
0.0101446621	0.7490209341	N	SRP,DIFP
0.0015492202	1.7635111809	Y	SRP,DIFP,3MX,3MXLOW,3MX4,3MXNC,3MXNC,3MXN
0.0001577379	3.8402044773	Y	SRP,DIFP,CMPU

0.0016154469	3.4891803265	Y	SRP,DIFP,CMPU
0.0009306652	4.4135394096	Y	SRP,DIFP,TRQ,CMPU
0.0010402465	NULL	Y	SRP,DIFP,CMPU
0.0005402145	3.2673454285	Y	SRP,DIFP,CMPU
0.0013342439	1.1807327271	Y	SRP,DIFP,CMPU
0.0025236513	1.9318797588	Y	SRP,DIFP,CMPU
0.0012998402	1.0713489056	Y	SRP,DIFP,CMPU
NULL	0.5653800964	Y	SRP,PAPPRP,MNS,DIFP,TRQ,2MX,2MXCON,2MXR2
0.0012165596	0.7232490182	Y	SRP,PAPPRP,MNS,DIFP,TRQ,2MX,2MXCON,2MXR2
0.0071664494	0.8857387304	N	SRP,DIFP,TRQ,SUFP,2MX,NSIP
0.0136446385	1.3626453876	N	SRP,DIFP,TRQ,3MX,3MX6
0.0196213182	0.9871698618	N	SRP,DIFP,TRQ,2MX,2MXNCD,EVDEXC,EVDEXC,SUFP
0.0037098073	1.1939495802	Y	SRP,DIFP,TRQ,SUFP,CMPU
0.0057241283	1.2526935339	N	SRP,DIFP,CMPU
0.0045377947	2.9580709934	Y	SRP,DIFP,TRQ,CMPU
0.0016834708	1.3617852926	Y	SRP,DIFP,TRQ,CMPU
0.0001717848	1.7790282965	Y	SRP,DIFP,TRQ,SUFP,CMPU
0.0091453185	0.6478973031	N	SRP,DIFP,TRQ,QFIH,QCFRQ
0.0032070801	0.7440193892	Y	SRP,DIFP,TRQ,CMPU
NULL	0.7885186076	N	SRP,DIFP,TRQ,1SS20L,1SSNCD,SUFP
0.0036128003	3.2961173058	Y	SRP,DIFP,TRQ,CMPU
0.0073597031	1.9847227335	Y	SRP,DIFP,TRQ,SUFP,CMPU
0.0050171087	1.5067733526	N	SRP,DIFP,CMPU
0.0088571180	1.4874495268	Y	SRP,DIFP,TRQ,CMPU
0.0043876674	1.3366142511	Y	SRP,DIFP,TRQ,CMPU
0.0005390263	1.1163094044	Y	SRP,DIFP,TRQ,SUFP,CMPU
0.0222531985	1.5061515570	N	SRP,DIFP,TRQ,CMPU
0.0009076163	3.4201178551	Y	SRP,DIFP,TRQ,CMPU
0.0047759255	0.8023933768	Y	SRP,SPPDNA,DIFP,1S9L10
0.0065642702	0.9458190799	N	SRP,SPPDNA,DIFP,1SS20L
0.0188108310	1.6170022488	N	SRP,DIFP,TRQ,3MX,2MXIND
0.0027822156	1.9081703424	Y	SRP,DIFP,TRQ,CMPU
0.0017992890	2.4099872112	Y	SRP,SPPDNA,DIFP,CMPU
NULL	2.9289386272	N	SRP,DIFP,1SS,1SSNCD
0.0024537058	1.0468084812	Y	SRP,SPPDNA,DIFP,2MX,2MX7,2MXNC,2MXNC,2MXNC
0.0227336120	0.8593848348	N	SRP,SPPDNA,DIFP,2MX,2MX7,2MXNC,2MXNC,2MXNC
0.0194439739	0.8111746311	N	SRP,SPPDNA,DIFP,1SS20L
0.0029154904	0.7091525197	Y	SRP,SPPDNA,DIFP,CMPU
0.0024621719	0.9761220217	Y	SRP,DIFP,TRQ,CMPU
0.0101788500	1.0694649220	N	SRP,DIFP,TRQ,MIX,MIX8,MIX5,MIX5,MIX5
0.0053540808	1.2635129690	N	SRP,DIFP,TRQ,MIX,MIX2,MIX5,MIX5
0.0037158770	1.0000766516	Y	SRP,SPPDNA,DIFP,TRQ,SUFP,CMPU
0.0061796317	1.3214204311	N	SRP,DIFP,TRQ,CMPU,SUFP
0.0102432007	2.5217037201	Y	SRP,DIFP,TRQ,QFIH,QCFRQ
0.0010736041	2.0970346928	Y	SRP,DIFP,TRQ,CMPU,SUFP
0.0025639855	2.7016732693	Y	SRP,DIFP,TRQ,CMPU
0.0024867314	3.0446751118	Y	SRP,DIFP,TRQ,CMPU
0.0042030793	2.6455101967	Y	SRP,DIFP,TRQ,CMPU
0.0048494325	2.0855777264	Y	SRP,DIFP,TRQ,CMPU
0.0286090299	9.9733028412	Y	SRP,DIFP,TRQ,CMPU

0.0272965413	2.0137901306	N	SRP,DIFP,CMPU
0.0113797933	1.5563131571	N	SRP,DIFP,TRQ,3MX,2MXIND,3MXNC,3MXNC,3MXNC,S
0.0101058586	1.6141134501	N	SRP,DIFP,TRQ,CMPU
0.0079394933	2.7573015690	N	SRP,DIFP,TRQ,CMPU
0.0041677291	1.6824148893	Y	SRP,DIFP,TRQ,CMPU
0.0009735587	5.6944642067	Y	SRP,DIFP,TRQ,CMPU
0.0023536528	1.9945317507	Y	SRP,DIFP,TRQ,CMPU
0.0176699571	6.5021452904	Y	SRP,DIFP,2MX,2MXIND,2MXNC,PRNCID
0.0015661094	1.7931858301	Y	SRP,DIFP,TRQ,CMPU
0.0039616288	1.1974593401	Y	SRP,DIFP,TRQ,CMPU
0.0040011192	2.0069584846	Y	SRP,DIFP,TRQ,CMPU
0.0094843432	0.9605963826	N	SRP,DIFP,TRQ,3MX,3MXNC,2MXIND,3MX7
0.0051531657	0.4670690596	Y	SRP,SPPDNA,DIFP,SUFP,1SS
0.0023525681	0.4771764278	Y	SRP,SPPDNA,DIFP,2MX,2MXCON,2MXRCU
0.0003604254	1.4437714815	Y	SRP,DIFP,TRQ,CMPU
0.0013929618	1.6175091267	Y	SRP,DIFP,TRQ,CMPU
0.0168732107	1.5422792435	N	SRP,DIFP,TRQ,2MX,2MX7,2MXNC,SUFP
0.0092661446	1.3661799431	Y	SRP,DIFP,TRQ,SUFP,3MX,3MXCON,3MXR6
0.0099357488	1.0599370003	N	SRP,DIFP,TRQ,SUFP,1SS20L
NULL	2.1887936592	Y	SRP,NDNAD,TRQ,PPUCP,SUFP
0.0018719111	5.7435717583	Y	SRP,DIFP,TRQ,CMPU
0.0134131070	1.2697790861	N	SRP,DIFP,TRQ,CMPU
0.0051554912	0.7934753895	Y	SRP,PAPPRP,MNS,DIFP,TRQ,2MX,2MX7,2MXNC,2MXM
0.0159702878	0.8032224178	N	SRP,SPPDNA,DIFP,SUFP,1SS20L,1SSNCD
0.0052621253	1.5945173502	Y	SRP,DIFP,TRQ,CMPU
0.0023084448	0.9960867167	Y	SRP,LDIS,DIFP,TRQ,CMPU
0.0077506485	1.7671389580	N	SRP,DIFP,TRQ,CMPU
0.0021682424	3.6469101906	Y	SRP,DIFP,TRQ,CMPU
0.0066096098	2.8612122536	Y	SRP,DIFP,TRQ,CMPU
0.0044267625	3.5922248363	Y	SRP,DIFP,TRQ,CMPU,SUFP
0.0035640993	25.0870628357	Y	SRP,DIFP,TRQ,SUFP,CMPU
0.0034924066	3.5277531147	Y	SRP,DIFP,TRQ,SUFP,CMPU
0.0072765946	1.8555098772	N	SRP,DIFP,TRQ,SUFP,CMPU
0.0092353970	1.7567080259	N	SRP,DIFP,TRQ,SUFP,2MX,2MX7,2MXNC
0.0069838860	1.4364426136	N	SRP,DIFP,TRQ,SUFP,3MX,3MXLOW,3MXINC
0.0038329309	7.0831227303	Y	SRP,PAPPRP,MNS,DIFP,TRQ,SUFP,CMPU
0.0270945933	2.0794239044	N	SRP,DIFP,TRQ,3MX,3MX7
0.0078275111	5.3604531288	Y	SRP,DIFP,TRQ,CMPU
0.0086161690	0.8419950008	N	SRP,SPPDNA,DIFP
0.0139549747	1.7367578745	N	SRP,DIFP,TRQ,MIX,MIX8
0.0168085620	1.5731102228	N	SRP,DIFP,TRQ,2MX,2MXNC,2MX7
0.0096560884	0.9235055447	N	SRP,DIFP,TRQ,2MX,NSIP
0.0008954645	0.8946689367	Y	SRP,NDNAD,TRQ,CMPU
0.0048659495	0.9483433366	Y	SRP,DIFP,TRQ,2MX,NSIP
0.0047617983	1.0482540131	Y	SRP,DIFP,TRQ,2MX,NSIP
0.0118828565	1.1496583223	N	SRP,DIFP,TRQ,NSIP,3MX
0.0002115436	3.3746623993	Y	SRP,DIFP,PSTN,TRQ,SUFP,CMPU
0.0178950578	1.4253244400	N	SRP,DIFP,CMPU
0.0101995002	2.6909191608	Y	SRP,DIFP,3MX,3MXNC
0.0213027168	1.3319915533	N	SRP,DIFP,CMPU

0.0051643034	1.3693217039	Y	SRP,DIFP,CMPU
0.0121862674	1.0160713196	N	SRP,DIFP,CMPU
0.0055648279	1.3198553324	Y	SRP,DIFP,CMPU
0.0134622529	1.0556244850	N	SRP,DIFP,TRQ,MIX,NSIP
0.0118480120	1.0222127438	N	SRP,DIFP,TRQ,CMPU
0.0042678677	2.6035628319	Y	SRP,DIFP,CMPU
0.0047158552	2.8414595127	Y	SRP,DIFP,CMPU
0.0082144532	2.7328095436	N	SRP,DIFP,SUFP,CMPU
0.0152042406	2.4080803394	N	SRP,DIFP,MIX,MIX5
0.0039141444	0.9543620348	Y	SRP,SPPDNA,DIFP,TRQ,1SS,1SS20L
0.0032109942	1.1723400354	Y	SRP,SPPDNA,DIFP,TRQ,2MX,2MXNC
0.0034165182	2.9837133884	Y	SRP,DIFP,TRQ,CMPU
0.0051388354	1.0407823324	N	SRP,DIFP,TRQ,CMPU
0.0167291239	2.7452917099	Y	SRP,DIFP,TRQ
0.0127838077	1.1035996675	N	SRP,SPPDNA,DIFP,PSTP,TRQ,SUFP,1SSAKN,PSTI

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EXC,EVDEXC,EVDEXC,EVDEXC,EVDEXC,EVDEXC

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C,2MXNC,2MXNC,2MXNC,2MXNC,2MXNC,2MXNC,2MXNC,2MXNC,2MXNC,2MXNC,2MXNC,SCSNC,SCSNC

SCSNC,SCSNC,SCSC7,SCINMX,SCSNC,SCSNC,SCSNC,SCLOW,SCSNC,SCSNC,3MXNC

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Cathie Allen

From: O'Malley.TroyS(CC) <[redacted]
Sent: Monday, 14 March 2022 12:46 PM
To: Cathie Allen
Subject: NDNAD DIFP PRIORITY
Attachments: NDNAD_DIFP_Priority.xlsx

Cathie

Please find attached the extract of samples with Analytical Priority as requested.

Troy

Cathie Allen

From: Cathie Allen
Sent: Monday, 14 March 2022 12:52 PM
To: Justin Howes
Subject: Data
Attachments: NDNAD_DIFP_Priority.xlsx

Hi Justin

Here's the data, with the priority added to one column. Enjoy!

Cheers
Cathie

Cathie Allen **BSc, MSc (Forensic Science) (She/Her*)**
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

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

p 07 [redacted] **m** [redacted]
a 39 Kessels Road, Coopers Plains, QLD 4108
e [redacted] **w** www.health.qld.gov.au/fss

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

*If you're wondering about the use of pronouns She/Her on this signature block, I encourage you to read some resources available here

Cathie Allen

From: Cathie Allen
Sent: Monday, 14 March 2022 4:25 PM
To: Justin Howes
Subject: RE: report

No problem Justin, I understand that it's a big data set.

Cheers
Cathie

Cathie Allen **BSc, MSc (Forensic Science) (She/Her*)**
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

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

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

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

*If you're wondering about the use of pronouns She/Her on this signature block, I encourage you to read some resources available here

From: Justin Howes <[redacted]
Sent: Monday, 14 March 2022 4:04 PM
To: Cathie Allen <[redacted]
Subject: report

Hi Cathie, sorry I got sidetracked trying to sort data and found some duplicates….

I will do the report first thing in the morning – I have the data.

Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

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

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

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.

Request Date	Request made by	Scope of Request
22-May-20	Cathie Allen, Managing Scientist	Report to be created that captures Date, Time, Barcode, Result, Scientist who entered the result, Scientist who reviewed the result - data to be captured for a scientist who had reviewed a result. Report to be created that captures Date, Time, Barcode, Result, Scientist who entered the result, Scientist who reviewed the result - data to be captured for a scientist who had entered a result.
18-Feb-22	Cathie Allen, Managing Scientist	Data regarding samples within the DIFP range and the DNA results obtained if they had been through microcon concentration for a period of approx 4 years

Quote Provided	If lab proceeded with request	Date of request
No quote provided, work undertaken via the Support Arrangement	The request was progressed	22-May-20
Quote provided via email	The request was progressed	2-Mar-22

Date of bdna providing data
Report within the Forensic Register on 11 June 2020
2 Mar 2022
4 Mar 2022
9 Mar 2022
14 Mar 2022

From: Paula Brisotto <[redacted]
Sent: Friday, 12 January 2018 11:37 AM
To: [redacted]
Subject: As requested.
Attachments: Report_Evaluation of the efficacy of Microcons_v2.doc

Hey Justin,

It's all good here. Fairly quiet. Kylie has sent an email to RT1 in yours and Amanda's absence letting them know they can go to her for help.

Take it easy.

Thanks,
Paula

In the matter of the *Commissions of Inquiry Act 1950*
Commissions of Inquiry Order (No. 3) 2022
Commission of Inquiry into Forensic DNA Testing in Queensland

STATEMENT OF DALE FRIEBERG

I, **Dale Frieberg,** of 200 Roma Street, Brisbane, Queensland, 4001 state as follows:

1. The following statement is provided in response to a notice I received from the Commission of Inquiry into Forensic DNA Testing in Queensland requiring me to give information in a written statement regarding my knowledge of matters set out in the Schedule attached to that notice.

Attached and marked "Exhibit 1" is a copy of that notice.

Question 1(a): Explain why the Executive Briefing Note and draft letter was prepared, in lieu of the Ministerial Briefing Note prepared by Inspector David Neville.

Briefing Notes

2. Briefing Notes are used by the Queensland Police Service ("the QPS") to convey information both within and outside the organisation.

3. Briefing Notes within the QPS can take a number of forms. The type of Briefing Note depends on the nature of the issue being raised, the timeliness in which a response or information is require and its intended audience.

4. The forms of Briefing Notes used within the QPS are as follows:

   (a) verbal communication;

   (b) email correspondence;

(c) summaries for the Assistant Commissioner ("AC") of the Operations Command;

(d) Operational Matters of Note for the QPS Board of Management – this is collated by the AC of each Region or Command and forwarded accordingly;

(e) Possible Parliamentary Questions ("PPQ");

(f) Executive Briefing Note ("EBN") – this is an internal document used to brief the Senior Executive for escalation to the Commissioner through the chain of command. The person drafting the EBN will commonly include draft letters or memorandums for the Deputy or the Commissioner to adopt; and

(g) Ministerial Briefing Note ("MBN") – this is used to escalate the issue from the Commissioner to the Minister.

5. EBNs and MBNs are generally of a similar format, with exception of the cover sheet.

6. The Executive Member may exercise their discretion to convert an EBN into an MBN or vice versa at any time.

7. When an EBN is submitted and received by the Commissioner, the Commissioner may then brief the relevant Minister or others with the information contained therein.

Background

8. In **late November 2021 to early December 2021**, there was increased media coverage around the inadequacies of the Queensland Health Forensic and Scientific Services ("QHFSS") laboratory. The published articles related to the Shandee Blackburn murder investigation.

9. Around that same time, Inspector David Neville ("Inspector Neville") and I were having regular conversations about the deficiencies of DNA testing in the QHFSS laboratory.

[redacted] .. [redacted]
Witness

10. Inspector Neville told me that he had raised the issues with the Managing Scientist, Ms Catherine Allen ("Ms Allen"). Inspector Neville said that Ms Allen had undertaken to provide the QPS with a report reviewing the data on the testing issues identified by Inspector Neville.

11. On **6 December 2021**, I received an email from Ms Allen advising that she intended to have the Shandee Blackburn case file sent to the Australian Federal Police ("AFP") for peer review.

12. I appraised Acting AC David French ("AAC French") of these issues by sending him regular updating emails.

Attached and marked "Exhibit 2" are copies of the Briefing Notes that I sent to AAC French in relation to the issues identified above.

Decision to choose Executive Briefing Note

13. In **February 2022**, I had a conversation with Inspector Neville. He told me that he had not received the report that Ms Allen told him she would provide.

14. We remained concerned about the issues with DNA testing at QHFSS and the delay in the provision of the above report. That led to our decision to prepare a Briefing Note.

15. We initially agreed that the Briefing Note would take the form of an MBN. We had further conversations about this and determined that it was more appropriate to convert the MBN into an EBN at first instance.

16. The reason this decision was made was because it was important for the issues to be raised through the chain of command. This organisational structure is of vital importance within the QPS.

17. Inspector Neville and I felt that there was no cooperation on the part of QHFSS to address the issues we had raised at our level. It was on that basis that we felt it was prudent to escalate the issues to those higher than us in the chain of command.

[redacted]

18. We considered it essential that AAC French, the Deputy and the Commissioner were properly briefed on the issues. We felt that the submission of the EBN placed them in a position where they could discuss the issues in detail and make decisions as to the appropriate steps to be taken.

19. The EBN also provided an opportunity for the Commissioner to send the accompanying letter drafted by Inspector Neville to the Director-General of the Department of Health, Mr John Wakefield PSM ("the Director-General").

20. The Director-General was the Commissioner's equivalent within Queensland Health. It is usual practice for the QPS to send these types of interdepartmental letters when EBNs are submitted.

21. The decision as to whether an EBN is converted into a MBN usually rests with the AC, the Deputy or the Commissioner.

Question 1(b): Describe in detail any meetings, discussions or correspondence you were involved in regarding the Ministerial Executive Briefing Note, Executive Briefing Note and draft letter.

22. I was aware that Inspector Neville was conducting an internal review of the success rate of obtaining a DNA profile for samples initially reported as "DNA insufficient for further processing". We had regular verbal conversations about these issues throughout **December 2021**.

23. We continued our verbal discussions about the issues with the QHFSS lab DNA testing upon Inspector Neville's return from annual leave in **February 2022**. These discussions led to our decision to prepare a Briefing Note.

24. It was initially agreed that Inspector Neville would draft an MBN given his extensive involvement and knowledge of the issues surrounding DNA testing.

25. Inspector Neville prepared the MBN on or around **14 February 2022**.

26. Inspector Neville and I continued to discuss the form of the Briefing Note verbally (see paragraphs 13 to 19 of this statement).

27. All my conversations with Inspector Neville in relation to the preparation of the Briefing Note were verbal. Our conversations were informal and very regular, so I did not make any notes.

28. I received an email from Inspector Neville on 22 February 2022 confirming that he changed the draft MBN to and EBN and had prepared a supporting letter addressed to the Director-General.

Attached and marked "Exhibit 3" is a copy of the email sent from Inspector Neville on 22 February 2022.

29. I reviewed the draft EBN and supporting letter on **22 February 2022**.

30. I supported the content drafted by Inspector Neville and arranged for Sergeant Karen Heit ("Sergeant Heit") to submit the EBN and the supporting letter to AAC French's office on that date.

Attached and marked "Exhibit 4" is a copy of the email submitting the EBN and supporting letter to AAC French on 22 February 2022.

31. It was expected that the EBN and the supporting letter would be forwarded through the chain of command to the Commissioner.

32. Additionally, on **22 February 2022**, I received an email from Sergeant Heit advising that the QPS had received an email sent on behalf of the Office of the Minister for Health and Ambulance Service. The email sought urgent advice from the QPS for an upcoming parliamentary session.

Attached and marked "Exhibit 5" is a copy of the email chain dated 22 February 2022.

33. On **24 February 2022**, I forwarded an email I received from Inspector Neville earlier that afternoon to the Support Officer of the Office of the Forensic Services Group. The email was addressed to Ms Allen and reiterated his concerns about DNA testing performed by QHFSS. I forwarded the email so it could be raised with Superintendent Bruce McNab ("Superintendent McNab") upon him taking up the Superintendent role in the Forensic Services Group on the following Monday.

[redacted]

Attached and marked "Exhibit 6" is a copy of the email sent to the Support Officer of the Office of the Forensic Services Group on 24 February 2022.

34. I concluded my secondment with the Forensic Services Group on the afternoon of **24 February** 2022. I returned to my position as the Superintendent of the Ethical Standards Command.

35. On **27 February 2022**, Superintendent McNab commenced in the role of Superintendent of the Forensic Services Group.

36. I have had no further involvement in this matter since my return to the Ethical Standards Command.

37. Whilst I have not been directly involved with the Forensic Services Group since my departure on **24 February 2022**, I am aware of the following matters:

(a) On **31 March 2022**, Ms Jenna De Marco (Acting Support Officer in the Office of the Superintendent of the Forensic Services Group) ("Ms De Marco") sent an email to AAC French following up on the EBN and supporting letter I had submitted on **22 February 2022**; and

Attached and marked "Exhibit 7" is a copy of the email sent from Ms De Marco on 31 March 2022.

(b) Inspector Neville told me that he was subsequently called to Minister Mark Ryan MP's office by the Commissioner. I understand that the Commissioner told Inspector Neville that she had not been briefed about the issues raised in the EBN and supporting letter he drafted.

TAKEN AND DECLARED before me at Brisbane in the State of Queensland 4000 this 2nd day of November 2022

[redacted]

Dale Frieberg

Witness

Daniel John Barter
Solicitor
McGinness & Associates Lawyers

Exhibit 1

Notice number: 2022/00305

COMMISSION OF INQUIRY INTO FORENSIC DNA TESTING IN QUEENSLAND

Section 5(1)(d) of the *Commissions of Inquiry Act 1950*

REQUIREMENT TO GIVE INFORMATION IN A WRITTEN STATEMENT

To: Dale Frieberg

Of: Queensland Police Service

I, Walter Sofronoff KC, Commissioner, appointed pursuant to Commissions of Inquiry Order (No. 3) 2022 to inquire into certain matters pertaining to forensic DNA testing in Queensland require you to attend to give a written statement to the Commission pursuant to section 5(1)(d) of the *Commissions of Inquiry Act 1950* in regard to your knowledge of the matters set out in the Schedule annexed hereto.

YOU MUST COMPLY WITH THIS REQUIREMENT BY:

Giving a written statement signed and witnessed as a declaration in accordance with the *Oaths Act 1867* to the Commission of Inquiry on or before **5.00pm on 31 October 2022** by delivering it to Level 21, 111 George Street, Brisbane.

A copy of the written statement must also be provided electronically by email at [redacted] with the subject line "Requirement for Written Statement".

If you believe that you have a reasonable excuse for not complying with this notice, you will need to satisfy me of this by the above date.

DATED this 27th day of October 2022

[redacted]

Walter Sofronoff KC
Commissioner
Commission of Inquiry into Forensic DNA Testing in Queensland

Notice 2022/00305

Schedule of topics for statement

Superintendent Dale Frieberg

Executive Briefing Note

1. Explain in detail your involvement in an Executive Briefing Note titled "POTENTIAL ISSUES WITH TESTING OF DNA BY QUEENSLAND HEALTH FORENSIC AND SCIENTIFIC SERVICES" and draft letter addressed to Dr John Wakefield (**attached**).
    a. Explain why the Executive Briefing Note and draft letter was prepared, in lieu of the Ministerial Briefing Note prepared by Inspector David Neville (**attached**).
    b. Describe in detail any meetings, discussions or correspondence you were involved in regarding the Ministerial Executive Briefing Note, Executive Briefing Note and draft letter.
    c. Attach any documents relevant to (a) and (b) above.

Exhibit 2

Frieberg.DaleJ[ESC]

From: Frieberg.DaleJ[OSC]
Sent: Monday, 29 November 2021 15:05
To: French.DavidA[OSC]
Subject: RE: DNA testing

OFFICIAL

It does happen. Dave is very good at providing it.

Dale Frieberg APM
Superintendent | Forensic Services Group | Queensland Police Service | [redacted]

OFFICIAL

From: French.DavidA[OSC] [redacted]
Sent: Monday, 29 November 2021 15:00
To: Frieberg.DaleJ[OSC] [redacted]
Subject: RE: DNA testing

I would think as part of our client feedback it should be raised.

Does this happen regularly?

David French |
Acting Assistant Commissioner
Operations Support Command
Queensland Police Service
[redacted]

From: Frieberg.DaleJ[OSC] <Frieberg.DaleJ@police.qld.gov.au>
Sent: Monday, 29 November 2021 14:50
To: French.DavidA[OSC] <French.David@police.qld.gov.au>
Subject: FW: DNA testing

OFFICIAL

Given the sensitivities around QH at present, I welcome your view.

Dale Frieberg APM

[redacted]

OFFICIAL

From: Neville.DavidH[OSC] [redacted]
Sent: Monday, 29 November 2021 12:58
To: Frieberg.DaleJ[OSC] [redacted]
Subject: DNA testing

Dale
On Friday I was advised of a potential issue with DNA testing in relation to the Rene Latimore murder investigation which was solved over the weekend. The initial results reported for 10 samples were "DNA insufficient for further testing". Given the importance of the samples, QH was asked to retest them. After these items were retested, each yielded a profile that could be linked to a person with a likelihood ratio of >100 Billion.

Exhibit Number	Exhibit type	Label	Location	Initial result	Result after
[redacted]	Swab	RB60 - Top of backrest of chair	in Bedroom 1	DNA INSUFFICIENT FOR FURTHER PROCESSING	[redacted]
	Trace DNA Kit	RB22 - Left calf	of decedent	DNA INSUFFICIENT FOR FURTHER PROCESSING	
	Swab	Item V28	collected from the sides and rear of the mobile phone in the centre console top compartment	DNA INSUFFICIENT FOR FURTHER PROCESSING	
	Swab	Item V9	collected from the interior driver side A Pillar door trim	DNA INSUFFICIENT FOR FURTHER PROCESSING	
	Fabric	RB78a - Excise of bloodstains	from pink track pants located in Bedroom 1	DNA INSUFFICIENT FOR FURTHER PROCESSING	
	Trace DNA Kit	RB109a - Tapelift of exterior	condom wrapper	DNA INSUFFICIENT FOR FURTHER PROCESSING	
	Fingernail Scraping	left Nails	LATIMORE Rene* SS21J1697 PM Samples	DNA INSUFFICIENT FOR FURTHER PROCESSING	

[redacted]					[redacted]
	Swab	Item SB7 - Trace DNA swab	collected from inner condom packaging	DNA INSUFFICIENT FOR FURTHER PROCESSING	
	Swab	Item SB1a- Trace DNA swab	collected from cartridge case	DNA INSUFFICIENT FOR FURTHER PROCESSING	
	Epithelial Fraction	RB110a - Exterior shaft	Condom	DNA INSUFFICIENT FOR FURTHER PROCESSING	

During the initial part of testing the amount of DNA present is quantified. The sample only goes on to be profiled if it is over a certain threshold. Given what has occurred, I think this threshold needs to be reviewed. Are you happy for me to raise this with QH.

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

Frieberg.DaleJ[ESC]

From: Frieberg.DaleJ[OSC]
Sent: Thursday, 2 December 2021 12:27
To: French.DavidA[OSC]
Subject: RE: Blackburn matter

OFFICIAL

Yes interesting

Dale Frieberg APM

[redacted]

OFFICIAL

From: French.DavidA[OSC] [redacted]
Sent: Thursday, 2 December 2021 12:22
To: Frieberg.DaleJ[OSC] [redacted]
Subject: RE: Blackburn matter

Thanks Dale,

I see the announcement (the Australian) that the inquest is being re-opened.

David French |
Acting Assistant Commissioner
Operations Support Command
Queensland Police Service
[redacted]

INTEGRITY PROFESSIONALISM COMMUNITY RESPECT & FAIRNESS

From: Frieberg.DaleJ[OSC] [redacted]
Sent: Thursday, 2 December 2021 12:08
To: French.DavidA[OSC] [redacted]

Frieberg.DaleJ[ESC]

From: Frieberg.DaleJ[OSC]
Sent: Thursday, 2 December 2021 12:08
To: French.DavidA[OSC]
Cc: Neville.DavidH[OSC]; Support Officer FSG[OSC]; Strategy and Performance OSC
Subject: FW: Blackburn matter
Attachments: FW: Op Lima Zimzala; DNA testing

OFFICIAL

Morning AAC

Please see below link – a lot of media on this topic and it is continuing as you would be aware.

Attached also are emails pertaining to DNA and the Blackburn matter.

Cathie Allen who is the Managing Scientist, Police Services Stream, Forensic and Scientific Services (Prevention Division) of Queensland Health. Part of her area of responsibility revolves around DNA.

Dave has raised an issue with regard to another murder (Rene Latimore) which has some similarity to the Blackburn murder currently being featured regularly in the media. In the case of Latimore, DNA samples provided to QH were deemed to be DNA insufficient. On further testing they yielded results.

In conversation this week that Dave has had with Cathie Allen, Cathie has in Dave's view attempted to shift risk/blame back to the QPS indicating it is incumbent on the QPS to prioritise testing and that we should be monitoring all results and request reworks when a sample yields an unusual result. The concern here for us is that police are not DNA experts and would not have knowledge of the likelihood of a particular sample yielding a profile based on a quantification threshold (relying on the expert advice of the scientist – who has provided advice previously there was insufficient DNA to get a result – contrary to the outcome when retested).

Ms Allen in her conversation also made an accusation that there must be someone from thew QPS leaking information to the media in the most recent press regarding their processes.

On a side note, Dave has raised also whether there needs to be a review of what the threshold value should be – Cathie advised there was no need as they had ample data to support their processes.

For information in event something comes QPS way.

D

Dale Frieberg APM

[redacted]

OFFICIAL

From: Neville.DavidH[OSC] <[redacted]>
Sent: Thursday, 2 December 2021 10:15

Frieberg.DaleJ[ESC]

From: Frieberg.DaleJ[OSC]
Sent: Monday, 6 December 2021 12:24
To: French.DavidA[OSC]
Cc: Strategy and Performance OSC; Support Officer FSG[OSC]
Subject: FW: Peer Review of Forensic DNA Analysis casefile

OFFICIAL

AAC

I will call you about this, but I agree with Dave. There has been no consultation with us regarding this approach by QH.

D

Dale Frieberg APM

[redacted]

OFFICIAL

From: Neville.DavidH[OSC] <[redacted]
Sent: Monday, 6 December 2021 12:10
To: Frieberg.DaleJ[OSC] <[redacted]
Subject: FW: Peer Review of Forensic DNA Analysis casefile

Dale
I would like to raise my concerns about QHFSS releasing case information to a third party without the consent of the QPS. This information including everything in the casefile is confidential in nature and should not have been released without the permission of the QPS.

The QPS has agreed for testing to be undertaken by QHFSS on the condition that it meets the requirements of ISO17025. That includes:
4.2.1 Maintaining confidentially of information provided to it by the customer or created during laboratory testing.
7.1.1 c) Obtaining customer approval before activities are to be performed by an external provider.

It is a breach of the standard for QHFSS to have made this decision without our approval. It may also breach Qld information privacy laws.

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

From: Cathie Allen [redacted]
Sent: Monday, 6 December 2021 11:19
To: Frieberg.DaleJ[OSC] [redacted]
Cc: Lara Keller [redacted]; Neville.DavidH[OSC] [redacted]
Subject: Peer Review of Forensic DNA Analysis casefile

Hi Dale

Recent negative media articles regarding the work undertaken in the Forensic DNA Analysis laboratory for an unsolved homicide case has generated a number of enquiries from the Minister's Office, the DG's office, the Coroner and the QPS.

With respect to the DNA analysis aspect of this case, FSS feel it prudent to have the DNA casefile peer reviewed by an independent DNA practitioner, and as such, we have engaged with Dr Sarah Benson, Chief Forensic Scientist, Operational Science and Technology of the AFP. Dr Benson has agreed to assign a forensic DNA expert to peer review the casefile, with a view to re-reviewing the reported DNA outcomes, provide any recommendations regarding any new processing that could be undertaken and place the laboratory in a good position if a new Inquest date is set in the future. If recommendations regarding new processing are put forward, FSS will engage with the QPS regarding their desire to undertake this, prior to any work being done (given the case is unsolved, and may use any remaining DNA extract).

We will be providing the casefile to the AFP, with the understanding that the review is being undertaken around their operational requirements, given no new Inquest date has been set.

Please let me know if you have any queries regarding this.

Cheers
Cathie

Cathie Allen BSc, MSc (Forensic Science) (She/Her*)
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

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

[redacted]

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

"If you're wondering about the use of pronouns She/Her on this signature block, I encourage you to read some resources available here

****

****

Exhibit 3

Frieberg.DaleJ[ESC]

From: Heit.KarenL[OSC]
Sent: Tuesday, 22 February 2022 12:53
To: Frieberg.DaleJ[OSC]
Subject: FW: EBN and letter under hand of commissioner
Attachments: EBN QHFSS DNA sample triaging.doc; Ltr to DG Health from COP re DNA sample triaging.doc

Should we include how much we pay QH for DNA samples?

Cheers

K

Karen Heit | Sergeant
Support Officer
Forensic Services Group
Operations Support Command
Queensland Police Service
[redacted]

From: Neville.DavidH[OSC] <Neville.DavidH@police.qld.gov.au>
Sent: Tuesday, 22 February 2022 12:28
To: Supt FSG <OSC-D-SuptFSBOffice@qldpolice.onmicrosoft.com>; Support Officer FSG[OSC] <SupportOfficerFSG@police.qld.gov.au>
Cc: Foxover.StephanP[OSC] <Foxover.StephanP@police.qld.gov.au>
Subject: EBN and letter under hand of commissioner

Hi
I have changed to EBN and included letter requesting a review

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

EXECUTIVE BRIEFING NOTE

SUBJECT: POTENTIAL ISSUES WITH TESTING OF DNA BY QUEENSLAND HEALTH FORENSIC AND SCIENTIFIC SERVICES

PURPOSE:

1. To inform the Commissioner of potential issues reported in the media relating to the testing of DNA samples by Queensland Health Forensic and Scientific Services.

BACKGROUND:

2. Queensland Health Forensic and Scientific Services (QHFSS) undertakes DNA testing on behalf of the Queensland Police Service (QPS). Since November 2021 QHFSS has received continuous criticism in *The Australian* newspaper about the DNA testing it performed as part of the 2013 investigation into the murder of Shandee Blackburn. The scope of the criticism has now widened to the threshold value used by QHFSS to determine if testing of a sample should continue.

3. In February 2018 QHFSS made a recommendation to QPS that testing of samples containing less than 0.008ng/uL of DNA should discontinue because the chance of obtaining a profile would be less than 2%. QHFSS advised that QPS could request testing to continue if the sample was critical to a case. Except for 'Priority One' samples, the QPS agreed to discontinue testing at that point as a matter of routine based on the advice.

4. Prior to this threshold being established, it was routine for samples with low amounts of DNA to undergo a process of concentration to improve the likelihood of attaining a profile. It is understood that the removal of this process as a matter of routine resulted in a significant cost saving for QHFSS.

5. On 14 November 2018 Inspector David Neville raised concern with Ms Cathie Allen, Managing Scientist, QHFSS that the triage process may be problematic after 3 out of 4 below threshold samples from a murder investigation yielded a result after QPS requested testing to continue. At that time QHFSS provided reassurance that the success rate would be lower than 2% and that the matter should be treated as an aberration.

6. On 26 November 2021 police investigating the murder of Renee Latimore raised concerns about 33 samples that were initially reported as having 'insufficient DNA for further testing'. When QHFSS was requested to continue with testing, 10 of them yielding a full profile.

7. Based on the results of the Latimore case, the DNA Management Section undertook a wider review of results achieved when the QPS requested testing to continue during the period of July to December 2021. This revealed 51 out of 160 samples provided a profile when the QPS requested testing to continue. This equates to a 30% success for samples that did not meet testing threshold.

8. As a result of the internal review, on 13 December 2021 Inspector Neville requested an explanation from Ms Allen as to why police were observing a 30% success rate for samples that were initially reported as 'insufficient DNA for further testing'. A request was also made for the threshold value to be reviewed to ensure it remained valid.

Continuation of Executive Briefing Note

SUBJECT: **POTENTIAL ISSUES WITH TESTING OF DNA BY QUEENSLAND HEALTH FORENSIC AND SCIENTIFIC SERVICES**

9. On 17 February 2022 *The Australian* published another article relating to the Shandee Blackburn case claiming that thresholds used by QHFSS to triage testing are too high. It claims that the Queensland lab requires crime scene samples to have the equivalent of at least 22 cells to be fully tested, otherwise they are deemed to have insufficient DNA. It claims that the threshold is double the 11 cells required in NSW, and almost three times the eight cells that the product manufacturer has used to obtain good quality DNA profiles. It alleges there is potentially a very large number of cases where offenders aren't being identified when they should be.

ISSUES:

10. Over the past 12-month period approximately 4500 samples were reported by QHFSS as having 'insufficient DNA for further testing'. This would include samples from both volume and major crime matters. The results of the internal review indicate a significant number of these (up to 30%) may have produced a profile if the samples were concentrated and testing continued.

11. QHFSS indicated that it has moved the portion of the budget previously used to fund the sample concentration process to another area of the business. As a result, it may seek additional funding from the QPS if the process is reimplemented as a matter of routine.

12. The truncation of testing of low concentration samples will also have saved significant processing and interpretation time within the laboratory. A lowering of the threshold for testing to continue will mostly likely increase testing turnaround times.

13. QHFSS is yet to address the concerns raised by Inspector Neville other than indicating they will respond in due course. These concerns were raised prior to this issue around thresholds being raised in the media.

14. A review of the sample triage processes undertaken at QHFSS is recommended to ensure the thresholds for further testing remain valid. A letter under the hand of Commissioner requesting such review is attached for consideration of signing.

RECOMMENDATION/S:

15. That the content of the briefing note be noted.

16. That the Commissioner sign the attached letter requesting an interdepartmental review of the sample triage processes implemented for DNA testing.

D FRENCH
A/ASSISTANT COMMISSIONER
OPERATIONS SUPPORT COMMAND

Contact Officer:
Inspector David Neville
Inspector, Biometrics
[redacted]

Continuation of Executive Briefing Note

SUBJECT: **POTENTIAL ISSUES WITH TESTING OF DNA BY QUEENSLAND HEALTH FORENSIC AND SCIENTIFIC SERVICES**

NOTED / SUPPORTED / APPROVED

Comment:

DEPUTY COMMISSIONER (CRIME, COUNTER-TERRORISM & SPECIALIST OPERATIONS)
/ /

NOTED / SUPPORTED / APPROVED

Comment:

DEPUTY COMMISSIONER (REGIONAL QUEENSLAND)
/ /

NOTED / SUPPORTED / APPROVED

Comment:

DEPUTY COMMISSIONER (SOUTHERN QUEENSLAND)
/ /

NOTED / SUPPORTED / APPROVED

Comment:

DEPUTY COMMISSIONER (STRATEGY & CORPORATE SERVICES)
/ /

COMMISSIONER
/ /

25 July 2022

Dr John Wakefield PSM
Director-General
Queensland Health
GPO Box 48 Brisbane, Queensland 4001 Australia

Dear Dr Wakefield

As you are aware, Queensland Health Forensic and Scientific Services (QHFSS) undertakes DNA testing on behalf of the Queensland Police Service (QPS).

In February 2018 QHFSS made a recommendation to QPS that testing of samples containing less than 0.008ng/uL of DNA should discontinue because the chance of obtaining a profile would be less than 2%. QHFSS advised that they would report samples below this threshold as 'insufficient DNA for further testing' and that QPS could request testing to continue if the sample was critical to a case. Except for 'Priority One' samples, the QPS agreed to discontinue testing at that point as a matter of routine based on the advice.

In December 2021 the QPS undertook a review of the success rate of obtaining a profile when it requested testing to continue for samples initially reported as 'insufficient DNA for further testing'. This revealed that 30% of the samples yielded a useable DNA profile when testing was continued.

I understand that the sample triage process may have resulted in considerable cost and time savings, however the relatively high success rates observed when testing is continued raises concerns in relation to the threshold value used. If the value is too high, it has the potential to result in offenders going undetected.

I have been keeping abreast of commentary in *The Australian* relating to DNA testing undertaken by QHFSS. On 17 February 2022 this widened to claims that thresholds used by QHFSS to triage testing are too high. It stated that the Queensland lab requires crime scene samples to have the equivalent of at least

22 cells to be fully tested, otherwise they are deemed to have insufficient DNA. It claimed that the threshold is double the 11 cells required in NSW, and almost three times the eight cells that the product manufacturer has used to obtain good quality DNA profiles.

I am not able to assess the basis or legitimacy of the claims made by *The Australian*, however they come at a time where similar concerns have been raised internally within my organisation.

Considering the current circumstances, I request that a review of the current DNA sample triage process be undertaken as a matter of urgency to ensure that the threshold value is still valid. Such a review should include benchmarking practices with other DNA laboratories within Australia.

I would request that an interdepartmental working party be established to undertake the review and offer the QPS to take a lead role. Should independent advice be required during the review, I would recommend this would occur by way of mutual agreement between both agencies.

The key point of contact within the QPS for the purposes of the review is Inspector David Neville, Biometrics, Forensic Services Group. His contact number is [redacted]

Yours sincerely

KATARINA CARROLL APM
COMMISSIONER

Exhibit 4

Bri McKenzie

From: Heit.KarenL[OSC] <[redacted]>
Sent: Tuesday, 22 February 2022 2:31 PM
To: Strategy and Performance OSC
Cc: Brits.DelindaC[OSC]
Subject: DOC22/274597 Ltr to DG Health re DNA Sample triaging & EBN QHFSS DNA sample triaging
Attachments: EBN QHFSS DNA sample triaging.doc; Ltr to DG Health from COP re DNA sample triaging.doc

Hi

Please find attached EBN and Letter under the hand of the Commissioner in relation to DNA sample triaging currently in place at QHFSS. This issue is currently in the media being highlighted by the Shandee Blackburn murder.

Cheers

K

Karen Heit | Sergeant
Support Officer
Forensic Services Group
Operations Support Command
Queensland Police Service
[redacted]

From: Heit.KarenL[OSC]
Sent: Tuesday, 22 February 2022 13:28
To: Brits.DelindaC[OSC] <[redacted]>
Subject: FW: EBN QHFSS DNA sample triaging

Please objectify and advise DOC no.

Docs can be moved to A/C's working folder.

Cheers

K

Karen Heit | Sergeant
Support Officer
Forensic Services Group
Operations Support Command
Queensland Police Service
[redacted]

From: Neville.DavidH[OSC] <[redacted]
Sent: Tuesday, 22 February 2022 13:02
To: Heit.KarenL[OSC] <[redacted]>
Subject: EBN QHFSS DNA sample triaging

Exhibit 5

Frieberg.DaleJ[ESC]

From: Heit.KarenL[OSC]
Sent: Tuesday, 22 February 2022 11:52
To: Frieberg.DaleJ[OSC]
Subject: FW: URGENT - Prepared for Parliament - URGENT DOT POINTS REQUIRED re DNA TESTING
Attachments: DNA compliance stats - charging district.xlsx

Copy for your records.

Cheers

K

Karen Heit | Sergeant
Support Officer
Forensic Services Group
Operations Support Command
Queensland Police Service
[redacted]

From: Heit.KarenL[OSC]
Sent: Tuesday, 22 February 2022 11:37
To: Strategy and Performance OSC [redacted]
Cc: Support Officer FSG[OSC] [redacted]
Subject: FW: URGENT - Prepared for Parliament - URGENT DOT POINTS REQUIRED re DNA TESTING

Hi

Please see below dot points and attached is the DNA Compliance Stats.

Cheers

K

Karen Heit | Sergeant
Support Officer
Forensic Services Group
Operations Support Command
Queensland Police Service
[redacted]

[redacted]

From: Neville.DavidH[OSC] [redacted]
Sent: Tuesday, 22 February 2022 11:30
To: Heit.KarenL[OSC] [redacted]
Subject: RE: URGENT - Prepared for Parliament - URGENT DOT POINTS REQUIRED re DNA TESTING

- There is no cap on the number of samples submitted in relation to crimes against the person. The samples are however prioritised based on probative evidential value and likelihood of testing success.
- The QPS does limit the number of samples submitted for volume crime offences. Officers are permitted to submit two samples in the first instance. Additional samples can be approved in the event that testing does not yield a result, if there is evidence of multiple offenders, or if the offence is linked to a more serious matter.
- The limiting of samples for volume crime matters is common practice across Australia. Research by the National Institute of Forensic Science demonstrated there is a diminishing likelihood of success when more than two samples are analysed for volume crime matters

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

From: Heit.KarenL[OSC] [redacted]
Sent: Tuesday, 22 February 2022 10:57
To: Foxover.StephanP[OSC] <[redacted]; Neville.DavidH[OSC] [redacted]
Cc: Frieberg.DaleJ[OSC] <[redacted]
Subject: FW: URGENT - Prepared for Parliament - URGENT DOT POINTS REQUIRED re DNA TESTING
Importance: High

Hi

Please see urgent request below.

Cheers

K

Karen Heit | Sergeant
Support Officer
Forensic Services Group
Operations Support Command
Queensland Police Service
[redacted]

Level 4, PHQ, 200 Roma Street, Brisbane
GPO Box 1440, BRISBANE, QLD 4001
[redacted] Support Officer FSG

From: Reynolds.PaulR[OSC] <[redacted]
Sent: Tuesday, 22 February 2022 10:43
To: Supt FSG <[redacted]
Cc: Strategy and Performance OSC [redacted]
Subject: FW: URGENT - Prepared for Parliament - URGENT DOT POINTS REQUIRED re DNA TESTING
Importance: High

Good morning

For urgent advice, please.

Per the below a response is sought as soon as possible.

Regards

Paul Reynolds
Inspector, Strategy and Performance
Operations Support Command
Queensland Police Service
[redacted]

From: MinisterialLiaison.Officer[HQ] <[redacted]
Sent: Tuesday, 22 February 2022 10:37
To: Strategy and Performance OSC <[redacted]
Cc: DEPUTY COMMISSIONER REGIONAL QUEENSLAND[NR] [redacted]; MinisterialLiaison.Officer[HQ] [redacted]
Subject: URGENT - Prepared for Parliament - URGENT DOT POINTS REQUIRED re DNA TESTING
Importance: High

Good morning,

The below email was received at the MINs office from the Office of the Minister for Health and Ambulance Services.

Health advise that the QPS apply a cap to forensic examination of DNA with respect to crimes against property but not crimes against the person.

Could urgent advice please be provided in relation to the below matter by **midday today, 22 February 2022 (or earlier if possible).**

Regards,

Judy Kidcaff
Support Officer
Commissioners Office | 200 Roma Street, Brisbane, QLD, 4000
[redacted]
Office of the Minister for Police and Corrective Services
and Minister for Fire and Emergency Services
1 William Street, Brisbane, QLD, 4000
[redacted]

From: Frances Stewart [redacted]
Sent: Tuesday, 22 February 2022 10:11
To: MinisterialLiaison.Officer[HQ] [redacted]
Cc: Ellen McIntyre [redacted]; Daniel Carvosso [redacted]
Subject: Prepared for Parliament - URGENT DOT POINTS REQUIRED re DNA TESTING
Importance: High

Hi Rob

Could we please get some urgent dot points on the below.

Health advise that the QPS apply a cap to forensic examination of DNA with respect to crimes against property but not crimes against the person.

Could you please advise/confirm asap.

Thanks,
Frances

From: Martin Philip [redacted]
Sent: Tuesday, 22 February 2022 8:30 AM
To: SDLO [redacted]
Cc: Luke Richmond [redacted]; Lucy Collier [redacted]
Darren Cann [redacted]
Subject: URGENT DOT POINTS REQUIRED BY 9AM - DNA TESTING
Importance: High

Good morning, can he dept please provide some urgent dot points by 9am addressing the claims made in this report in today's Australian, specifically that DNA tests had been "capped".

Police capped DNA tests as lab struggled EXCLUSIVE DAVID MURRAY NATIONAL CRIME CORRESPONDENT Queensland police "capped" the number of trace DNA samples being sent to a government-run forensics laboratory amid poor results, a shortage of scientists and a blowout in waiting times. A Queensland Audit Office report from 2019 details problems engulfing the Queensland Health Forensic and Scientific Services lab, now under scrutiny in the Shandee's Story investigative podcast. While the Palaszczuk government says there is no evidence of systemic failings in the lab, its auditors found entrenched problems with the potential for profound impacts on investigations. The report reveals that instead of extra staff being put on to manage the increasing demand for DNA analysis, the lab's budget and staff levels had shrunk. "A lack of planning and modelling has limited its ability to effectively

prepare for the increase in demand," it says. The report outlines how offenders can leave DNA at a crime scene in forms such as blood, sweat, skin cells and hair, but can also leave minute cells referred to as trace or touch DNA. In August 2018, "to manage the increasing demand", police capped the number of trace DNA exhibits that could be sent for analysis, the audit report states. Trace DNA samples had made up just over 60 per cent of DNA exhibits sent to the lab for analysis over the previous five years. Victims of crime likely had no idea samples from their cases were not being analysed to cut backlogs. "The Queensland Police Service based this decision on research published by the National Institute of Forensic Science, which highlighted that trace DNA is less likely to yield a DNA profile," the report states. The auditors agreed the lab's trace DNA results were poor, yielding profiles in only 12 per cent of cases. The Australian last week revealed the lab had set a very high threshold for the minimum DNA required for crime scene samples to be fully tested. The 22 cells required is double the 11 cells required in NSW. Forensic scientist Kirsty Wright, assisting the podcast series, is convinced the high threshold contributed to the poor results from trace DNA analysis. "So not only is the lab not generating DNA profiles when it should be, but their poor success rate has forced the hand of Queensland police to decide to limit the number of trace crime scene samples that are being sent," Dr Wright said. "I just find that an incredible response. It's a double whammy." The audit report states that despite a 21 per cent increase in the number of DNA exhibits analysed from 2013-14 to 2017-18, the DNA team had dropped from 65 full-time equivalent staff to 61 in the same period. The Forensic and Scientific Services budget to deliver forensic DNA services has decreased by about $1m over the same fiveyear period. Meanwhile, DNA exhibits 120 days or older had more than quadrupled, from 289 in 2013–14 to 1284 in 2017–18. "Queensland Health's Forensic and Scientific Services is struggling to keep pace with the increase in demand for DNA analysis," the auditors found. Queensland Health has declined to answer questions on the lab.

Martin Philip
Senior Media Advisor
Office of the Hon. Yvette D'Ath MP
Minister for Health and Ambulance Services
Leader of the House
[redacted]
1 William Street Brisbane

Queensland
Government

Exhibit 6

Frieberg.DaleJ[ESC]

From: Frieberg.DaleJ[OSC]
Sent: Thursday, 24 February 2022 14:42
To: Support Officer FSG[OSC]
Subject: FW: Testing thresholds

For office records. Dave will need to speak with Bruce at some stage and he will need to see the EBN we submitted.

Dale Frieberg APM
[redacted]

From: Neville.DavidH[OSC] <[redacted]
Sent: Thursday, 24 February 2022 13:21
To: Cathie Allen [redacted]>
Cc: Lara Keller <[redacted] Frieberg.DaleJ[OSC] <[redacted]
Subject: RE: Testing thresholds

Hi Cathie,
Thanks for the reply and also for the paper discussing the micro-con success rates. I have read the paper previously, however the explanation in your email sent yesterday made this a lot clearer. It was really helpful because there is a lot to assimilate when you don't work in the field.

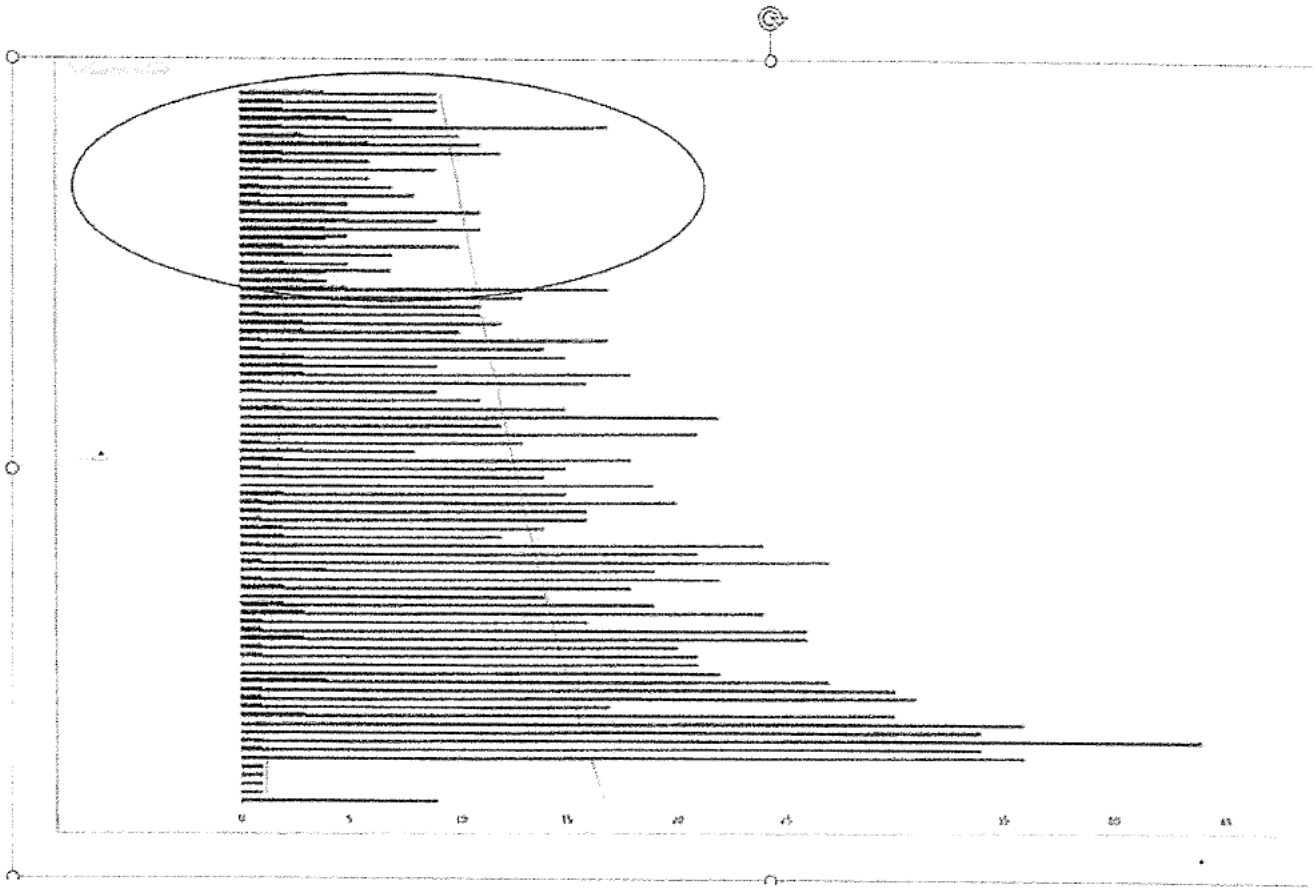
I wondered if you can clarify my understanding of the paper? The success rate of <2% relates to the likelihood of the process resulting in a new link rather than the likelihood of obtaining a profile. The actual success rate of obtaining a profile is roughly 10% overall according to Figure 1.

I'll be honest, using the number of new links to measure the value of analysis is very problematic because the probative value of the evidence will vary hugely depending on the sample type and location. Although I can see the logic, it does over simply the situation.

10% is much closer to 30% which is what we observed and our selection process may explain part of the gap in our success values. More importantly, I did some calculations based on the success rate shown in Figure 2 for samples with a quant value of over .006ng/uL. Above this quant the success rate is 24% which is even closer to our observation.

The current system of reporting places an onus on the QPS to make a decision as to whether testing should continue for samples under .0088ng/uL of DNA. Investigators are advised to let the DNA Management Section know if they seek for this to occur. This is problematic for members of the QPS to make a decision as to whether testing should proceed because they do not have access to information about the quality and quantity of DNA present. For this to actually work we need to have visibility over the quant and degradation values to make an informed decision. This could easily be resolved through a change in the FR. For a short time QPS members had visibility of this information due to a programming error, but it was switched off. I believe it is essential that this limited information be made available again for the current regime of reporting is to remain.

According to Figure 2, the likelihood of success appears to be much greater for samples above .006ng/uL (approx. 24%). Its also interesting to note that this accounts for relatively low proportion of samples below the .0088ng/uL.



Based on the information in this graph, I wondered if it might be worthwhile lowering the threshold.

I am not supportive at this point of returning to automatic processing of all of the samples above .001ng/uL. I think that would be a retrograde step and unnecessarily tie up the scientists. But I am very supportive of fine tuning the threshold.

In any case, your email has been incredibly helpful and it does resolve some of my concerns. However it also highlights a need for us to modify our practices. Can you please provide advice on the practicality of the suggestions I have made? Alternatively I would be very interested in any improvement suggestions you may have.

Thanks again and I look forward to hearing your thoughts.

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

From: Cathie Allen <[redacted]
Sent: Thursday, 24 February 2022 08:37
To: Neville.DavidH[OSC] <[redacted]
Cc: Frieberg.DaleJ[OSC] <[redacted], Lara Keller [redacted]
Subject: RE: Testing thresholds

Hi David

The laboratory has conducted an extensive validation process prior to the implementation of the current quantitation process. The validation outcomes were in line with the manufacturer's specification. From August 2018 onwards, if a sample obtains a quantitation value of 0.001 ng/uL or below, the laboratory reports this to the QPS as 'No DNA Detected'. If a sample obtains a quantitation value between 0.001ng/uL and 0.0088ng/uL, the laboratory reports this to the QPS as 'DNA insufficient for further processing' (expanded QPRIME results supplied below). These values are listed in the Options paper attached that was provided to the QPS. Samples that obtain a quantitation value greater than 0.0088ng/ug are processed through the DNA profiling step and results obtained are reported. Its FSS's understanding that forensic officers review DNA results within the context of the case and can request testing or submit additional items for testing.

No DNA detected
This item/sample was submitted for DNA analysis, however no DNA was detected above the limit of detection at the quantitation stage. No further processing was conducted on this item.

DNA insufficient for further processing
This item/sample was submitted for DNA analysis, however the amount of DNA detected at the quantitation stage indicated the sample was insufficient for further processing (due to the limitations of current analytical and interpretational techniques). No further processing was conducted on this item. Please contact Forensic DNA Analysis if further information is required.

The theoretical values regarding human cells to derive a DNA profile are not used within the laboratory. The laboratory uses values obtained from the quantitation process that provide the approximate amount of human DNA available within the sample.

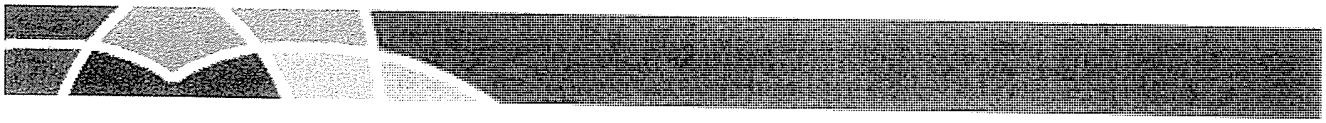
Each year, the forensic laboratories will exchange information regarding profiling kit and equipment used, however details regarding quantitation values has not been exchanged or collated so I'm unable to comment or draw comparisons to other jurisdictions. Validation studies conducted within each laboratory ensures that the method or equipment is fit for purpose within that laboratory environment, so it's not unexpected that different laboratories would have slightly different thresholds for quantitation or limit of detect for DNA profiles (as different equipment and kits are used in the different laboratories).

The in-house validation of the current QuantiFiler Trio system showed that the laboratory could reliably detect DNA down to concentrations of 0.001ng/uL, however the manufacturer has reported that the system has single source sensitivity only down to 0.005ng/uL. At these lower concentrations of DNA, there are more stochastic effects that can occur and thereby affect the interpretation of the DNA profile. Quantity and quality of the DNA obtained from a sample determines the ability to obtain a DNA profile.

If the QPS request a 'DNA insufficient' sample to be processed, it first undergoes a concentration step then amplification and associated DNA interpretation (excluding Priority 1 samples). The concentration step is required to give the sample the best opportunity to obtain a 'useful' DNA profile (ie useful to load to the NCIDD or meaningful comparison to other profiles obtained within the case).

Once we've received the quote from bdna regarding when an enhancement can be added to the FR for data extraction, we will be able to provide a timeframe regarding analysis of the data and provision of a report.

Cheers
Cathie



Cathie Allen BSc, MSc (Forensic Science) (She/Her*)
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

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

p [redacted]
a
e

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*If you're wondering about the use of pronouns She/Her on this signature block, I encourage you to read some resources available here

From: Neville.DavidH[OSC] <[redacted]
Sent: Wednesday, 23 February 2022 8:51 AM
To: Cathie Allen [redacted]
Cc: Frieberg.DaleJ[OSC] <[redacted] Lara Keller [redacted]
Subject: RE: Testing thresholds

This email originated from outside Queensland Health. DO NOT click on any links or open attachments unless you recognise the sender and know the content is safe.

Dear Cathie

Thank you for your reply to my email, however the response does not address the main query posed. I am seeking information from you in relation to the comments in the Australian claiming that the thresholds in Queensland are twice that of other states and three times higher than the manufacturer's recommended value. These claims in the national newspaper come at a time when the QPS has raised similar concerns around testing triage thresholds. Unfortunately the gears have shifted since our meeting on 1 February due these claims in the media and I am being asked questions in relation to these very issues.

I need to also further clarify my comment that the QPS had 'cherry picked' samples. The dataset that was provided included the barcodes of samples that the QPS requested to continue testing after receiving a result 'insufficient DNA for further testing'. Some of these were selected because we found it unusual for the sample type to yield low DNA. This included samples from blood and a used condom. The fact that these produced low quant values is concerning to some extent. However, the majority of them were selected due to the probative value of the sample rather than the sample type. For Operation Amulet alone, this included 33 samples with 10 later providing a full profile. Yes, the sample selection may have had some impact, however it could not explain the vast difference between >2% and 30% success rate.

Having said this, I do appreciate the work that you have done so far in reviewing the dataset. I understand that this may not be a simple task. I know that we share a common interest in ensuring the effectiveness of DNA in enhancing community safety. To that effect, could you please provide an estimated timeframe for completion.

For clarity, could you please provide advice on the threshold values used with QHFSS as a matter or priority including how they accord with other jurisdictions. I assume that this information will be readily available within your procedures.

Kind Regards

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

From: Cathie Allen <[redacted]>
Sent: Tuesday, 22 February 2022 16:32
To: Neville.DavidH[OSC] <[redacted]>
Cc: Frieberg.DaleJ[OSC] <[redacted]> Lara Keller [redacted]
Subject: RE: Testing thresholds

Hi David

During the Bi-Monthly QPS / QHFSS meeting on the 1st of February, I provided a verbal update to you and Supt Frieberg regarding this. Minutes from this meeting are yet to be circulated (it was recorded), I have detailed notes that I took during the meeting and I've referred to those for this email.

I advised that due to the community transmission of COVID-19 affecting Forensic DNA Analysis staff members and the two urgent cases that the QPS requested we process (a number of items), slow progress had been made on this request. At the meeting, you provided an assurance that you understood the situation that both the QPS and FSS were in due to the community transmission of COVID-19 affecting the workforces.

During the meeting, you advised that you were aware that the QPS had 'cherry-picked' particular samples to be tested further, and that this may be the reason behind the results that were achieved.

The data that is required to be analysed is within the FR, and FSS have submitted a request to bdna for a quote to extract the data required. Once we have received the quote and approved it, and then received and analysed the data, we will provide a report to the QPS regarding this.

Cheers
Cathie

Cathie Allen BSc, MSc (Forensic Science) (She/Her*)
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

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

[redacted]

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From: Lara Keller [redacted]
Sent: Monday, 21 February 2022 11:22 AM
To: Neville.DavidH[OSC] [redacted]
Cc: Frieberg.DaleJ[OSC] [redacted]; Cathie Allen [redacted]
Subject: RE: Testing thresholds

Good morning David

Cathie is off duty today, so I have asked for an update from within the team today. I do know that Cathie has been following this up already.

Thanks and Kind Regards
Lara

Lara Keller B App Sc (MLS), Grad Cert Health Mgt, MAIMS, CMgr FIML
A/Executive Director

Forensic and Scientific Services
Prevention Division, Queensland Health

[redacted]

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From: Neville.DavidH[OSC] [redacted]
Sent: Monday, 21 February 2022 10:21 AM
To: Cathie Allen [redacted]
Cc: Frieberg.DaleJ[OSC] [redacted]; Lara Keller [redacted]
Subject: FW: Testing thresholds

Dear Cathie
I understand the difficulty of the ongoing coverage by the *The Australian* of the Shandee Blackburn case. This must be causing significant stress for you and your staff.

Unfortunately I have been drawn into comment internally on peripheral matters raised by the outlet on 18 February 2022.

article.

It claims that the Queensland lab requires crime scene samples to have the equivalent of at least 22 cells to be fully tested, otherwise they are deemed to have insufficient DNA. It claims that the threshold is double the 11 cells required in NSW, and almost three times the eight cells that the product manufacturer has used to obtain good quality DNA profiles.

I know you are busy, but since 1 December 2021 I have raised concerns in relation to the truncating of testing based on DNA quant values because of the significant number of below threshold samples yielding a profile when testing is continued. This remains a high priority matter for the QPS. To date I have not received any feedback or explanation as to difference between the predicted (<2%) and observed success rates (30%) for samples that reportedly contained a low concentration.

Could you please provide advice as to how the Queensland threshold for testing accords with other jurisdictions. Can you also please advise the outcome of any internal review that you have undertaken based on the information I provided. I need this information as a matter of urgency to brief the executive in relation to this matter.

Regards

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

From: Neville.DavidH[OSC] <[redacted]
Sent: Friday, 17 December 2021 17:23
To: Cathie Allen <[redacted]
Cc: Frieberg.DaleJ[OSC] <[redacted]> [redacted]
Subject: Re: Op Tango Amunet

Hi Cathie
Thanks for the clarification. That was my understanding too. I was of the belief that QHFSS stopped doing this as a matter of routine for low quant samples because there was a lower than 2 percent chance of success. However, QPS has found the success rate to be 30 percent when we requested this to be done. It is the difference between these success rates that I am interested in.

Have a good weekend

David Neville
Inspector, FSG
[redacted]

From: Cathie Allen [redacted]
Sent: Friday, December 17, 2021 5:06 pm
To: Neville.DavidH[OSC]
Cc: Lara Keller; Frieberg.DaleJ[OSC]
Subject: RE: Op Tango Amunet

Hi David

Thank you for the follow-up email regarding samples within this case.

To ensure that we're all on the same page, I'd like to clarify the process. If samples that have been deemed 'insufficient DNA for further processing' are processed further, they all first undergo a concentration step, followed by amplification. This is in contrast with samples that are not deemed in this range, as these samples amplification, without a concentration step. Just wanted to draw to your attention that there is additional work undertaken on the DNA extract to attempt to achieve a DNA result for the samples deemed 'insufficient DNA for further processing'.

Cheers
Cathie

Cathie Allen BSc, MSc (Forensic Science) (She/Her*)
Managing Scientist
Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022
Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health
[redacted]

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From: Neville.DavidH[OSC] [redacted]
Sent: Friday, 17 December 2021 12:04 PM
To: Cathie Allen [redacted]

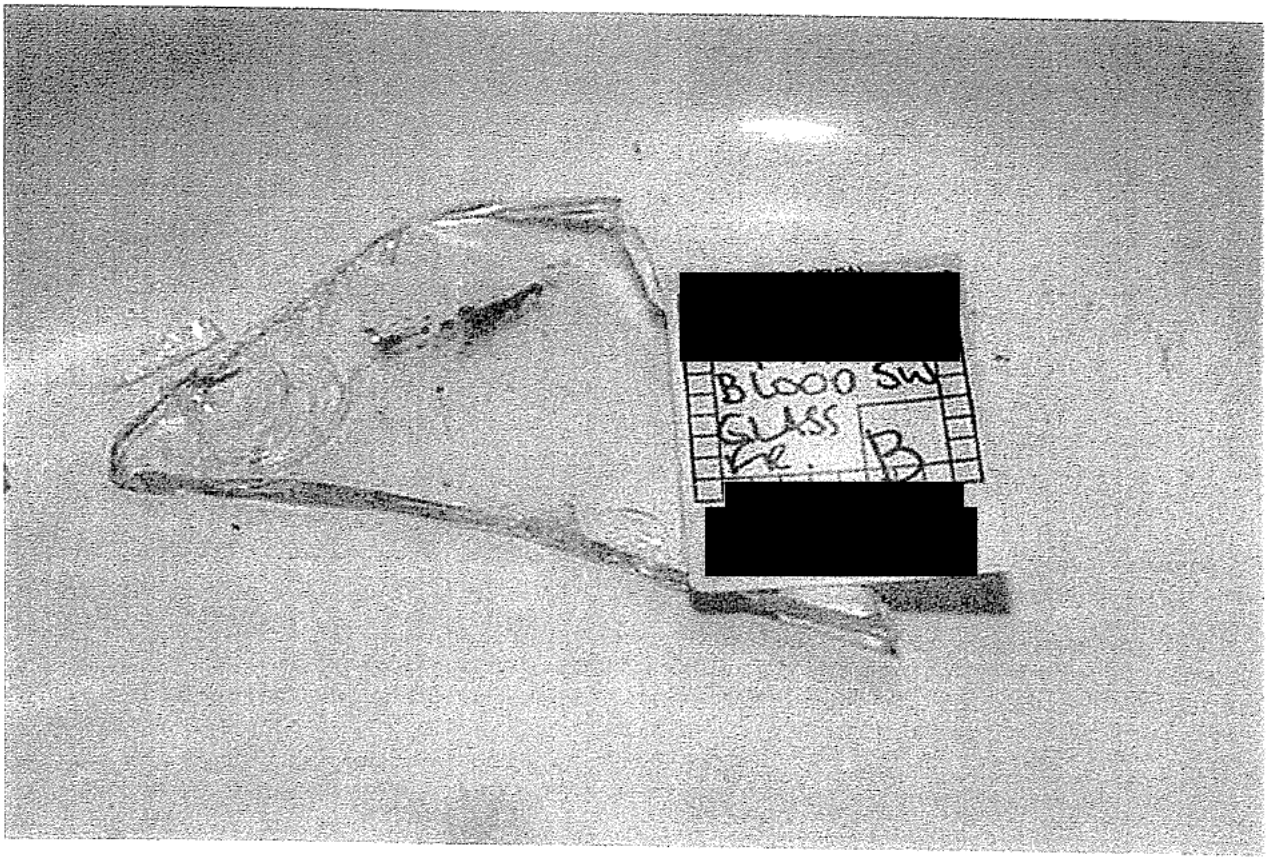
Cc: Lara Keller <[redacted]; Frieberg.DaleJ[OSC] <[redacted]
Subject: RE: Op Tango Amunet

Hi Cathie
In addition to the items on the list provided previously, last week we requested a blood swab [redacted] to be retested which was originally reported as "insufficient DNA for further testing". This sample was taken from blood on a broken shard of glass as depicted in the photo below.

Given the nature of the stain and inert substrate, we were surprised with the original result which is what prompted the request to further test. Today we were advised that subsequent testing yielded a single source 20 loci profile. This was an excellent result solving the crime which would have been otherwise missed.

The image below is attached to the exhibit screen which was visible to the laboratory staff. The results of presumptive testing are also included on that screen. I wondered if lab staff use this information when making a decision on stopping testing?

Forwarded for you information and consideration along with the other material provided.



David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

[redacted]

From: Neville.DavidH[OSC] [redacted]
Sent: Thursday, 16 December 2021 12:56
To: Cathie Allen <[redacted]
Cc: Frieberg.DaleJ[OSC] <[redacted]; Lara Keller [redacted]
Subject: Re: Op Tango Amunet

Hi Cathie
Thanks, this is a high priority for us, we would appreciate advice as soon as possible please.

David Neville
Inspector, FSG
[redacted]

From: Cathie Allen <[redacted]
Sent: Thursday, December 16, 2021 12:42 pm
To: Neville.DavidH[OSC]
Cc: Frieberg.DaleJ[OSC]; Lara Keller
Subject: RE: Op Tango Amunet

Hi David

Thank you for your email and feedback regarding this. We will review scientific data available to us and will provide further advice to the QPS in due course.

Cheers
Cathie

Cathie Allen **BSc, MSc (Forensic Science) (She/Her*)**
Managing Scientist
Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022
Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health
[redacted]

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From: Neville.DavidH[OSC] <[redacted]
Sent: Monday, 13 December 2021 2:06 PM
To: Cathie Allen <[redacted]
Cc: Harris.LibbyA[OSC] <[redacted]
Subject: RE: Op Tango Amunet

Hi Cathie
Since sending you my last message I found some correspondence from February 2018 where QHFSS made a recommendation to QPS that testing of samples that contained less than 0.008ng/uL of DNA should discontinue because the chance of obtaining a profile was less than 2%. Samples below this threshold were previously micro concentrated in an effort to attain a profile. Based on the advice from QHFSS, the QPS agreed to discontinue testing including micro concentration under such circumstances and the result would be reported as "DNA Insufficient for further testing" (DIFFT). I am assuming this is the information I was seeking in the below request.

Based on the results obtained for Operation Tango Amunet, I asked my staff to undertake a wider review of the success rate of further testing of items that were originally reported as DIFFT during 2021. This revealed 51 out of 160 samples provided a profile when the QPS requested testing to continue. These items are listed in the attached.

On 14 November 2018 I raised similar concern in relation to Operation QUEBEC CLARIFY after 3 out of 4 samples yielded a result when QPS requested testing to continue. At that time QHFSS provided reassurance that the success rate would be lower than 2% and that the matter should be treated as an aberration. As a result the QPS agreed to continue the truncation of testing for items below the threshold quantity of DNA and limit automated micro concentration to P1 samples only.

Given the result of the recent cases where continued testing was successful, might it be timely to review the practice of truncating testing of lower quant items? For instance, is the threshold value still valid? Also, with the implementation of the latest version of STRMix that can deconvolute more complex mixtures, is it more likely to get a result now?

I think the 30% success rate of retesting warrants a little further examination to make sure we are maximising our chances of solving crime, particularly for major crime matters.

I look forward to discussing this further with you.

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

From: Neville.DavidH[OSC]
Sent: Friday, 3 December 2021 10:07
To: Cathie Allen [redacted]
Subject: RE: Op Tango Amunet

Thanks Cathie
I appreciate the timely feedback. Based on our conversation the other day, I am assuming these discussions occurred in 2008. Is there any correspondence that was provided to base this decision on that you can provide, please? For our refence and moving into the future, what is the actual percentage that your dataset has indicated? Obviously this information will be helpful in guiding future requests for retesting.

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

From: Cathie Allen <Cathie.Allen@health.qld.gov.au>
Sent: Friday, 3 December 2021 09:55
To: Neville.DavidH[OSC] <Neville.DavidH@police.qld.gov.au>
Cc: Justin Howes <Justin.Howes@health.qld.gov.au>
Subject: RE: Op Tango Amunet

Hi David

Thanks for the additional information on those samples from that particular case. We'll have a look into them and get back to you when we can.

After we had conducted a review of a large dataset, it was found that below a particular quantitation threshold and in line with manufacturer's specifications, a very small percentage of samples may provide some type of DNA profile, if they proceeded through DNA processing. This information was provided to the QPS, and the QPS advised that it would prefer that those samples that didn't exceed the quant threshold were not processed through to a DNA profile. We've monitored this and have found that with a larger dataset, the small percentage didn't vary.

We'll provide advice for this particular case when we're able to.

Cheers

Cathie

Cathie Allen BSc, MSc (Forensic Science) (She/Her*)
Managing Scientist
Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022
Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health
[redacted]

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From: Neville.DavidH[OSC] <[redacted]
Sent: Wednesday, 1 December 2021 1:48 PM
To: Cathie Allen <[redacted]
Cc: Justin Howes [redacted]
Subject: RE: Op Tango Amunet

Hi Cathie
To provide further context, it has been raised with me that 33 items were examined with advice being received, "DNA Insufficient for further testing". A request was made for these items to be further worked. Ten of these then returned a result with persons being identified with LRs of >100 billion. I have attached a spreadsheet that includes the results. II wondered if there was a particular reason for this case as to why approx. 30% of the samples yielded a result after the work was requested. Can you please advise what the actual threshold is and advice as to whether this needs to be reviewed.
Finally, sorry to sound demanding, can you also provide information on your expected likelihood of success in normal casework (i.e the likelihood of DNA insufficient samples yielding a result if testing is continued).

Cheers

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

From: Neville.DavidH[OSC]
Sent: Wednesday, 1 December 2021 10:24
To: Cathie Allen <[redacted]
Subject: Op Tango Amunet

Hi Cathie
I wondered if you might be available at some time today to have a brief chat about some results from Op Tango Amunet. If Justin was available too, that might be helpful. Can we teams please?

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

Exhibit 7

Bri McKenzie

From: Support Officer FSG[OSC] <[redacted]
Sent: Thursday, 31 March 2022 3:36 PM
To: Strategy and Performance OSC
Cc: Support Officer FSG[OSC]
Subject: FW: DOC22/274597 Ltr to DG Health re DNA Sample triaging & EBN QHFSS DNA sample triaging
Attachments: EBN QHFSS DNA sample triaging.doc; Ltr to DG Health from COP re DNA sample triaging.doc

Good afternoon,

Could I please seek an update on this EBN and Letter?

Please note, the correct Objective number for this matter is **DOC22/274519.** The above one does not exist.

Regards,
Jenna

Jenna De Marco
Acting Support Officer
Office of the Superintendent
Forensic Services Group
Operations Support Command
Queensland Police Service
[redacted]

I am positively bedeviled with meetings et cetera….

INTEGRITY PROFESSIONALISM COMMUNITY RESPECT & FAIRNESS

Our values are at the core of who we are and what we do each day

From: Heit.KarenL[OSC] <[redacted]
Sent: Tuesday, 22 February 2022 14:31
To: Strategy and Performance OSC [redacted]
Cc: Brits.DelindaC[OSC] [redacted]
Subject: DOC22/274597 Ltr to DG Health re DNA Sample triaging & EBN QHFSS DNA sample triaging

Hi

Please find attached EBN and Letter under the hand of the Commissioner in relation to DNA sample triaging currently in place at QHFSS. This issue is currently in the media being highlighted by the Shandee Blackburn murder.

Cheers

K

Karen Heit | Sergeant
Support Officer
Forensic Services Group
Operations Support Command
Queensland Police Service
[redacted]

From: Heit.KarenL[OSC]
Sent: Tuesday, 22 February 2022 13:28
To: Brits.DelindaC[OSC] <[redacted]
Subject: FW: EBN QHFSS DNA sample triaging

Please objectify and advise DOC no.

Docs can be moved to A/C's working folder.

Cheers

K

Karen Heit | Sergeant
Support Officer
Forensic Services Group
Operations Support Command
Queensland Police Service
[redacted]

From: Neville.DavidH[OSC] <[redacted]
Sent: Tuesday, 22 February 2022 13:02
To: Heit.KarenL[OSC] <[redacted]
Subject: EBN QHFSS DNA sample triaging

In the matter of the *Commissions of Inquiry Act 1950*
Commissions of Inquiry Order (No. 3) 2022
Commission of Inquiry into Forensic DNA Testing in Queensland

STATEMENT OF BRUCE McNAB

I, **Bruce McNab,** of 200 Roma Street, Brisbane, Queensland, 4001, state as follows:

The following statement is provided in response to a notice I received from the Commission of Inquiry into Forensic DNA Testing in Queensland requiring me to give information in a written statement regarding my knowledge of matters set out in the Schedule attached to that notice. Attached and marked **'Exhibit 1'** is a copy of that notice.

Background

1. I am the Superintendent, Forensic Services Group, Queensland Police Service.

2. I do not have a current CV.

Role

3. I was sworn into the Queensland Police Service on the 28th of October 1989. Since that time, I have worked in several roles in regional Queensland primarily as a Detective or in charge of Detectives. In 2015 I was appointed to the rank of Superintendent as the District Officer Mackay District. In 2018 I took up the role of Superintendent, Operations Commander Forensic Services Group.

4. For much of 2021 I was relieving as the Operations Commander Covert and Specialist Operations Group, and Detective Superintendent, Financial and Cyber Crime Group. I returned to my role in FSG in late February 2022.

Executive Briefing Note

5. [redacted]

[redacted] Noting that, I have endeavoured to respond to the questions posed in the Notice from memory and to the best of my recollection.

6. I had no part in drafting the Executive Briefing Note (EBN) in question.

7. I do not know what material and information was relied upon in preparation of the EBN and draft letter addressed to Dr John Wakefield. This was prepared and submitted prior to my return to FSG in late February 2022.

8. When I returned to Forensic Services Group in late February 2022, I was advised by Inspector Dave Neville that an EBN was in existence regarding his concerns over testing thresholds adopted by Queensland Health, and this EBN was at the Assistant Commissioner, Operations Support Command office. The EBN had not been progressed to the Commissioner of Police's office.

9. I recall that shortly after I received that advice, Inspector Neville and I raised the concerns in writing regarding the DNA thresholds to Lara Keller and Cathy Allen. In either this meeting or shortly after Keller advised me they would review correspondence around this issue that Neville had provided and I understand was of the same issue as the EBN, further Keller of Queensland Health gave the QPS an undertaking to respond in writing to the issues raised by Inspector Neville. I cannot recall if this was verbally or in writing

10. I made a decision to wait for Queensland Health's response before briefing the Commissioner through an amended EBN. I had hoped that, in light of Inspector Neville's correspondence, Queensland Health would change their position around the status of the current testing thresholds, and if not, this information, and the reasoning of Health as to their decision not to change the threshold would be important to include in the EBN so the Commissioner was properly informed. I advised Neville of this course of action and requested the office of the Ac (OSC) return the EBN to my office for subsequent amendment upon receipt of the information from Health.

11. I cannot recall the deadline for Health to respond but I think it was in March 2022.

12. I did not at any time agree to withdraw the EBN to the Commissioner of Police.

[redacted] ..... [redacted]

Bruce McNab Witness

13. I had concerns about the testing thresholds as they existed at that time, and [redacted], these concerns were never reduced.

14. I was briefed by Neville as to what steps his team was taking to remain vigilant in the interim, and that this increased surveillance from a QPS end was not sufficient and could not replace a simple change in thresholds by Health, which was the not just the most appropriate, but the most common-sense approach to the issue. I also regularly briefed my AC as to the status of our requests, and our frustration.

15. I was later verbally advised by Keller that Health would not provide the report as they had received legal advice which was delaying the release of the response. I expressed to her then that this was completely unacceptable, and the response must be released to us. The response was subsequently released. I cannot tell you the date of either her advice it wasn't going to be released or its release. The advice was verbal by telephone initially, as I remember I was surprised and I had to ask her to repeat it. Keller may have responded in writing as well but I do not recall. I do recall the actual response to the concerns of Neville was in writing and was received by email.

[redacted]

TAKEN AND DECLARED before me at Cooroy in the State of Queensland this 8TH day of November 2022

[redacted] ..... [redacted] .....

Bruce McNab

Witness

Helen Sheridan Bernays JP (Qual)

JUSTICE OF THE PEACE (QUALIFIED) QUEENSLAND GOVERNMENT Reg.No. 109297 DEPT. OF JUSTICE & ATTORNEY-GENERAL

[redacted] ..... [redacted] .....

Bruce McNab

Witness

EXHIBIT 1

Notice number: 2022/00306

COMMISSION OF INQUIRY INTO FORENSIC DNA TESTING IN QUEENSLAND

Section 5(1)(d) of the *Commissions of Inquiry Act 1950*

REQUIREMENT TO GIVE INFORMATION IN A WRITTEN STATEMENT

To: Bruce McNab

Of: Queensland Police Service

I, Walter Sofronoff KC, Commissioner, appointed pursuant to Commissions of Inquiry Order (No. 3) 2022 to inquire into certain matters pertaining to forensic DNA testing in Queensland require you to attend to give a written statement to the Commission pursuant to section 5(1)(d) of the *Commissions of Inquiry Act 1950* in regard to your knowledge of the matters set out in the Schedule annexed hereto.

YOU MUST COMPLY WITH THIS REQUIREMENT BY:

Giving a written statement signed and witnessed as a declaration in accordance with the *Oaths Act 1867* to the Commission of Inquiry on or before **5.00PM on 31 October 2022** by delivering it to Level 21, 111 George Street, Brisbane.

A copy of the written statement must also be provided electronically by email at [redacted] with the subject line "Requirement for Written Statement".

If you believe that you have a reasonable excuse for not complying with this notice, you will need to satisfy me of this by the above date.

DATED this **27th day of October 2022**

[redacted]

Walter Sofronoff KC
Commissioner
Commission of Inquiry into Forensic DNA Testing in Queensland

Notice 2022/00306

Schedule of topics for statement

Superintendent Bruce McNab

Background

1. State your current rank and position in the Queensland Police Service.
2. State your qualifications, experience and relevant positions held. Alternatively, please furnish a CV.

Role

3. Outline all positions you held within the Queensland Police Service between 1 January 2018 to present.

Executive Briefing Note

4. Explain in detail your involvement in an Executive Briefing Note titled "POTENTIAL ISSUES WITH TESTING OF DNA BY QUEENSLAND HEALTH FORENSIC AND SCIENTIFIC SERVICES" and draft letter addressed to Dr John Wakefield (both **attached**). At a minimum, address the following:
    a. Explain your understanding of why the Executive Briefing Note and draft letter were prepared.
    b. Explain who was involved in the preparation of the Executive Briefing Note and draft letter.
    c. Explain your understanding of what material and information was relied upon in preparation of the Executive Briefing Note and draft letter.
    d. Describe in detail any meetings, discussions or correspondence you were involved in regarding the Executive Briefing Note and draft letter.
    e. Identify who made the decision not to progress the Executive Briefing Note and draft letter, and explain why the decision was made. Describe any meetings, discussions or correspondence you were involved in regarding this decision.
    f. Explain whether you took any steps to ensure the issues raised in the Executive Briefing Note and draft letter were otherwise addressed.

g. Attach any documents relevant to (a) – (f) above, including all documents you refer to in your answers to those questions

In the matter of the *Commissions of Inquiry Act 1950*
Commissions of Inquiry Order (No. 3) 2022
Commission of Inquiry into Forensic DNA Testing in Queensland

STATEMENT OF TROY SHAN O'MALLEY

I, Troy Shan O'MALLEY of the 41 Peachdale Street, Queensland, 4173, state as follows:

The following statement is provided in response to a notice I received from the Commission of Inquiry into Forensic DNA Testing in Queensland requiring me to give information in a written statement regarding my knowledge of matters set out in the Schedule attached to that notice. Attached and marked '**Exhibit 1**' is a copy of that notice.

Background

Current Employment

1. I am currently the Managing Director (Forensic) at bdna Pty Ltd a provider of professional services and forensic case management software. My current duties include leading the development of the bdna|forensic-register (FR) for the Queensland Police Service, Queensland Heath Forensic & Scientific Services, South Australia Police, Victoria Police, Australian Federal Police and the Application Architect for the Australian Criminal Intelligence Commission and Home Affairs, National Criminal Intelligence System Application (NCIS).

2. A copy of my CV is attached and marked '**Exhibit 2'.**

Previous employment with Queensland Police Service

3. My employment with the Queensland Police Service (QPS) commenced on 27 October 1986. I was sworn in as a Constable on 8 May 1987 performing general duties until transferring to the Forensic and Technical Services Branch in December 1990. The majority of my thirty years of service was in the Forensic and Technical Services Branch (Forensic Services Group).

4. I performed the duties of Senior Sergeant, Forensic Technology Coordinator from 10 February 2003 until the position was upgraded. I then acted in the position of

[redacted] .... [redacted] .....
Troy Shan O'Malley Witness

JUSTICE OF THE PEACE (QUALIFIED) DEPT. OF JUSTICE & ATTORNEY-GENERAL Reg.No.: 12111

Inspector, Forensic Technology Coordinator from 20 December 2010 till my resignation on 16 February 2018.

5. My duties as the Forensic Technology Coordinator did not directly involve DNA Testing or Analysis.

6. My duties as the Forensic Technology Coordinator included the development and maintenance of the QPS Forensic Register, a case management application used (in part) for recording the collection on DNA evidence, transmission of case and exhibit information to Queensland Health Forensic and Scientific Services (QHFSS) and receiving notifications that items had been received for testing and the results of the DNA Testing and Analysis.

7. I further developed the QPS Forensic Register with my team, in partnership with QHFSS, to replace AUSLAB through the implementation of electronic workflows, processes and reporting associated with DNA Testing and Analysis.

Options Paper

8. In early 2018, I was performing the duties of the Inspector, Forensic Technologies Coordinator, Forensic Services Group.

9. I have some recollection of the Options Paper, meeting on 2 February 2018 and subsequent outcomes as described in the notice **'Exhibit 1'**. I do not however have a recollection of when or how I first became aware of the Options Paper and as I am no longer a member of the QPS, documents relating to that period are not in my possession. I do not have any independent recollection of discussions or correspondence prior to the meeting, nor do I have any independent recollection of when I reviewed the Options Paper.

10. I recall the meeting attendees included Forensic Services Group Superintendent Dale Frieberg, Acting Inspector Ewen Taylor and Managing Scientist Cathie Allen however I have no memory or independent recollection of who else attended the meeting, the agenda or discussions.

[redacted]

JUSTICE OF THE PEACE (QUALIFIED) Reg.No.: 12777 JUSTICE & ATTORNEY-GENERAL

Troy Shan O'Malley Witness

11. I attended the meeting in my capacity as Inspector, Forensic Technologies Coordinator, to provide advice on any Information Technology changes that may be necessary for the QPS or for QHFSS. I was routinely involved in meetings where there were potential Information Technology changes necessary to support a change either, in electronic workflows, processes, electronic records, auditing or reporting associated with DNA Testing or Analysis.

12. I recall that the Options Paper provided a review by QHFSS of the likelihood of obtaining a usable DNA profile for searching, through the routine step of automatic concentration of the DNA extracts, where the initial DNA Quantification Step indicated a low concentration of DNA. I do not recall the exact concentration, nor do I have any independent recollection of the discussion.

13. I recall, that due to the low likelihood of success based on the review, that the outcome was to stop the testing at the DNA Quantification Step, preserve the sample, and provide advice to QPS with an explanation of why testing had been stopped and for QPS to decide whether to undertake further testing, based on the circumstances of the case.

14. This was subsequently implemented through an update to the Forensic Register and the addition of a new QHFSS DNA result mnemonic and associated expanded explanation. The result with expanded explanation was automatically reported to the QPS DNA Results Management Unit and then uploaded to QPrime for the advice of police investigators.

TAKEN AND DECLARED before me at Brisbane in the State of Queensland this 14 day of September 2022

[redacted]

Troy Shan O'Malley

[redacted]

Witness

JUSTICE OF THE PEACE (QUALIFIED) Reg.No.: 42177 DEPT. OF JUSTICE & ATTORNEY-GENERAL

[redacted]

Troy Shan O'Malley

[redacted]

Witness

JUSTICE OF THE PEACE (QUALIFIED) Reg.No.: 42177 DEPT. OF JUSTICE & ATTORNEY-GENERAL

Commission of Inquiry into Forensic DNA Testing in Queensland

Ph 07 3003 9722 | enquiries@dnainquiry.qld.gov.au | PO Box 12028, George St Qld 4003 | www.dnainquiry.qld.gov.au

Our ref: 2022/00152

Wednesday 7 September 2022

Mr Troy O'Malley
Managing Director
bdna
Level 9, 231 North Quay
BRISBANE QLD 4000

By email: [redacted]

Dear Mr O'Malley

REQUIREMENT TO PRODUCE A STATEMENT TO THE COMMISSION OF INQUIRY INTO FORENSIC DNA TESTING IN QUEENSLAND

Please find enclosed a notice requiring you to produce a statement to the Commission of Inquiry into Forensic DNA Testing in Queensland (the Commission) established by *Commissions of Inquiry Order (No 3) 2022*.

The statement is required to address the matters set out in the attachment to the notice.

The statement must be provided to the Commission by **midday 14 September 2022**.

When preparing the statement, please note the following requirements:

(a) A draft statement should be provided to the Commission at least 2 days in advance of the due date to allow the Commission to ensure the statement addresses all the topics in the requirement before it is finalised and signed. This will assist to ensure further statements or amendments are kept to a minimum.

(b) The statement should be provided in the format as in the enclosed template. Each paragraph should, as far as possible, be confined to a distinct portion of the subject matter. Documents attached to the statement should be clearly identified using exhibit numbers. The statement and exhibits should be numbered sequentially. If there are multiple exhibits, an index should be prepared. We encourage the use of appropriate headings to separate topics.

(c) The statement should be signed and witnessed as a declaration in accordance with the *Oaths Act 1867* (Qld).

A scanned copy of the final signed statement must be provided by email to enquiries@dnainquiry.qld.gov.au.

If you require any further information or clarification, please contact my office on 07 3003 9702 or enquiries@dnainquiry.qld.gov.au.

Yours sincerely,

[redacted]

Jess Wellard
Executive Director
Commission of Inquiry into Forensic DNA Testing in Queensland
(enclosed)

Notice number: 2022/ 00152

COMMISSION OF INQUIRY INTO FORENSIC DNA TESTING IN QUEENSLAND

Section 5(1)(d) of the *Commissions of Inquiry Act 1950*

REQUIREMENT TO GIVE INFORMATION IN A WRITTEN STATEMENT

To: Troy O'Malley

Of: bdna

I, Walter Sofronoff QC, Commissioner, appointed pursuant to Commissions of Inquiry Order (No. 3) 2022 to inquire into certain matters pertaining to forensic DNA testing in Queensland require you to attend to give a written statement to the Commission pursuant to section 5(1)(d) of the *Commissions of Inquiry Act 1950* in regard to your knowledge of the matters set out in the Schedule annexed hereto.

YOU MUST COMPLY WITH THIS REQUIREMENT BY:

Giving a written statement signed and witnessed as a declaration in accordance with the *Oaths Act 1867* to the Commission of Inquiry on or before **12.00pm on 14 September 2022** by delivering it to Level 21, 111 George Street, Brisbane.

A copy of the written statement must also be provided electronically by email at [redacted] with the subject line "Requirement for Written Statement".

If you believe that you have a reasonable excuse for not complying with this notice, you will need to satisfy me of this by the above date.

DATED this 7th day of September 2022

[redacted]

Walter Sofronoff QC
Commissioner
Commission of Inquiry into Forensic DNA Testing in Queensland

Notice number: 2022/ 00152

Schedule of topics for statement

Troy O'Malley

bdna

Background

1. State your qualifications, experience and relevant positions held. Please attach a current CV.
2. State the duties of your current position.
3. Describe any previous experience with forensic DNA testing or analysis.

Options Paper

4. In early 2018, a document titled *A review of the automatic concentration of DNA extracts using Microcon Centrifugal Filter Devices: Options for QPS consideration* (**Options Paper**) was presented to the Queensland Police Service (**QPS**). Describe the role you held within the QPS at the time the Options Paper was presented.
5. Explain when and how you first became aware of the Options Paper.
6. Explain your involvement in a meeting on 2 February 2018 with Cathie Allen, Paul Csoban, Superintendent Dale Frieberg and Acting Inspector Ewen Taylor about the Options Paper, including identifying:
    a. Why you attended the meeting.
    b. Who you discussed or corresponded with, when, and what was said, prior to the meeting.
    c. Any documents you reviewed prior to, or during, the meeting.
    d. What was discussed in the meeting and by whom, and your role in those discussions.
    e. What occurred as a result of the meeting, and your understanding of the reasons for those actions.
    f. Attach any notes, emails, correspondence or other documents you have in relation to this meeting.
7. Explain your understanding of the options presented in the Options Paper at the time of the meeting.

bdna

Areas of Expertise

- Forensic Technologies
- Stakeholder liaison & management
- Team Leadership
- Program & project management
- Agile development process
- Commercial management
- Strategy planning & execution

Special Interests/Talents

- Baseball

Troy O'Malley

Managing Director (Forensic)

Profile Overview

Troy is a highly skilled IT professional and a former Queensland police officer with 30 years' experience. He performed the role of Inspector, Forensic Technologies Co-ordinator and has provided expert evidence for numerous cases nationwide.

He was chair and co-author of the National Institute of Forensic Science (NIFS) Australasian Guidelines for Digital Imaging Processes, Deputy Chair of the NIFS Electronic Evidence Specialist Advisory Group and the architect and principle technical developer of the Queensland Police Service (QPS) Interactive Crime Scene Recording System (ICSR), Forensic CCTV Demultiplexing System (DeMux) and the QPS Forensic Case Management System (Forensic Register).

Troy received QPS Meritorious Service, National Police and National Service Medals Queensland Premier's Award for the QPS Forensic Mobile Data Project, Prime Minister's Awards for Excellence in Public Sector Management in partnership with Queensland Health for the Queensland DNA Improvement Strategy and recognised by the ANZPAA NIFS for his publication 'Forensic informatics enabling forensic intelligence'.

Summary of Key Roles

Queensland Police Service
Lead Consultant, media-log Upgrade and Re-development, 2021 to current

ACIC – Home Affairs
NCIS Application Architect – 2021 - Current

South Australia Police Force
Lead Consultant, forensic-register Upgrade and Re-development, 2020 - Current

Queensland Police Service
Lead Consultant, forensic-register Upgrade and Re-development, 2018 - Current

Australian Federal Police
Team Lead – Forensic Management System (FMS) 2017 - Current

Queensland Police Service (QPS)
Forensic Technologies Co-ordinator – QPS Forensic Register Case Management System 2003 - 2018

bdna

History of Experience

Queensland Police Service

Lead Consultant, QPS media-log

2021 – Current

- Troy leads the bdna development team in the redevelopment and upgrade of the bdna media-log product.
- Manages Agile Development Process and Software Engineering Team.

South Australia Police

Lead Consultant, Forensic Case Management System (forensic-register)

2020 – Current

- Troy leads the bdna development team for the forensic-register upgrade and re-development.
- Provides strategic advice to South Australia Police with respect to forensic Case Management and laboratory Information Management System design and development.

Queensland Police Service

Lead Consultant, QPS Forensic Case Management System (forensic-register)

2018 – Current

- Troy leads the bdna development team for the upgrade and re-development of the forensic-register product.
- Provides strategic advice to Queensland Police Service and Queensland Health Forensic and Scientific Services with respect to Forensic Case Management and laboratory Information Management System design and development.
- Leads the incorporation of innovative and advanced technology processes to enhance the forensic-register product through industry research, collaboration and consultation.

Australian Federal Police

Lead Consultant, Forensic Management System (FMS)

2017 – Current

- Troy leads the bdna development team for the FMS Project at the AFP.
- The project has successfully implemented a tailored version of the forensic-register into the AFP environment which is used by over 600 AFP users across Australia.

Queensland Police Service

Forensic Technologies Coordinator

2003 – 2018

- Troy was the principal software designer and developer of the QPS Forensic Register Case Management System which was later extended to include a Forensic Laboratory Information Management System for Queensland Health Forensic and Scientific Services.

- The QPS Forensic Register, which has been implemented and continuously developed over an 19 year period, has been recognised as Australia's only integrated Forensic Case Management and Laboratory Information Management System providing efficient end to end processing capability for forensic evidence.

Queensland Police Service

Electronic Recording Section

1990 – 2003

- Troy supported policing operations using his extensive experience and background in AV, IT and software engineering.
- Troy performed numerous technical advisory roles including as a Deputy Chair of the Electronic Evidence Specialist Advisory Group and provided guidance both nationally and internationally in relation to appropriate management of electronic/digital evidence. This resulted in the production of nationally and internationally recognised Guidelines for Digital Imaging Processes informing the broader forensic community in relation to best practice in the field.
- Troy was the principal developer for the design, development and implementation of numerous technological advances including the Interactive Crime Scene Recording (ICRS) system. This system is used by QPS personnel to comprehensively document crime scenes enabling realistic recreations which can then be visualised by members of the court during prosecutions.

Queensland Police Service

General Duties

1986 – 1990

- Troy performed General Duties policing in the Gold Coast Region.

QTQ 9

Broadcast Technician

1984 – 1986

- Troy was responsible for quality control and maintenance of all equipment relating to video clarity, signal strength, and audio quality for recorded and live broadcasts at the television network.

Education and Memberships

Electrical Engineering (Computer Systems)
Graduate Diploma Business
Australian and New Zealand Forensic Science Society Member

Notice number: 2022/00141

COMMISSION OF INQUIRY INTO FORENSIC DNA TESTING

IN QUEENSLAND

Section 5(1)(d) of the *Commissions of Inquiry Act 1950*

STATEMENT OF LUKE RYAN

I, **Luke Ryan,** care of Queensland Health Forensic and Scientific Service, Senior Scientist, do solemnly and sincerely declare that:

1. On 6 September 2022, I was requested to provide a statement in response to Notice 2022/00141 "Requirement to Give Information in a Written Statement" ('the Requirement').

Background

Question 1 - State your qualifications, experience and relevant positions held. Alternatively, please furnish a current CV.

2. A copy of my CV is attached at **LR-01 Attachment 1 - Luke Ryan Resume.**

Question 2 - State the duties of your current position.

3. Please refer to my CV (see paragraph [2] above) and the Position Description for the HP5 Forensic Scientist Advanced. The Position Description is attached as **LR-02 Attachment 2 - JEDii 1814 Forensic Scientist - Advanced_CJEU 08_08_12.**

Question 3 - State the duties of the previous positions you held.

4. Please refer to my CV and the Position Description for the HP5 Forensic Scientist (see paragraphs [2] and [3] above).

Options Paper

[redacted] [redacted]

Luke Ryan Witness

*Question 4 - In February 2018, a document titled A review of the automatic concentration of DNA extracts using Microcon Centrifugal Filter Devices: Options for QPS consideration (**Options Paper**) was presented to the QPS. Describe the role you held within the forensic DNA laboratory at the time the Options Paper was presented to the QPS.*

5. At this time I held the HP5 Forensic Scientist, Advanced position as the Senior Scientist for the Analytical Team. Please refer to my CV and the Position Description for the HP5 Forensic Scientist Advanced (see paragraphs [2] and [3] above).

Question 5 - Explain when and how you first became aware of the Options Paper.

6. I cannot recall specifically when I first became aware of the Options Paper. New projects are raised and discussed in Management Team meetings and this would likely be the first time I became aware of the Options Paper, referred to initially as Project #184. I have reviewed Management Team meeting minutes, and Project #184 was first included in the minutes of the meeting held on the 11th of May 2017. It is likely this is the first time I became aware of this project.

Question 6 - What involvement, if any, did you have in the decision to finalise Project 184 and prepare the Options Paper? Explain your involvement in detail, with reference to material and information you had access to in relation to the decision, and any meetings, discussions or correspondence you were involved in regarding the decision.

7. On the 30th of November 2017, Justin Howes requested all members of the Management Team (i.e., Allan McNevin, Amanda Reeves, Cathie Allen, Kirsten Scott, Kylie Rika, Luke Ryan, Paula Brisotto, Sharon Johnstone and Wendy Harmer) to review a report titled "Project #184 – Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence". A copy of the email from Justin Howes is attached at **LR-03 20171130 - 1250 - Attachment 3 - JAH email to LBR 30-11-2017**. A copy of the project report is attached at **LR-04 201711 - Attachment 4 Report_Evaluation of the efficacy of Microcons_v1**.

Luke Ryan Witness

8. I reviewed this report and provided feedback to Justin Howes on the 1st December, 2017 by email. A copy of this email is attached at **LR-05 20171201 - 0850 - Attachment 5 - LBR email to JAH 184 feedback 01-12-2017.**

9. On the 8th January 2018, I received two update emails from Justin Howes regrading this project. Copies of these two emails are attached at **LR-06 20180108 - 0904 - Attachment 6 - JAH email 08-01-2018** and **LR-07 20180108 - 1647 - Attachment 7 - JAH email 08-01-2018 #2**. The second email included a revised report for Project #184 which was included for feedback. A copy of this report is attached at **LR-08 201801- Attachment 8 - Report_Evaluation of the efficacy of Microcons_v2.**

10. On the 9th of January 2018 I provided my feedback on the revised report to Justin Howes in a series of emails. A copy of this email trail is attached at **LR-09 20180109 - 0910 - Attachment 9 - LBR and JAH email comms 09-01-2018**. Based on a review of my records, this email exchange on 9th January 2018 was the final time I provided feedback on the Project #184 report.

11. I provided feedback on the contents of the Project #184 report but was not involved in the decision to prepare this report as an Options Paper. I was also not involved in the final decision making regarding the options presented in the Project #184 report or the Options Paper.

Question 7 - If you had no involvement in the decision to finalise Project 184 and prepare the Options Paper, or consideration leading to that decision, what is your understanding, and explain the basis for your understanding of the following:

a. Who made that decision;

12. I was not involved in the decision and do not know who made the decision. I would only be speculating based on the names on the Options Paper that those persons were involved in making the decision.

Luke Ryan Witness

b. When the decision was made;

13. I was not involved in the decision and do not know when the decision was made. I would only be speculating however I assume the decision was made sometime prior to the issue date on the Options Paper.

c. The reason for the decision;

14. I was not involved in the decision and do not know the reason for the decision. The fact that it is an Options Paper suggests to me that it was designed to provide QPS with a range of options for consideration.

d. The material or information on which the decision was made.

15. I was not involved in this decision. I do not know what material or information was relied upon in the decision to finalise Project 184 and prepare the Options Paper, or consideration leading to that decision.

Question 8 - Explain your role in reviewing the Options Paper prior to it being presented to the QPS. Summarise any feedback you gave in relation to the Options Paper, including verbal discussion, the basis for your views and the response of Cathie Allen and Justin Howes.

16. I have reviewed my records and cannot find any record of me reviewing the Options Paper in its final form. I reviewed the final report for Project #184, which was a precursor to the Options Paper, as described in paragraphs [7], [8], [9], [10] and [11].

All the facts and circumstances declared in my statement, are within my own knowledge and belief, except for the facts and circumstances declared from information only, and where applicable, my means of knowledge and sources of information are contained in this statement.

I make this solemn declaration conscientiously believing the same to be true and by virtue of the provisions of the *Oaths Act 1867*.

TAKEN AND DECLARED before me at Brisbane in the State of Queensland

[redacted] [redacted]

Luke Ryan Witness

this 13th day of September 2022.

[redacted]

Luke Ryan

[redacted]

Witness E. H. GASTEEN Solicitor

SCHEDULE OF EXHIBITS

Question 1
LR-01 - Attachment 1 - Luke Ryan Resume
Question 2
LR-02 Attachment 2 - JEDii 1814 Forensic Scientist - Advanced_CJEU 08_08_12.
Question 6
LR-03 20171130 - 1250 - Attachment 3 - JAH email to LBR 30-11-2017
LR-04 201711 - Attachment 4 Report_Evaluation of the efficacy of Microcons_v1
LR-05 20171201 - 0850 - Attachment 5 - LBR email to JAH 184 feedback 01-12-2017
LR-06 20180108 - 0904 - Attachment 6 - JAH email 08-01-2018
LR-07 20180108 - 1647 - Attachment 7 - JAH email 08-01-2018 #2
LR-08 201801- Attachment 8 - Report_Evaluation of the efficacy of Microcons_v2
LR-09 20180109 - 0910 - Attachment 9 - LBR and JAH email comms 09-01-2018

Luke Ryan - Resume

42 Balonne Court
Upper Coomera, QLD 4209
Phone: [redacted]
Email W: [redacted]
Email H: [redacted]

Tertiary Qualifications:

2016 Diploma of Management, TAFE Queensland

2011 Diploma of Government (Security), Attorney General's Department

2002 Master of Science (Forensic Science), Griffith University

1998 Bachelor of Science (Biochemistry), University of Queensland

Awards:

2008 Qld Police Service Award for Excellence in Policing Operations, State Gold Award.

2008 Australian Federal Police Operations Medal – Operation Alliance.

2001 Griffith University Award for Academic Excellence for Studies in Master of Science.

Appointments:

- DNA Analyst – Appointed under the Evidence Act 1977
- Justice of the Peace (Qualified)

Presentations and Training:

- HIDS Conference 2021, Virtual
- HIDS Conference 2020, Virtual
- HIDS Conference 2019, Kobe, Japan
- QUT University Lecturer – CVB225 Forensic Biology and Analytical Toxicology
- Griffith University Lecturer - 1001ESC Intro to Forensic Science
- DNA Analysis and Interpretation training – Japanese HID University Seminar Series
- QPS Scientific Officer training – annually
- Forensic Medical Officer/Forensic Nurse Examiner conference presentation – 2013

Forensic DNA Analysis Projects – Projects Managed

- 3500xL Genetic Analyzer Validation for Reference samples Amplified with Powerplex®21 using Direct Amplification
- 3500xL Genetic Analyzer Validation for Extracted Reference Samples Amplified with Powerplex®21

- Testing of Updated Quantifiler® DNA Quantification Kit
- Validation of Quantifiler® Trio
- Verification of Cleaning Reagents (Trigene Advance, Viraclean, Virkon, Pyroneg, Decon, Cavicide, F10SC) for use in Forensic DNA Analysis
- Validation of the QIAsymphony® SP/AS Modules
- Verification of PowerPlex®21 New Internal Lane Standard and Matrix
- Validation of Hamilton STARlet A for Quantification and Amplification Assay Setup
- Validation of Hamilton® STARlet C for Capillary Electrophoresis Setup
- Validation of two QuantStudio™ 5 Real-Time PCR Systems
- Verification of Maxwell®16 for Retain Supernatant
- Massively parallel sequencing as an investigative tool
- Validation of QIAsymphony SP for Bone Extraction
- Verification of QIAsymphony® SP for Teeth Extraction
- Verification of QIAsymphony SP/AS
- Verifiler™ Plus Trial
- Verification of ProFlex™96 Well PCR System using PowerPlex®21
- Verification of QIAsymphony following change to QSL3
- Proteinase K Verification
- Verification of Maxwell® FSC Instruments
- Impact of magnetic fingerprint powders on bead-based trace DNA extraction and STR profiling
- Verification of DCS v4 on 3500xL
- Development of Queensland Biogeographical Ancestry and Externally Visible Characteristic Data Set for the Prediction of Ancestry and Phenotype
- VeriFiler™ Plus Validation

Publications

- Luke Ryan, Megan Mathieson, Tegan Dwyer, Marcus Edwards, Libby Harris, Matt Krosch, Daniel Power, Paula Brisotto, Cathie Allen & Ewen Taylor (2020): Massively parallel sequencing as an investigative tool, Australian Journal of Forensic Sciences, DOI:10.1080/00450618.2020.1781251

Employment History

February 2014 – current: Senior Scientist – Analytical Team, Forensic DNA Analysis, Queensland Health.

Responsibilities and achievements:

- DNA Analyst gazetted under Section 133A of the Evidence Act 1977.
- Manage the Analytical Team to ensure that samples are processed within expected timeframes and to high levels of quality.
- Investigate and report on quality investigations within the Analytical Team.
- Manage a team of scientists including conducting performance reviews, coordinating training programs and mentoring senior staff.
- Manage research and development and validation projects for new techniques and instruments, including the Ion Chef and Genestudio S5 Plus for massively parallel sequencing, 3500xL Genetic Analyzer, Quantifiler Trio and QuantStudio 5, QIAsymphony SP/AS DNA automated extraction platform,

Maxwell FSC extraction instrument and STARlet liquid handlers for PCR and capillary electrophoresis reaction preparation.
- Coordinate and document preventative maintenance, repair and calibration of a range of scientific instruments.
- Maintain and review all Analytical Standard Operating Procedures (SOPs) and Training Modules (TMs).
- Coordinate training for Analytical Team including maintenance of competencies.
- Ensure Analytical Team compliance with NATA accreditation under ISO 17025, including routine operations and validation of new processes.
- Profile interpretation and reporting, including the use of STRmix.
- Participate in decision making and strategic planning as Management Team member.

Higher Duties – HP6 Team Leader, Evidence Recovery and Quality, Forensic DNA Analysis, Queensland Health.

- Performed Acting Team Leader Role multiple times between 2013 and current for periods up to 6 months.
- Manage and develop the Evidence Recovery, Analytical and Quality and Projects Teams within Forensic DNA Analysis
- Monitor training and resource levels within the Evidence Recovery and Quality Team, and coordinate resources to ensure workflow is efficient and turnaround times are maintained
- Present weekly Evidence Recovery and Quality Team progress reports to the Managing Scientist
- Assist the Managing Scientist in setting strategic direction for Forensic DNA Analysis, and contribute to the planning and implementation of strategies to ensure organisational goals are achieved
- Participate in the Quality Program, including using QIS2 appropriately to maintain a high standard of quality in the laboratory, including updating and reviewing SOP's, approving OQI's, monitoring reviews and notifications of staff within sub-teams
- Chair Forensic DNA Analysis and Management Team meetings where required
- Provide high level scientific services to QPS, DPP and other clients
- Liaise with Clients (QPS, Judicial Officers, QPS DRMU, QHFSS Senior Management) regarding priority samples, collection, sampling, DNA testing, additional testing, and explanations of DNA profile interpretation
- Manage feedback from clients in relation to communication, work processes, turnaround times (including complaints), and developing actions and process improvements
- Represent Forensic DNA Analysis at meetings with internal and external clients
- Provide guidance and feedback in relation to projects conducted and implemented within Forensic DNA Analysis

February 2013 – February 2014: Senior Scientist – Evidence Recovery Team, Forensic DNA Analysis, Queensland Health.
Responsibilities and achievements:

- DNA Analyst gazetted under Section 133A of the Evidence Act 1977.
- Manage the Evidence Recovery Team to ensure that items submitted by QPS are examined within expected timeframes and to high levels of quality.
- Ensure presumptive screening results are entered, reviewed and reported to meet QPS investigative timeframes and requirements.
- Manage a team of scientists, including conducting performance reviews, training modules and mentoring.
- Coordinate training for Evidence Recovery Team including maintenance of competencies.
- Maintain competency in and perform Evidence Recovery techniques includes examination of items, presumptive screening tests (saliva, semen, spermatozoa, blood), photography, note taking and review of presumptive results.
- Redesigned Examination of Items SOP and Examination of Sexual Cases SOP and associated TMs.
- Ensure Evidence Recovery Team compliance with NATA accreditation under ISO 17025, including routine operations and validation of new processes.
- Fulfill duties as a court reporting scientist including case management and use of STRmix.
- Participate in decision making and planning as a member of the Management Team.

November 2010 – February 2013: Specialist Advisor – Source Security, Radiation Health Unit, Queensland Health.
Responsibilities and achievements:

- Manage the Radiation Security Team to ensure performance targets are met, including processing time critical health and non-health related applications and submissions.
- Conduct Performance Appraisal and Development planning.
- Manage Queensland's radiation source security activities including the cradle to grave tracking of radiation sources and be Queensland's point of contact for national radiation source tracking activities for state and federal government agencies.
- Lead the development and technical review of security plans and transport security plans to document radiation security arrangements and business continuity planning for a range of external public and private clients, in accordance with relevant legislation, standards and codes of practice.
- Manage security for Queensland Government's Radioactive Waste Store (QGRWS), including business continuity planning and upgrade QGRWS security measures ($250K budget).
- Design and manage the National Sealed Source Register, including electronic interfaces, bulk data migration and routine upload of Queensland radioactive sources.
- Manage the national police and ASIO background checking for radiation licence applicants, and make recommendations regarding an applicant's suitability to access security enhanced radioactive sources.

- Conduct detailed onsite and desktop audits to monitor licensee compliance with the Radiation Safety Act 1999 (the Act), security plans, transport security plans and codes of practice. Issue Act instruments where deficiencies are identified and monitor implementation and continuous improvement.
- Lead security-related policy development at the national level and ensure the implementation of adequate security provisions in the Act.
- Participate in responses to radiation safety or security incidents and accidents.
- Maintain SECRET National Security Clearance and protect classified information from compromise, loss or unlawful disclosure.
- Conduct duties as Fire Warden, including inducting new staff.

October 2006 – November 2010: Senior Research Officer – Risk Analysis Research Unit Manager, Counter-Terrorism Strategic Policy Branch (CTSPB), Queensland Police Service (QPS).
Responsibilities and achievements:

- Manage and supervise the Risk Analysis Research Unit within the CTPSB. Conduct Performance Appraisal and Development Plans and training needs analysis.
- Conduct environmental scans to identify "Queensland Terrorism Priority Sites" and prioritise these sites based on their evaluated terrorism risk. Risk is quantified using in-house developed Priority Site Security Risk Analysis methodology.
- Produce detailed Security Risk Assessments for high risk Queensland Priority Sites using methodology based on the AS/NZS ISO 31000:2009 Risk Management.
- Use Security Risk Assessments developed for high risk Queensland Priority Sites to produce location specific scalable Security Contingency Plans and Business Continuity Plans to enhance protective security during normal operations or to be activated during periods of heightened alert.
- Liaise and negotiate with members of the QPS senior executive, senior regional QPS officers and owners/operators of Queensland Priority Sites regarding the conduct and implementation of Security Risk Analyses and Business Continuity Plans and development of operational planning.
- Prepare risk management plans and implement risk mitigation strategies for QPS and national, multijurisdictional counter-terrorism exercises.
- Provide policy advice and produce policy position papers for National Counter-Terrorism Committee meetings for the Deputy Commissioner (Specialist Operations).
- As the CTSPB Security Manager, produce, maintain and implement CTSPB physical and administrative security policies, procedures and training in accordance with the Protective Security Policy Framework and Protective Security Manual. Manage the handling, storage and audit of electronic and hard copy classified information.
- Conduct operational terrorism research to enhance and guide the QPS's strategic, operational and tactical terrorism prevention capabilities.
- Produce, maintain and implement the Terrorism Prevention Framework, the QPS approach to terrorism prevention, for which I was awarded the Queensland Police Service Award for Excellence in Policing Operations, State Gold Award.
- Maintain SECRET National Security Clearance.

January 2005 – October 2006: Supervising Scientist – Results Management, Forensic Biology, Queensland Health Scientific Services
Responsibilities and achievements:

- DNA Analyst gazetted under Section 133A of the Evidence Act 1977.
- Supervise the Results Management Team, including management of workloads to meet targets and reduce backlogs, conduct Performance Appraisal and Developments, training needs analysis and resolve workplace conflict.
- Supervise and manage the initial data migration and routine upload, matching, reporting and data integrity of Qld DNA profiles for the CRIMTRAC National DNA Database.
- Liaise and negotiate with the QPS and other state/territory forensic laboratories regarding DNA links for the CRIMTRAC National DNA Database.
- Maintain personal competency and train staff in presumptive testing and examination of exhibits.
- DNA profile interpretation and reporting to the QPS.
- Preparation of written statements and provide oral DNA evidence in Qld courts.
- Conduct training for staff in the use of Auslab, DNA analysis and interpretation using Genotyper and the DNA link procedure including the use of the CRIMTRAC National DNA Database.
- Design, coordinate and conduct the moot court training and mentoring program, including digital recording and review of oral evidence.
- Participate in the implementation of Auslab for Forensic Biology. Design and implement the Auslab "Link" recording and reporting functions.
- Conduct duties as Fire Warden, including inducting new staff.

November 2002 – January 2005: Case Scientist – Major and Volume Crime Teams, Forensic Biology, Queensland Health Scientific Services
Responsibilities and achievements:

- DNA Analyst gazetted under Section 133A of the Evidence Act 1977.
- Maintain personal competency and train staff in the examination and presumptive testing of exhibits.
- Preparation of written statements and provide oral DNA evidence in Qld courts.
- DNA profile interpretation and reporting to the QPS.
- Conduct Disaster Victim Identification examinations.
- Maintain continuity and traceable audit trails of all samples and exhibits.
- Perform testing and validation of FTA paper for reference sampling.
- Participate in NATA audits.
- Conduct duties as Fire Warden, including inducting new staff.

February 2000 – November 2002: Case Technician - Forensic Biology, Queensland Health Scientific Services
Responsibilities and achievements:

- Perform DNA extraction, quantification and analysis using ABI 3700 and ABI 3100 instruments.
- Analysis and interpretation of DNA profiles using Genescan and Genotyper.
- Conduct and assess training for staff on all Analytical area roles and responsibilities.

- Maintain, decontaminate and calibrate Analytical instruments.
- Maintain continuity and traceable audit trails of all samples and exhibits.

October 1999 – February 2000: Laboratory Technician, Virology Department, Queensland Health Scientific Services
Responsibilities and achievements:

- Provision of diagnostic assays for various viral infections.
- Receipt and storage of patient medical samples.
- Operation under strict work place health and safety guidelines.
- Maintenance of laboratory consumables.

Referees

Ms Paula BRISOTTO: Team Leader – Forensic DNA Analysis, Queensland Health.
Ph: (07) [redacted]

Ms Cathie ALLEN: Managing Scientist – Police Services Stream, Queensland Health.
Ph: (07) [redacted]

Queensland Government

Health Services Support Agency

Job ad reference:	
Role title:	Forensic Scientist - Advanced
Status: (Permanent/Temporary) (Full-time/ Part-Time) (Casual)	Permanent Full Time. Please note future vacancies of a temporary, full time and part time nature may also be filled through this recruitment process.
Unit/Branch:	DNA Analysis Unit
Division/District:	Forensic and Scientific Services Health Services Support Agency
Location:	Coopers Plains
Classification level:	HP5 Reference: JEDii 1814 08/08/2012
Salary level:	
Closing date:	
Contact:	Cathie Allen
Telephone:	[redacted]
Online applications:	www.health.qld.gov.au/workforus or www.smartjobs.qld.gov.au
Fax application:	[redacted]
Post application:	Recruitment Services - Corporate & Statewide, Locked Mail Bag 7004, Chermside Centre, CHERMSIDE QLD 4032
Deliver application:	

About our organisation

Queensland Health's purpose is to provide safe, sustainable, efficient, quality and responsive health services for all Queenslanders. Our behaviour is guided by Queensland Health's commitment to high levels of ethics and integrity and the following **five core values**:

- **Caring for People:** We will show due regard for the contribution and diversity of all staff and treat all patients and consumers, carers and their families with professionalism and respect.
- **Leadership:** We will exercise leadership in the delivery of health services and in the broader health system by communicating vision, aligning strategy with delivering outcomes, taking responsibility, supporting appropriate governance and demonstrating commitment and consideration for people.
- **Partnership:** Working collaboratively and respectfully with other service providers and partners is fundamental to our success.
- **Accountability, efficiency and effectiveness:** We will measure and communicate our performance to the community and governments. We will use this information to inform ways to improve our services and manage public resources effectively, efficiently and economically.
- **Innovation:** We value creativity. We are open to new ideas and different approaches and seek to continually improve our services through our contributions to, and support of, evidence, innovation and research.

Purpose

Provide authoritative advice applying an expert level of knowledge, skills and experience in the area of Forensic Biology and operate as a State-wide reference point for forensic advice and advocacy. To manage the Forensic and Scientific Services, DNA Analysis Unit – to ensure the provision of an integrated, comprehensive, cost effective and quality forensic service in line with the policies, guidelines and strategies of Forensic and Scientific Services.

Your key responsibilities

- Fulfil the responsibilities of this role in accordance with Queensland Health's core values, as outlined above.
- As a recognised forensic expert and DNA Analyst, demonstrates a specialist level of knowledge, skills and experience and clinical leadership within DNA Analysis, Forensic and Scientific Services and is recognised for servicing at a state-wide level. Duties are performed through the independent application of forensic expertise and the use of established specialised techniques, to facilitate complex, critical discipline specific clinical decisions with minimal supervision.
- Accountable for providing independent high level forensic services, based on work performed by others, to all key stakeholders incorporating the interpretation of results, the use of information relating to the National Criminal Investigation DNA Database, and the provision of expert testimony on work performed within the laboratory in accordance with legislative requirements.
- Demonstrated high level management skills, especially in the areas of operational management and resource allocation with respect to new and existing samples, to be processed within an agreed timeframe.
- Provide specialist clinical advice to peers and relevant stakeholders regarding service delivery, on a state wide level, demonstrating involvement and participate in providing strategic direction to DNA Analysis and key stakeholders.
- Demonstrated ability to manage a medium sized team, including high level interpersonal skills including conflict management, ensuring that the team works cooperatively and with effective communication with clients internal and external to the laboratory, chairing weekly team meetings and being involved in the decision making process as part of the DNA Analysis Management Team.
- Ensure the development of scientific knowledge and expertise by supporting active learning and professional development of DNA Analysis Unit staff under your line management.
- Represent the DNA Analysis Unit laboratory group (Forensic & Scientific Services) which includes participation in decision making and strategic planning at a state-wide level.
- Represents Queensland Health at a state-wide level in the provision of expert forensic scientific evidence in all tiers within the court system.
- Applies high level evidence and judgement in advising senior management on quality service improvements to ensure that DNA Analysis complies with all relevant legislative, administrative and professional standards to meet NATA/ISO accreditation/certification requirements.
- Responsible for a high level of formal daily management of a medium-sized discipline-specific professional team. Responsibilities include performance appraisal, assistance with performance management, training of HP3 and HP4 staff, maintenance of appropriate standard operating procedures, appropriate management of allocated resources, assistance and input into strategic planning at a Department level and responsibility for the monitoring of professional standards and quality outcomes from staff and work unit.

Qualifications/Professional registration/Other requirements

- The successful applicant must hold a tertiary qualification, or equivalent, in science from a recognised university or tertiary institution.
- In some circumstances and following consultation, Queensland Health staff may be required to participate in 24 hour shift, on-call or weekend roster arrangements.

- Appointment to this position requires proof of qualification and if applicable registration or membership with the appropriate registration authority or association. Certified copies of the required information must be provided to the appropriate supervisor/manager, prior to commencement of clinical duties.

Are you the right person for the job?

You will be assessed on your ability to demonstrate the following key attributes. Within the context of the responsibilities described above, the ideal applicant will be someone who can demonstrate the following:

- Demonstrated extensive expertise and understanding of the contemporary discipline of forensic biology, with demonstrated abilities in a range of relevant procedures, techniques, instrumentation and quality assurance systems, including the use of computer systems.
- Demonstrated ability to solve scientific problems, generate ideas and innovations, introduce new technology and actively participate in the processes of change and continuous improvement.
- Demonstrated interpersonal skills for working in a team both as a member and as a leader; the ability to consult and communicate scientific/technical information effectively both orally and in writing including presentation of expert testimony in a court of law.
- A demonstrated commitment to the principles of quality management and continuous quality improvement and a contemporary knowledge of NATA/ISO accreditation/certification.
- Demonstrated ability to supervise and manage staff in line with quality human resource management practices with particular reference to employment equity, anti-discrimination, occupational health and safety and ethical behaviour.

How to apply

Please provide the following information to the panel to assess your suitability:

- Your current CV or resume, including referees. You must seek approval prior to nominating a person as a referee. Referees should have a thorough knowledge of your work performance and conduct, and it is preferable to include your current/immediate past supervisor. By providing the names and contact details of your referee/s you consent for these people to be contacted by the selection panel. If you do not wish for a referee to be contacted, please indicate this on your resume and contact the selection panel chair to discuss.
- A short statement (maximum 2 pages) on how your experience, abilities, knowledge and personal qualities are relevant for the role, taking into account the key responsibilities and attributes noted in the 'Are you the right person for the job?' section.

About the Health Services Support Agency

Working in the Health Services Support Agency (HSSA) is an opportunity to creatively and productively contribute to improving the provision of health services to the people of Queensland. HSSA is a learning organisation, committed to developing our people through training, support and leadership programs. We offer challenging opportunities to allow you to explore your potential. HSSA promotes a healthy balance between your work and personal life, provides flexible work hours, paid parental leave and study leave options.

We look forward to working with you!

HSSA is a division of Queensland Health that aims to deliver safe, sustainable and appropriate services to enhance health care throughout Queensland. It provides these services through

- Diagnostic and Scientific Services
- Procurement Logistics and Health Technology Services
- Clinical Support Services

http://www.health.qld.gov.au/hssa/home.htm

Pre-employment screening

Pre-employment screening, including criminal history and discipline history checks, may be undertaken on persons recommended for employment. The recommended applicant will be

required to disclose any serious disciplinary action taken against them in public sector employment. In addition, any factors which could prevent the recommended applicant complying with the requirements of the role are to be declared.

Roles providing health, counselling and support services mainly to children will require a Blue Card. Please refer to the Information Package for Applicants for details of employment screening and other employment requirements.

Salary Packaging

To confirm your eligibility for the Public Hospital Fringe Benefits Tax (FBT) Exemption Cap please contact the Queensland Health Salary Packaging Bureau Service Provider – RemServ via telephone 1300 30 40 10 or http://www.remserv.com.au.

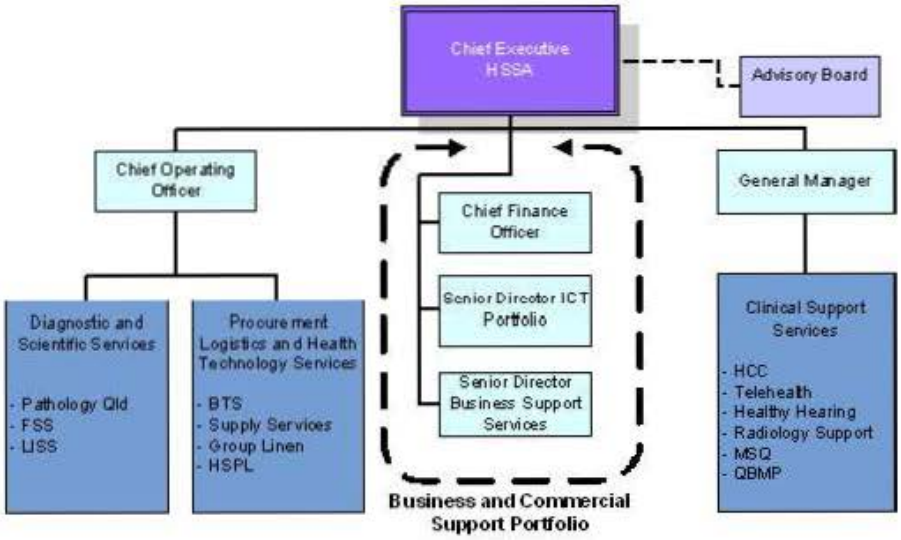
Disclosure of Previous Employment as a Lobbyist

Applicants will be required to give a statement of their employment as a lobbyist within one (1) month of taking up the appointment. Details are available at http://www.psc.qld.gov.au/library/document/policy/lobbyist-disclosure-policy.pdf

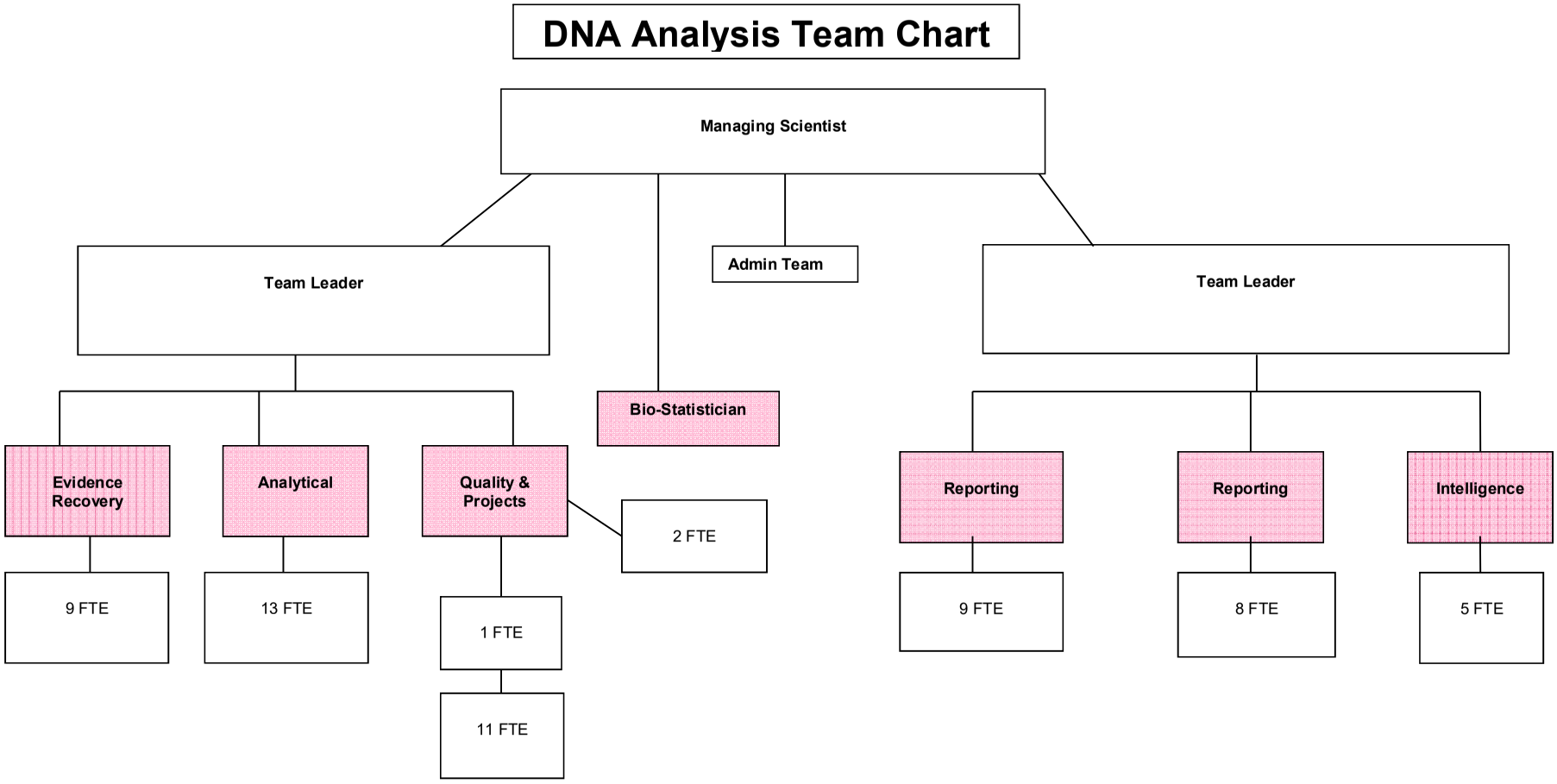
Probation

Employees who are permanently appointed to Queensland Health may be required to undertake a period of probation appropriate to the appointment. For further information, refer to Probation HR Policy B2 http://www.health.qld.gov.au/hrpolicies/resourcing/b_2.pdf

ORGANISATIONAL CHART



DNA Analysis Team Chart



Luke Ryan

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]

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
[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.

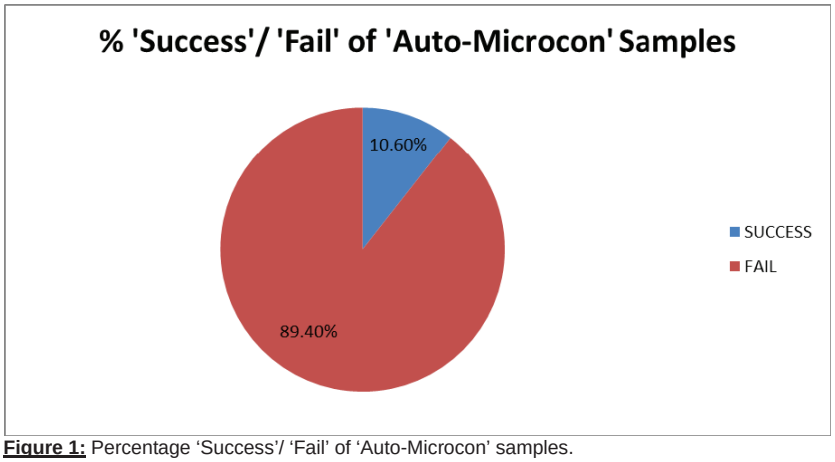


Figure 1: Percentage 'Success'/ 'Fail' of 'Auto-Microcon' samples.

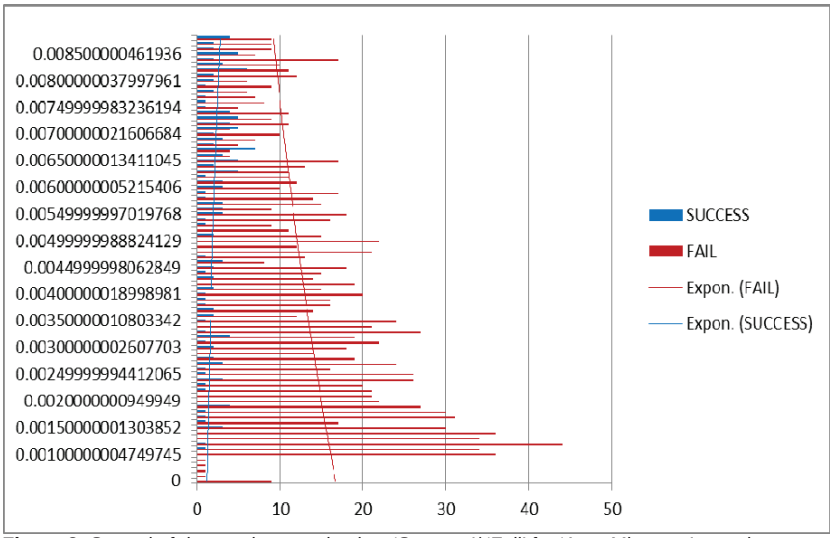


Figure 2: Spread of data and categorised as 'Success'/ 'Fail' for 'Auto-Microcon' samples.

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).

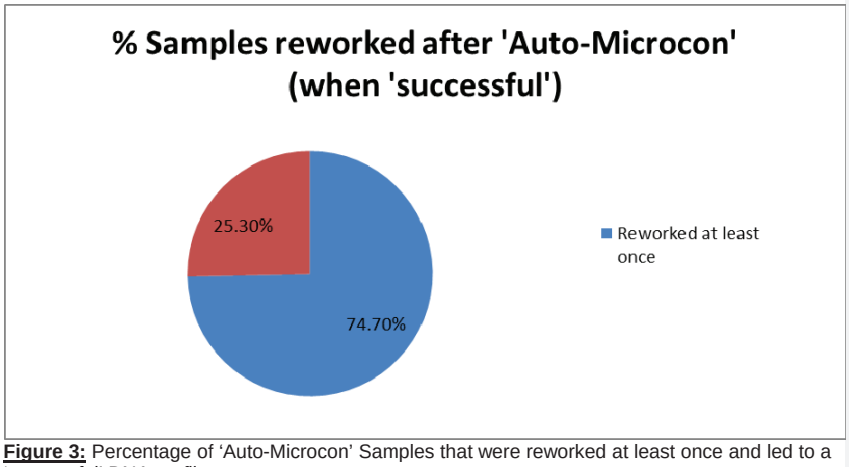


Figure 3: Percentage of 'Auto-Microcon' Samples that were reworked at least once and led to a 'successful' DNA profile outcome.

In putting the data behind Figures 2 and 3 together, if an 'auto-microcon' process was not conducted and was subsequently requested by the client for samples in this Quantification range, there would be approximately a 10% chance of obtaining a 'successful' DNA profile interpretation. Furthermore, in order to achieve that outcome, approximately 75% of these 'successful' samples would have needed a further rework. This means, for these samples, there would be a turnaround time factor for the client to consider, and in a potential fee-for-service model with requesting clients, being prepared to have increased processing costs associated with these low-quant samples would be a client consideration.

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.

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.

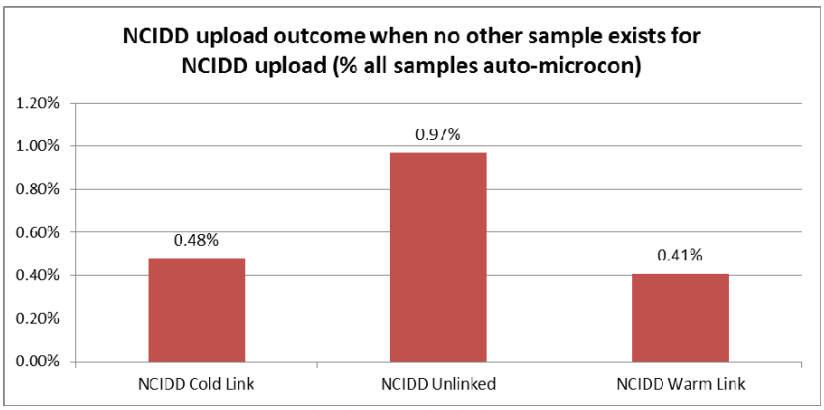


Figure 4: NCIDD outcome for samples that were loaded to NCIDD

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

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

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

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

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

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

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

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

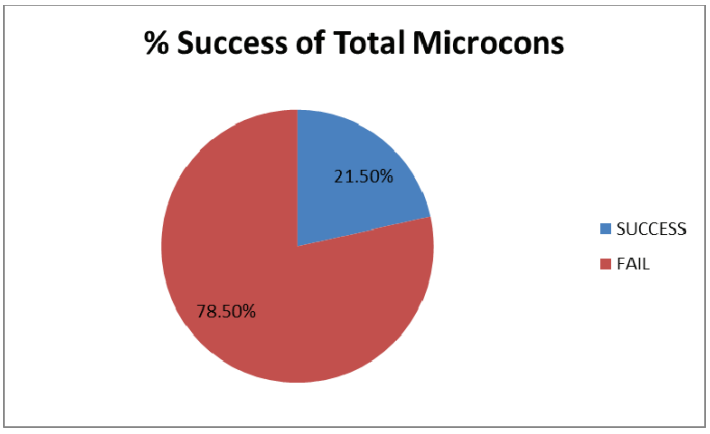


Figure 5: Percentage 'Success'/ 'Fail' of all Microcon® samples ('combined' data).

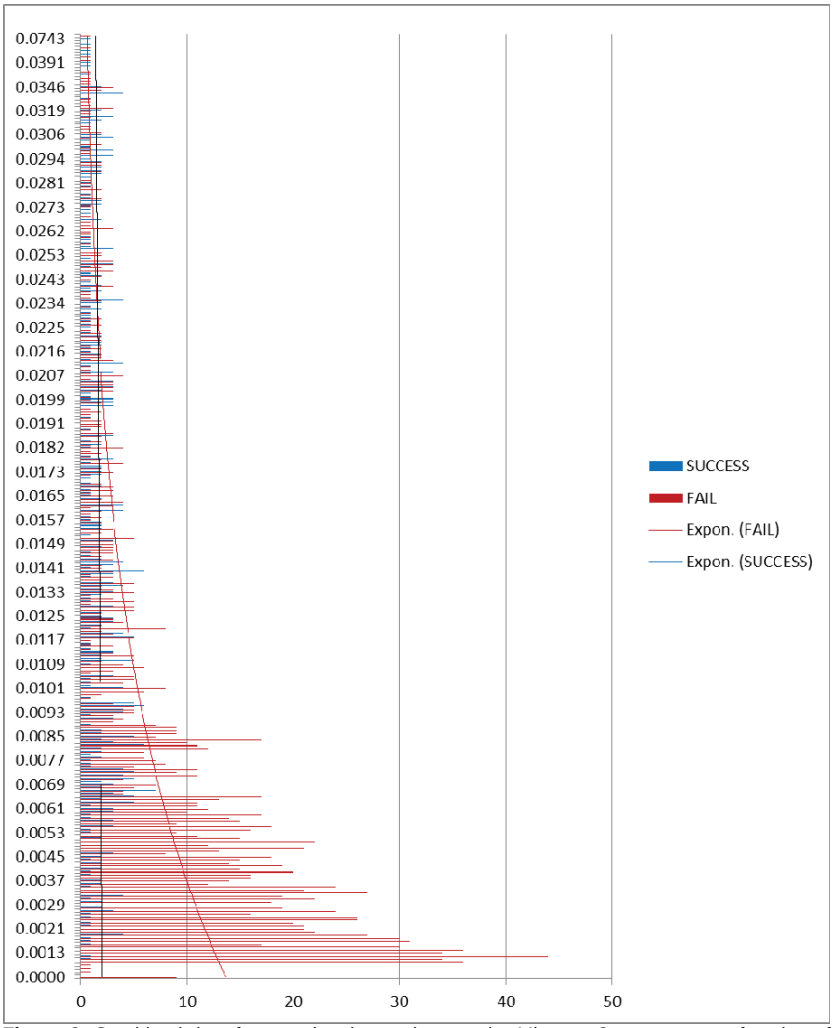


Figure 6: Combined data for samples that underwent the Microcon® process as a function of Quantification value.

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

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

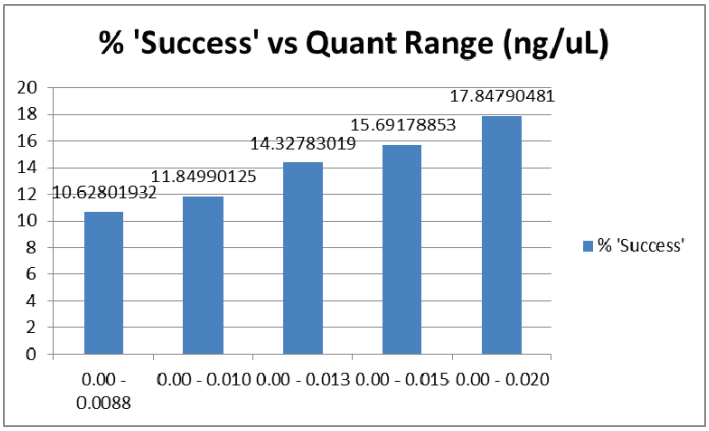


Figure 7: Percentage 'success' for samples that underwent a Microcon® process

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

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

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

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

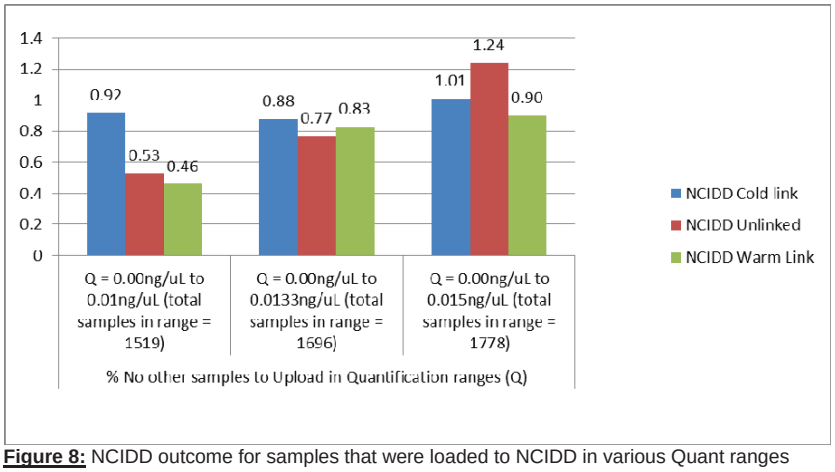


Figure 8: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

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

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

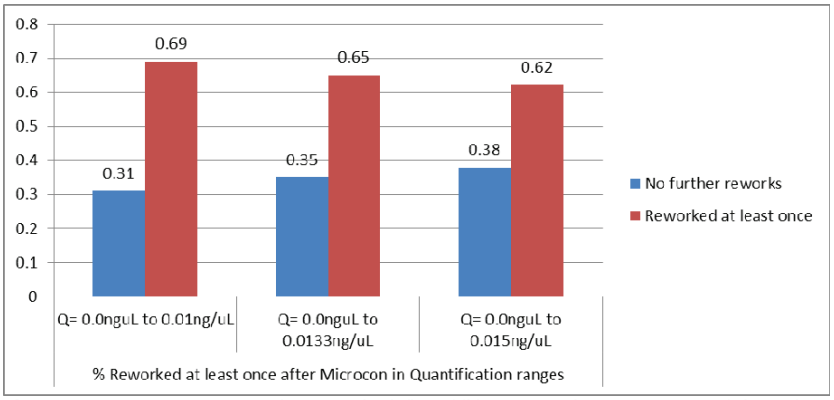


Figure 9: Percentage of samples reworked (in addition to a Microcon® process) in various Quantification ranges.

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

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

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

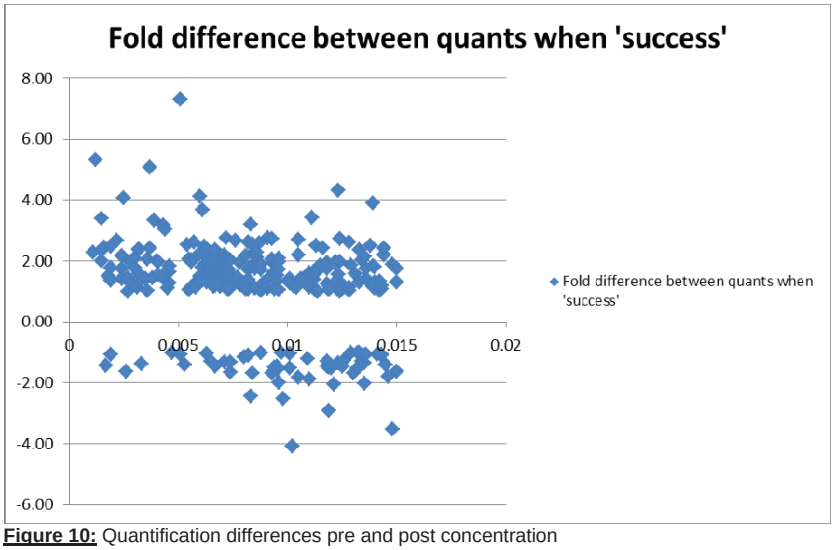


Figure 10: Quantification differences pre and post concentration

The findings are not unexpected as the scatter focusses mostly around two-fold increases in Quantification. It was also not unexpected to observe the variable results. 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.

2. Cease processing all Priority 3 samples up to the Quantification value of 0.0133ng/uL (template of 200ng).

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

4. Re-analyse Priority 2 samples in the range 0.0088ng/uL to 0.0133ng/uL after a six month period of processing to evaluate whether Recommendation 2 can be extended to Priority 2 samples.

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

~~7.~~8. References

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

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

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

Luke Ryan

From: Luke Ryan
Sent: Friday, 1 December 2017 8:50 AM
To: Justin Howes
Subject: RE: Project #184 for review

Hi Justin
Looks good to me. Just a few minor formatting comments:

Figure 2 – maybe reduce to 4 decimal places?, also add X and Y axis labels
Figure 6 – add X and Y axis labels
Figure 7 – reduce decimals in labels
Figure 10 – re-format legend so that graph has more room
Thoughout – sometimes the ® is superscript and sometimes not (sorry that's very picky)

Thanks
Luke

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

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]

Luke Ryan

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**

[redacted]

Luke Ryan

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**

[redacted]

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

Version history

Version	Date	Changed by	Description
1.0	30/11/2017	Justin Howes	Document Created.
2.0	09/01/2018	Justin Howes	Post Management feedback

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
Kerriy-Anne Lancaster	A/ 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 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.

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.

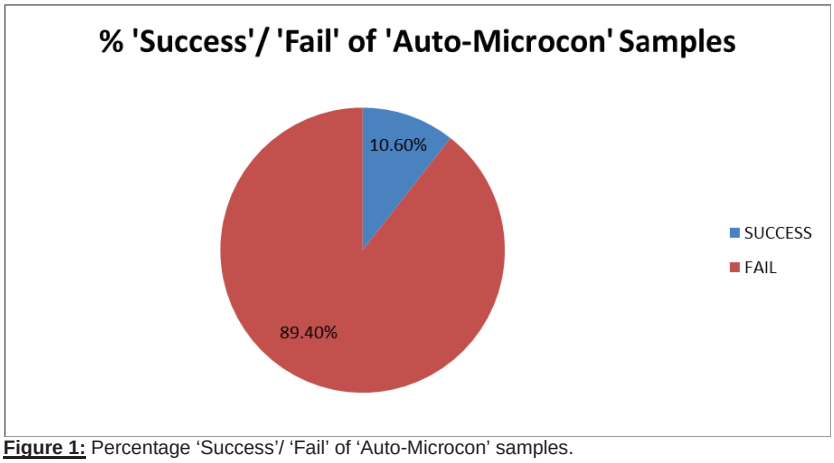

Figure 1: Percentage 'Success'/ 'Fail' of 'Auto-Microcon' samples.

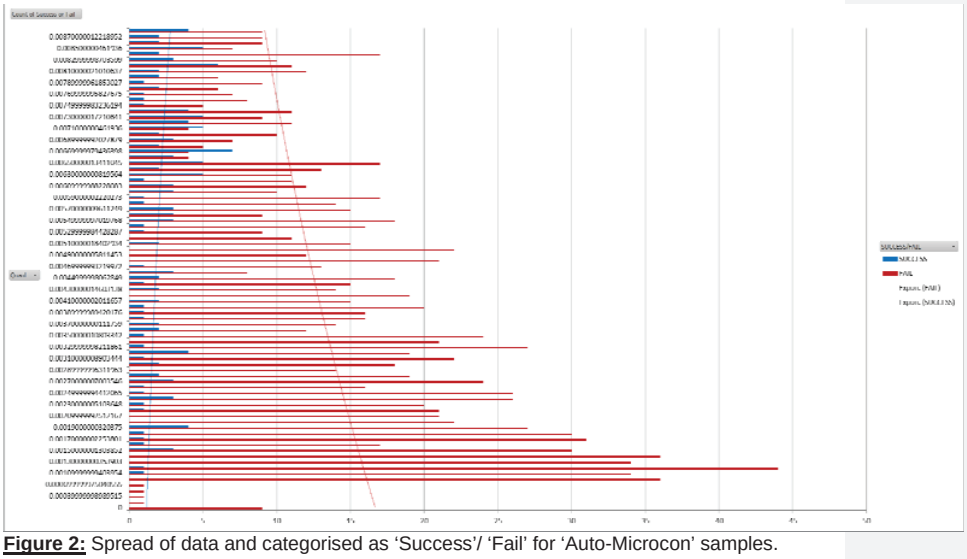

Figure 2: Spread of data and categorised as 'Success'/ 'Fail' for 'Auto-Microcon' samples.

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.

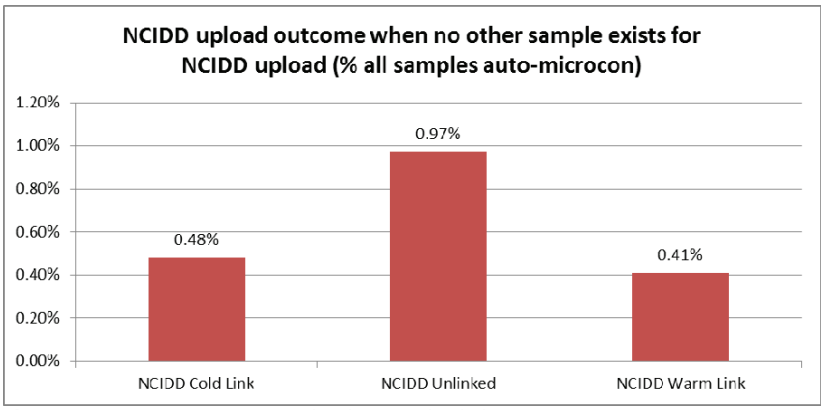

Figure 3: NCIDD outcome for samples that were loaded to NCIDD

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.

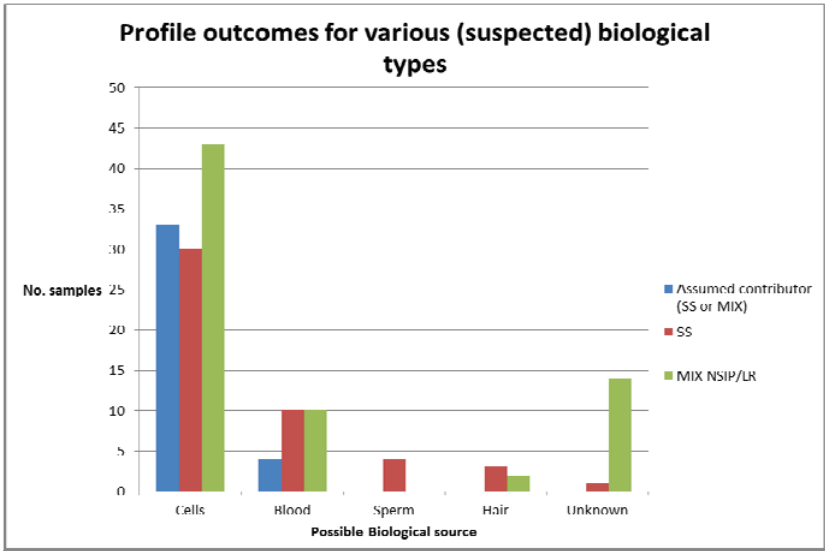

Figure 4: Profile outcomes for various (suspected) biological types

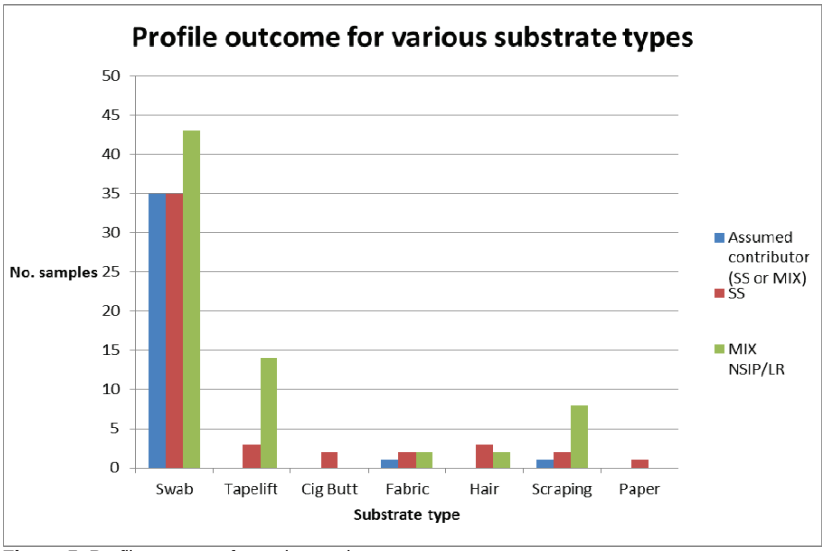

Figure 5: Profile outcome for various substrate types

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).

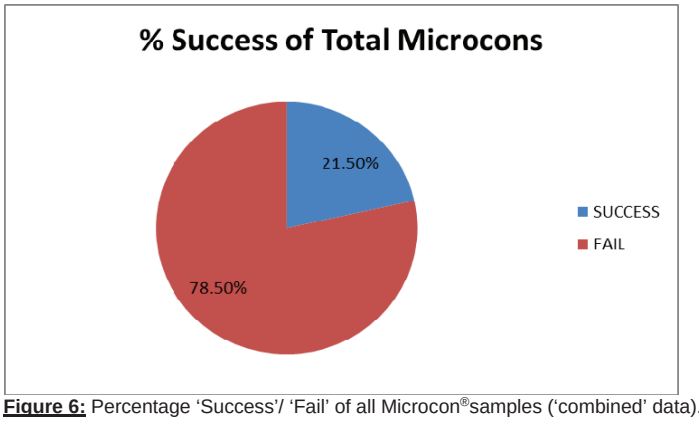

Figure 6: Percentage 'Success'/ 'Fail' of all Microcon®samples ('combined' data).

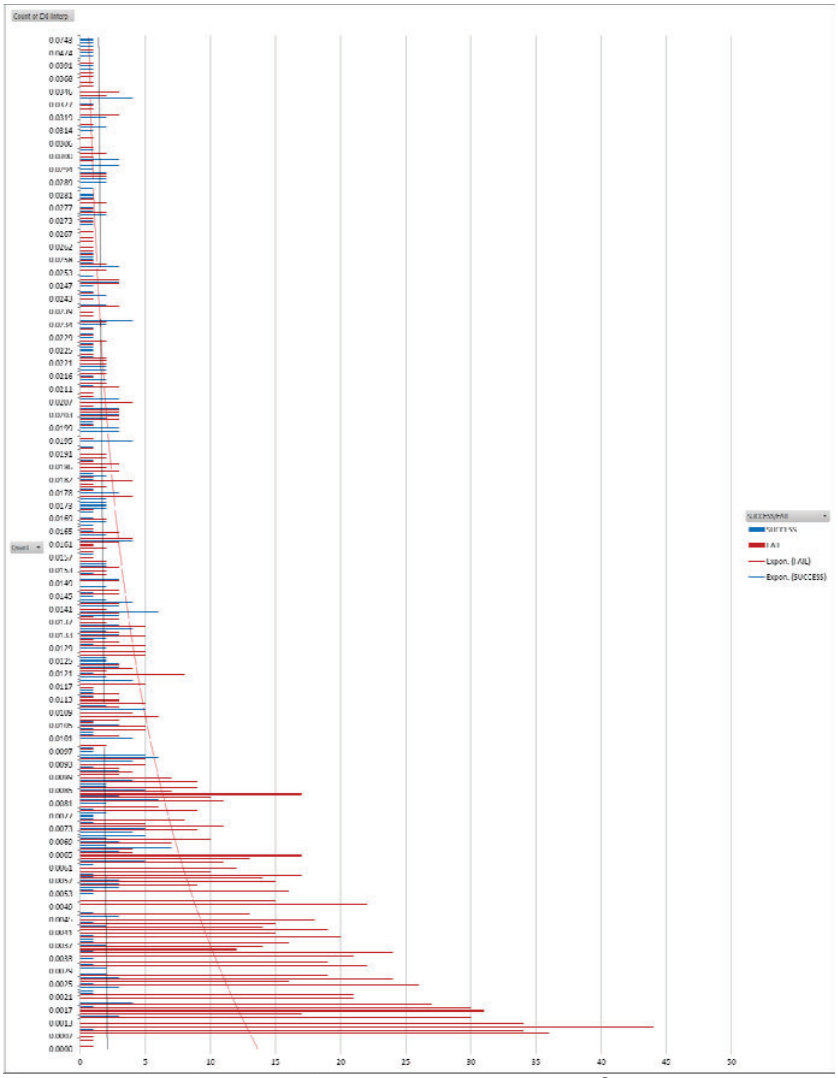

Figure 7: Combined data for samples that underwent the Microcon® process as a function of Quantification value.

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.

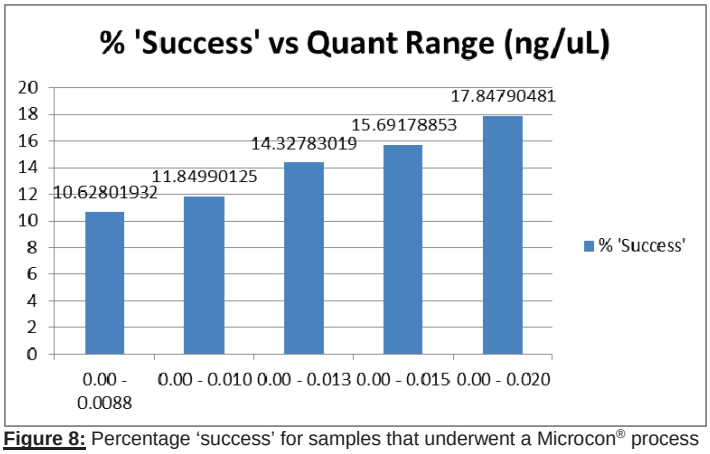

Figure 8: Percentage 'success' for samples that underwent a Microcon® process

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

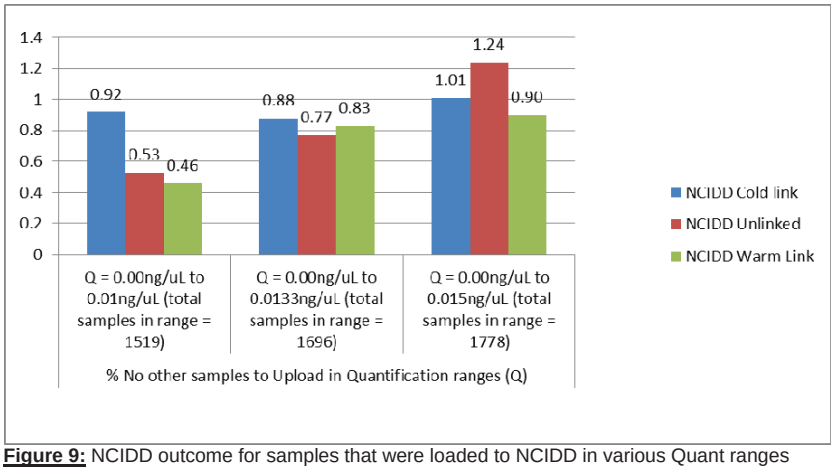

Figure 9: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

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'.

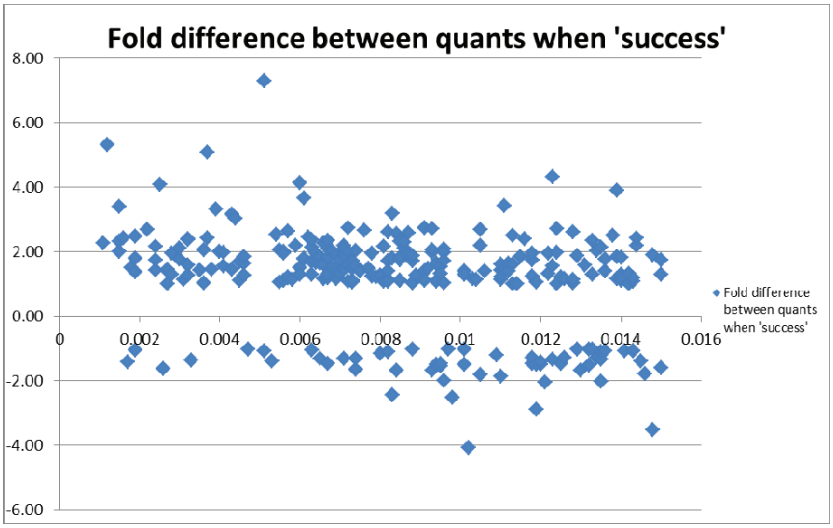

Figure 10: Quantification differences pre and post concentration

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

    a. Priority 1 samples (Critical Priority); and

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

2. Automatically send result information via the Forensic Register to QPS at Quantification stage for samples in the Quant range: 0.001ng/uL to 0.0088ng/uL. This result information is recommended to be the exhibit result line of 'DNA Insufficient for Further Processing'. This recommendation is an extension to the current 'No DNA Detected' process, which looks at Priority 2 samples yielding Quantification results of less than the Limit of Detection (0.001ng/uL).

3. After a six month period of processing, re-analyse samples that have had a Microcon® process performed and were in the initial Quantification range greater than 0.0088ng/uL, to evaluate whether the range from Recommendation 1 can be extended.

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

~~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.

Luke Ryan

From: Luke Ryan
Sent: Tuesday, 9 January 2018 9:10 AM
To: Justin Howes
Subject: RE: #184 report v2

Excellent good one

From: Justin Howes
Sent: Tuesday, 9 January 2018 8:50 AM
To: Luke Ryan
Subject: RE: #184 report v2

Hey, added to R1:

1. Cease 'auto-microcon' (Quant range: 0.001ng/uL to 0.0088ng/uL) processing for all samples of Priority 2 and 3 requested to be amplified with PowerPlex 21, with the following exceptions:

jah

Justin Howes
Team Leader – Forensic Reporting and Intelligence Team

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

[redacted]

From: Luke Ryan
Sent: Tuesday, 9 January 2018 8:41 AM
To: Justin Howes
Subject: RE: #184 report v2

Ok excellent. Might be worth specifying. I would either add a Scope section at the start (and say that recommendations apply to all P2 and P3 samples processed with PP21, or just specify in the Conclusion and Recommendations section – perhaps at start of recommendation 2? i.e. "For all Priority 2 and 3 samples processed with PP21, automatically….."

From: Justin Howes
Sent: Tuesday, 9 January 2018 8:35 AM
To: Luke Ryan
Subject: RE: #184 report v2

Hey, yes all samples. Do you think I should just expand this a bit?

jah

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

From: Luke Ryan
Sent: Tuesday, 9 January 2018 8:31 AM
To: Justin Howes
Subject: RE: #184 report v2

Hi Justin
Looks great, I assume the recommendations apply to P3 samples amped in PP21? I'm ready to sign.
Thanks
Luke

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

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**

[redacted]

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