SUPPLEMENTARY STATEMENT OF PAULA BRISOTTO

I, Paula Michelle Brisotto, care of Queensland Health Forensic and Scientific Service, Team Leader Evidence Recovery and Quality Team, Forensic DNA Analysis, do solemnly and sincerely declare that:

1. I am employed by Queensland Health Forensic and Scientific Service ('QHFSS').

2. I hold a Bachelor of Science from Griffith University, and a Master of Science in Forensic Science from Griffith University.

3. I have previously provided three statements to the Commissioner, dated 9 August 2022, 25 August 2022 and 21 September 2022. This is a supplementary statement to those previous statements.

4. This statement is in response to Notices 2022/00140 and 2022/00232.

5. I hold the position of Team Leader, Evidence Recovery and Quality Team, Forensic DNA Analysis, Police Services Stream at QHFSS at Coopers Plains. This is the team which undertakes the laboratory examination of samples of items for DNA.

6. As Team Leader of the Evidence Recovery and Quality Team, I have general oversight over approximately 30 to 40 staff and direct oversight over the three-sub team leaders (Evidence Recovery team, Analytical team and the Quality & Projects/Clinical Assistants team). The role of our team is to recover and then undertake the examination of samples of items for DNA, called analytical processing. The results are then sent to the Forensic Reporting and Intelligence Team ("FRIT") managed by Justin Howes for interpretation of the DNA profile, statistical analysis and reporting of the results, including to the QPS.

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7. My role includes:

   a. A variety of administrative duties including some relating to staffing, such as approving at a team level requests for leave;;
   b. responding to issues raised by line managers;
   c. liaising with line managers about day to day activities, including feeding back information such as might be provided by QPS;
   d. liaising with staff and line managers about technical aspects of our team's services that may have an impact on clients or require actioning by other teams;
   e. providing intel reports to QPS. My role in this respect generally deals with elimination sample matches being reported to the QPS;
   f. if required as a result of other senior scientists being on leave, reviewing technical work conducted by the team and signing off on such work;
   g. as part of the management team:
      i. reviewing and endorsing project proposals and reports;
      ii. attending weekly management team meetings;
   h. approving OQIs or quality improvements within my team;
   i. approving some financial requests up to the limit of my delegation. This includes purchasing common consumables and other times required for laboratory work. Although I have some level of financial delegation, I often also seek approval from Cathie Allen;
   j. endorsing professional development leave, which requires final approval from the Managing Scientist;
   k. preparing a weekly report to the Managing Scientist. This usually involves extrapolating information given to me by the line managers in their respective weekly reports to me about work received and work outstanding, as well as information about projects. I send the weekly report to Cathie Allen and also meet with her to discuss the report;
   l. on occasion, being an active participant in a proposal or project;
   m. liaising with members of my team on an ad hoc basis. This can occur in my office or on the laboratory floor. I have an open door policy so my team can see me at any time;

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n. attending to correspondence from QPS, such as Priority 1 requests. This information is sent to me, Cathie Allen and Justin Howes. When received, I will update the Forensic Register, advise staff where the samples are to be allocated and also inform them of any other requests I might have;

o. attending to general correspondence from my team, or anyone else in FSS;

p. when required, reviewing and accepting new SOPs or training modules. The Managing Scientist is the approver of all SOPs and training modules in QIS;

q. when required, meeting with Scientific Skills Development to discuss mandatory staff training or other FSS training requirements;

r. signing off, as required, on training competencies for staff, after a trainer and line manager finds them competent.

8. From early February 2015 to mid-July 2016, I was away from work on maternity leave. After returning to work in July 2016, until 16 January 2018, I worked a four-day week on Mondays, Tuesdays, Thursdays and Fridays. I generally worked approximately 6.6 hours a day, starting between 9:00am - 9:15am and finishing around 4pm – 4:15pm.

9. From Wednesday 17 January 2018 until Monday 22 January 2018, I was on leave and not at work. At that time, we did not have remote or external access to work emails and, as such, I could not check emails whilst on leave.

10. Upon returning to work on 22 January 2018, I worked reduced hours, to allow for school pickups. I still worked an eight day fortnight (not working on Wednesdays) however work hours were shorter, working around 5.5 hours a day. I would start work at around 9:15am and leave work between 2:30pm – 2:45pm. These work arrangements continued until around 12 February 2018, after which time I worked up to 5.5 hours on Mondays (generally finishing at 2.45pm), and 6.5-6.75 hours on Tuesdays, Thursdays and Fridays.

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EVIDENCE RECOVERY TEAM

11. The Evidence Recovery team includes forensic scientists and technicians. The Evidence Recovery team:

    a. prepares and records any examinations in the Forensic Register;
    b. submits samples to the Analytical team for processing;
    c. assesses the samples (which are received in a tube for processing) as fit for purpose for the extraction instruments;
    d. performs the microscopy for spermatozoa;
    e. performs the data entry task to run STRmix;
    f. provides the data/results of the STRmix to the reporting scientist for interpretation once available;
    g. undertakes the destruction of reference samples, when requested by QPS in the Forensic Register.

12. This is also explained in the duty statement, attached as **PB03** to my statement dated 21 September 2022.

13. *Explain what information Evidence Recovery staff input into the Forensic Register*

    a. Generally, the information the Evidence Recovery scientist input into the Forensic Register relates to the examination they have performed, and the record the results of any presumptive tests. These can be check boxes, and free text information in the examination summary. Staff will also select the relevant technique to progress through to analytical processing, for example differential lysis extraction.
    b. I do not perform these tasks, and therefore would need to rely on the relevant SOPs to indicate specifically what information the Evidence Recovery staff input for the different processes.

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14. *Explain what involvement the reporting scientists have in Evidence Recovery*

   a. I understand that the Senior Scientist of the Evidence Recovery team may be involved in providing an examination strategy if, for instance, there are large and/or whole items or SAIKs received for examination that require an examination strategy. The Senior Scientist of the Evidence Recovery Team is also a competent reporting scientist.

   b. If a reporting scientist is allocated a cold case, they may have involvement with the Evidence Recovery team if examination of items is required. They may discuss examination options with Evidence Recovery scientists or the Evidence Recovery Senior Scientist to ensure that what sampling they are undertaking is appropriate and best practice.

   c. One of the reporting scientists in FRIT, Angelina Keller, has competency in bone examination, and will undertake this task on a rostered basis within Evidence Recovery.

15. *Explain whether the Evidence Recovery staff receive any positive or negative feedback from Analytical or Reporting scientists about their work. Provide an example of feedback from each team.*

   a. I am not aware of any formal mechanism for feedback from the Analytical or Reporting scientists to the Evidence Recovery staff.

   b. At times, Cathie Allen may receive feedback for Priority 1 samples from QPS. This feedback is often communicated to the entire team (that is, Evidence Recovery, Analytical and Reporting Teams).

   c. I have also provided feedback to the Evidence Recovery Team line manager in relation to large numbers of examinations performed on SAIKs. The sort of feedback I usually give includes praising the team for their efforts and passing on my appreciation.

16. *Explain whether Evidence Recovery staff are provided or seek out the outcomes of the samples they collected from any other staff*

    a. If an interesting examination occurred, Evidence Recovery staff will follow the sample through, and feed back to the Evidence Recovery team on the outcomes.

    b. The majority of items received are in-tube samples, ready for processing on the instruments, so there may be little information known about the sample prior to submission for analytical processing.

ANALYTICAL TEAM

17. The Analytical team includes scientists and senior scientists and is managed by a Supervising Scientist. The Analytical team undertake processing to obtain a DNA profile. This process includes extraction, quantification, amplification, and capillary electrophoresis.

Analytical tasks

18. *Identify and explain the tasks undertaken in the Analytical section and the processes involved in each task, including, but not limited to:*

    a. *Manual Extraction*

        i. Manual extraction is DNA extraction performed on the Maxwell instruments. Manual extraction is also performed through Nucleospin for a specific sample type (paraffin tissue). Staff allocated to manual extraction also perform a pre-lysis step before the QIAsymphony auto-extraction, as this is a separate task, as well as any post-extraction processing.

        ii. On review of SOPs 34041, 34044, 35605, 34040 and 34132, I understand that it involves:

            1. preparing samples for automated DNA extraction i.e. performing pre-lysis of samples for QIAsymphony;

            2. performing DNA extractions using the Maxwell 16 and Maxwell FSC instruments;

            3. performing Nucleospin extractions;

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4. performing post-extraction processing of DNA extracts including Microcons, Nucleospin clean-ups, dilutions and transfers/pooling.

b. *Automatic Extraction*

i. Automatic extraction is extraction performed on the QIAsymphony instruments.

ii. On review of SOPs 34132 and 33756, I understand that it involves:

1. ensuring there are sufficient batches prepared and ready for automated DNA extractions i.e. both lysate and extract Nunc Bank-It™ tubes have been sorted and sequence checked.
2. performing DNA extractions using the QIAsymphony.
3. maintaining and calibratiing of QIAsymphony.

c. *Pre-PCR*

i. Pre-PCR is the process undertaken prior to amplification.

ii. The Pre-PCR tasks outlined in the duty statement are as follows:

1. Perform quantification and amplification of DNA extracts that have been processed by both manual and automated extraction methods using the Pre-PCR Hamilton STARlet instruments.
2. Carry out QC testing of Quantifiler Trio, PowerPlex 21 kits when necessary.
3. Make standards for quantification of DNA extracts and test them when required.
4. Perform manual quantification and amplification of DNA extracts as required.
5. Calibration and Maintenance of Hamilton STARlet instruments.

d. *CE*

i. Analytical staff undertake capillary electrophoresis ('CE') on amplified product using the 3500xL Genetic Analyser. SOP 34312 refers.

ii. The CE tasks outlined in the duty statement are as follows:

1. Prepare samples/plates for capillary electrophoresis.
2. Run plates on the 3500xL Genetic Analyser.

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3. Perform the CEQ check of CE batches after completion of the run
4. Create batches for and perform capillary electrophoresis of re-genescan samples and/or samples to be rerun.
5. Running quantification batches, checking QC parameters and exporting results.
6. Maintenance and calibration as required of 3500xL Genetic Analysers, 7500, Quant Studio 5 & Proflex instruments.

e. *Plate Reading*

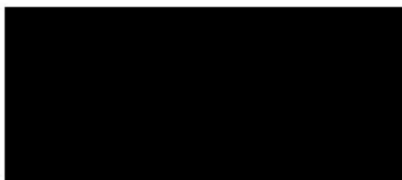
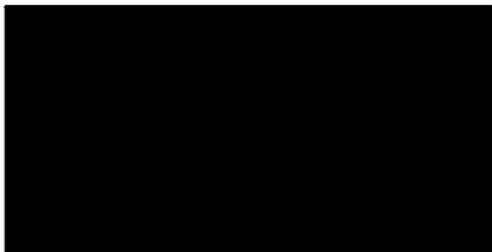
i. "Plate reading" refers to the interpretation of DNA profiles using the GeneMapper ID-X software. SOP 34112 refers. This task is shared across all teams and is performed by scientist and senior scientists (HP4).

f. *Testing reagents and kits*

i. All reagents used in quantification and amplification processes including kits, standards and quality controls are tested prior to routine used. This is to ensure the quality and validity of the results obtained from the processes.

ii. SOP 34514 *"Preparation & Testing of Quantification Standards, In-house DNA Controls, Quantification Kits and Amplification Kits"* details the methods and techniques performed within the Analytical section for:

1. The preparation of Quantifiler® Trio standards using the Hamilton Microlab® STARlet (STARlet) and LabElite® Integrated I.D. Capper™ (Decapper);
2. The testing of Quantifiler® Trio standards and assessing results against expected performance values;
3. The testing of Quantifiler® Trio kits and assessing results against expected performance values;
4. The preparation of in-house DNA controls; and
5. The testing of PowerPlex®21 kits and assessing results against expected performance values.

 ....  ...

g. *Preparing and testing quantitation standards*

i. See my response above.

ii. Also this process is detailed in SOP 34514 as follows:

> *"Quantifiler® Trio standards are used in every quantification reaction performed within Forensic DNA Analysis to create a five-point standard curve used to estimate the concentration of reference and casework samples.*

iii. The STARlet instruments are programmed to perform the automated preparation and testing of Quantifiler® Standards.

h. *Verifying pipetting instruments*

i. I understand from my review of SOPs 33756, 26628 and 34050 that verifying pipetting instruments includes the pipetting performance of each robotic platform and is assessed 3 monthly or when a component of a pipetting channel is replaced on the instrument. Testing is performed using the ARTEL MVS® system. All findings are recorded in the Forensic Recovery.

i. *Cross-contamination checks on pall processes*

i. Cross contamination checks are performed using positive and negative controls on all robotic platforms in accordance with SOP 34280 "*Environmental Monitoring*".

ii. These checks are performed every 6 months to monitor cross-contamination during DNA extraction (QIAsymphony SP and Maxwell 16 and FSC), quantification set-up (QIAsymphony AS) and amplification and CE set-up (Pre-PCR and CE STARlet instruments).

j. *Environmental monitoring*

k. Each line manager of the Analytical, Evidence Recovery and Quality and Projects Team will co-ordinate and / or conduct environmental monitoring of laboratory areas, including monitoring / reviewing of the results and carrying out appropriate actions that may arise from the results.

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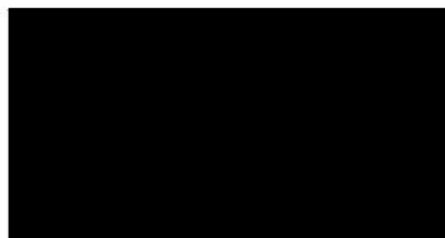
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l. SOP 34280 *Environmental Monitoring* provides the following:

"The purpose of environmental sampling is to monitor the environment for incidental/accidental DNA contamination (from staff, DNA samples, exhibits or other sources) to detect events that may detrimentally impact on sample processing/profiling within the Forensic DNA Analysis laboratory. It also assesses the efficacy of cleaning procedures within the Forensic DNA Analysis laboratories."

m. Environmental monitoring occurs monthly, taken before a deep clean of the laboratory areas (and after the routine daily clean). At least once a year, environmental sampling occurs before and after a deep clean.

19. *Outline the instruments and systems involved in each task. Attach any documentation relevant to each task*

a. The tasks for the Analytical Team are listed in the Duty statement (refer to **PB01** of my statement dated 21 September 2022).

b. I do not undertake these tasks and would refer to the SOPs for the details of the processes involved in each task.

20. *Explain how staff are assigned to each task*

a. My understanding is that, based on competency, staff are rotated to different tasks over the week by the Analytical HP4 Senior Scientist to ensure all core task are covered. Staff are generally allocated to one task, however, can perform other tasks on any given day. The only limitation is for staff allocated to CE, who cannot perform tasks in any pre-PCR rooms given they have been handling amplified product.

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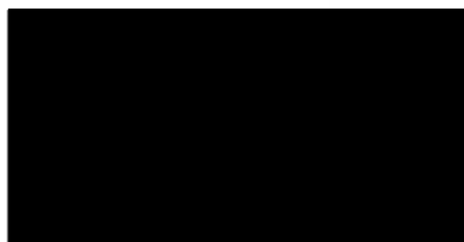

21. *Explain the extent of the analytical staff's ability to decide what process is undertaken on a sample*

    a. The analytical processing is driven by batch functionality (business rules within the Forensic Register), where the samples are allocated to an extraction worklist by the technique and method selected by Evidence Recovery.

    b. Batches and worklists are grouped by function (i.e. extraction, quantification, STR amplification capillary electrophoresis) and method (for example, Differential Lyiss, QIAsymphony pre-Lysis etc).

    c. At each batch completion, samples transition to the next processing step based on sample type, priority, process result and operator decision. Operator decision may relate to sending the sample for a dilution process if the DNA quantification is very high. There are flags programmed within the Forensic Register to assist with the assessment.

    d. Samples progress according to the applicable SOPs. Should anything occur outside of a SOP that requires advice to progress, this would be raised to the Senior Scientist of the Analytical team.

22. *Explain whether analytical staff can assist the Evidence Recovery Team or Reporting Team during busy times. Explain why or why not*

    a. The Analytical team can assist by replacing Reporting or Evidence Recovery staff in shared tasks, for example plate reading. This is a task that can take most of a day, and the Analytical staff often assist with this when requested.

    b. Other tasks cannot be undertaken as competency is required in most processes before staff can undertake that task. Many processes take some weeks or months to train in and require regular rotation through the task to consolidate the training and maintain competency.

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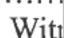

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23. *Explain whether analytical staff are provided with positive or negative feedback from you or other staff in relation to samples they processed. Provide an example of feedback*

a. I am not aware of any formal mechanism for giving feedback to Analytical staff in relation to samples they processed.

b. It can be difficult to give feedback on a particular sample as the through put and processing within the Analytical team is done though batches, so generally no one sample or samples are tracked.

c. If for instance a sampling issue is raised with staff, the discussion around the issue will be performed by the line manager, although I will be informed.

d. There may be feedback given on Priority 1 samples given as the request from the QPS is for an urgent turn around time. This feedback can be from the allocated reporting scientist, or may come through Cathie Allen passing on positive feedback from the QPS.

e. Attached to this statement is an email from Luke Ryan to Forensic DNA Analysis on 16 August 2021 with positive feedback regarding turn around times for Priority 1 samples as **PB129**.

QUALITY & PROJECTS/CLINICAL ASSISTANTS TEAM

24. The Quality & Projects/Clinical Assistants team is run by Kirsten Scott, a senior scientist as well as a HP3 senior scientist and clinical assistants. The clinical assistants provide support to the Evidence Recovery team and Analytical team as well as to Reporting team. This support includes taking photos of samples, tracking samples, creating sample batches or pulling samples from other locations. The performance of these tasks allow the scientists to focus on the core scientific work. Clinical assistants also undertake reference sample punching which involves using an instrument to punch the sample on to a plate which the scientist will use in various instruments.

25. Kristen Scott's role includes providing support for process improvements, verification or validation of new and/or alternative technologies and techniques, ensuring that the documentation required for projects is completed and filed, coordinating the

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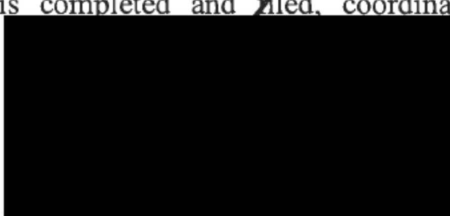

requirements for NATA audits and certification audit preparation, coordinating calibrations, reviewing all SOPs and training modules for Forensic DNA Analysis, and allocating proficiency tests to staff.

Information available

26. *Explain what information evidence recovery and analytical staff access when working on a sample (e.g. description of sample type, crime scene, pictures of sample, Forensic Register number etc.). Outline where this information is contained and how it is accessed*

   a. I do not perform these tasks, and therefore rely on the relevant SOPs to indicate specifically what information staff access during the work they perform.

   b. The majority of samples are received in a tube, ready for processing. The checks the Evidence Recovery team perform for these samples is an "in-tube check" to ensure the information on the item matches with the information in the Forensic Register, the seal is intact, the image is correct in the Forensic Register, and the sample is suitable for processing on the automated instruments. Most screening tests are performed by the QPS prior to receipt at Forensic DNA Analysis and this information is visible to Forensic DNA Analysis staff on the Forensic Register. The information is contained within the Exhibit record in the FR.

   c. Evidence Recovery staff will also assess the Exhibit Record for any presumptive screening test performed by the QPS, and any analytical advice check boxes ticked by the QPS that indicate presumptive screening tests for saliva, analysis for semen (microscopy) or dual analysis (with Forensic Chemistry) is required.

   d. Evidence Recovery scientists access further information for SAIKs, such as scanned medical notes from the examiner. These are loaded to the Forensic Register on receipt by FSS staff. If this information is not available, Evidence Recovery scientists will contact QPS to obtain the relevant information prior to examination to ensure the most appropriate testing is performed.

   e. The Analytical processing is driven by batch functionality (business rules within the FR), where the samples are allocated to an extraction worklist by the technique and method are selected at Evidence Recovery.

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f. Batches and worklists are grouped by function (i.e. extraction, quantification, STR amplification capillary electrophoresis etc) and method (for example, Differential Lyiss, QIAsymphony pre-Lysis, etc). At each batch completion, samples transition to the next processing step based on sample type, priority, process result and operator decision.

g. To perform these processes does not require the Analytical staff to assess the Exhibit testing page in the Forensic Register. Analytical staff will check for 'Analytical notes' within the Forensic Register entered by staff that may direct testing, for example '*Quant and hold*' which can be directed by the QPS on cold cases. These analytical notes are programmed to be visible from the batch screens they access through their normal processing.

27. *Explain what other information evidence recovery and analytical staff could access if they wished, and why they do not access it*

a. The same information is accessible to all Forensic DNA Analysis staff, however it depends on the process they are undertaking if they are required to look at certain information. This is defined in the SOPs.

b. For example, staff in the Analytical team undertaking an amplification process will have no need to access the Exhibit Testing page which contains presumptive screening information or photographs of an exhibit.

28. *Explain whether more detailed information about the sample would affect the way in which a sample is dealt with or processed by the evidence recovery or analytical teams*

a. Currently, if Evidence Recovery do not have the information they need to process a sample (such as SAIK notes), or a quality issue has been identified (for example an incorrect description) they will put the sample on hold and seek further information through a request / tasks process within the Forensic Register to the QPS. Once this is corrected, the sample will proceed.

b. The Analytical team process based on technique and method selected, so do not require access to further information to perform the analytical processing.

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c. Should changes to the way samples are processed in the Evidence Recovery and Analytical teams be made, and there was a requirement for additional information in order for these changes to be implemented, this would require changes to the Forensic Register. There may also be additional training required, depending on what information was requiring further assessment, and how that would direct the workflows.

PROJECT # 184

29. On 27 April 2017, I signed the proposed restart of Project #163, which was a project from 2015 proposed by Kylie Rika. This then became the new Project #184. Project #184 was driven primarily by Justin Howes. My understanding of the purpose of restarting the project was to look at the data to examine the benefit of testing for DNA within a certain quant range. My involvement was to be reviewing the project proposal and in turn any draft report or reports.

30. A draft report for Project #184 was prepared, by Justin Howes and Cathie Allen, and was circulated to the management team for their feedback on 30 November 2017. Feedback was required by Wednesday 20 December 2017.

31. The feedback for Project #184 went directly to Justin Howes. The usual process for projects was that feedback for a draft report was provided to the project team or at least the project manager on behalf of the team. In the case of Project #184, Justin Howes was the project manager.

32. I am now aware that the feedback for Project 184 was collated by Justin in a spreadsheet. Usually such a spreadsheet was saved in a folder which was accessible to all staff in Forensic DNA Analysis. I do not recall accessing this spreadsheet to view any other persons feedback regarding this project. This is not something I would generally do when I am not the author of the report. I don't believe I did so on this occasion.

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33. Sometimes, the feedback spreadsheet is provided to the management team as a reference point when further draft proposals or reports are circulated. This process was followed by some projects managers, though not usually where the feedback was minimal such as correcting typographical errors or formatting. Justin did not attach the feedback spreadsheet for Project #184 to his email of 8 January 2018, sending the second draft.

34. I was copied into an email from Allan McNevin to Justin Howes on 10 January 2018 which included Allan's feedback for the Project. This is the only feedback for Project #184 which I recall seeing or having any knowledge of at the time or that I have been able to find looking back at the records recently as having been provided to me. The feedback from Allan McNevin was in relation to version 2 of the Project Report and was supportive of the Project's recommendations.

35. At the time of the change in process which occurred as a result of the Options Paper that was presented to QPS in 2018, I do not believe I was aware of the feedback provided by Amanda Reeves and Kylie Rika to the draft reports for Project #184. Nor was I aware of any other staff members feedback, save for that of Allan McNevin as described above.

36. I agree that there is merit to testing at levels below .0088 ng/µL as there is a possibility that DNA profile information may be obtained below this level, which is supported by the statistics provided in the draft report. The question being raised in my understanding at the time was whether it should be automatically tested at low levels or only done at the request of QPS, depending on the particular matter and the importance in the investigation.

37. I have since looked at the spreadsheet that Justin Howes prepared, collating everyone's feedback. I cannot say whether the spreadsheet captured all of the feedback received by Justin, as I was only aware of Allan McNevin's feedback at the time.

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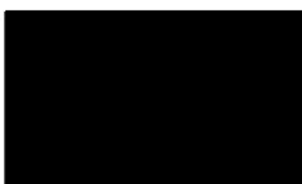
38. I provided written feedback to version 1 of the Project Report on 19 December 2017 (refer to **PB09** of my statement dated 21 September 2022). My feedback was as follows:

> *"I've reviewed and happy with the theory and recommendations.*
>
> *I asked Lisa to have a look in the FR training site to see how the process for P3 samples would work once they move to PP21. I will forward you the email summarising this.*
>
> *Once a decision is reached on the range for quant values, we will need to submit enhancements to VSTS and create/write manual procedures for P3 samples both through Analytical and reporting. These manual processes will be in place until the enhancements are in FR."*

39. As said, I was happy with the theory and recommendations that were included in the Project Report version 1. The remaining feedback I provided was in relation to the practicalities of how the samples would process through the Forensic Register, as well as the procedures and processes for the transition to PP21. I must have asked Lisa (our Forensic Register Subject Matter Expert in the Analytical team) to see how the change in process from Profiler Plus to PP21 would work using the Forensic Register training site. It appears from my wording, that a decision had not yet been made as to what the range would be for the quantification values that would differentiate what testing was to be conducted and in what circumstances.

40. In the feedback spreadsheet, there is an entry attributed to me on 9 January 2018. I do not have a recollection of providing this feedback to Justin. This particular entry does not appear to be a 'copy and paste' from an email like my feedback to version 1 and like many of the other feedback entries. I could not find any written feedback provided by email or otherwise by me. Normally, I would provide feedback in written form either by email, through track changes in the document, or handwritten on a printout.

.............

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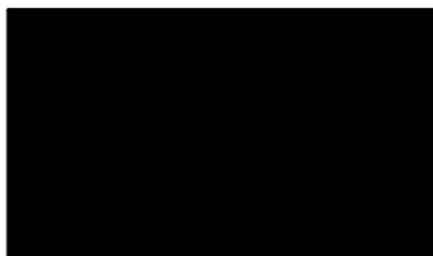...

41. It would be unusual for me to provide oral feedback to a project report. I do accept, however, that it is possible that I suggested to Justin that QPS should be the decision maker, as my view had been for some time that QPS had the ultimate say as to what progressed through testing. It was for Forensic DNA Analysis to make scientific decisions about testing processes but QPS had the choice about what was to progress through testing.

42. It was the case that Justin and I generally collaborated as Team Leaders and there certainly would have been opportunity for us to discuss the options being put to QPS for choosing.

43. Usually with projects and project reports, the subject is the implementation of a new laboratory instrument or process. Decision making about those matters is largely scientific in nature and so it is appropriate for the laboratory to decide the outcome. Here the subject matter of Project #184 and what became the Options Paper did involve data analysis of what was producing results that were of assistance, however, in the end a judgement needed to be made about the merits of what should be done.

44. All drafts of the Project #184 report concluded with a recommendation to "*Communicate the change in process to the QPS*". That did not sit with my understanding as what was the role of Forensic DNA Analysis and what was the role of QPS in making choices about progression through testing. The role of Forensic DNA Analysis was to provide QPS with the data and it was the role of QPS to make the choice.

45. From the email correspondence, I can see that version 2 of the Project Report was sent on 8 January 2022 at 4:47pm. As I left work at 4:16pm on that day, I would not have looked at Version 2 of the Project Report until I returned to work on 9 January 2018. I have searched through my emails and work calendar from 9 January 2018 and see that on that date I was in STRmix training which generally runs for between two to three hours. I did not send any emails on that day before 1.43pm, which was replying to an email received at 10.27am, suggesting to me that I had not been working on my computer much if at all that day before that time. I note that Justin's email asked for

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feedback for version 2 of the report before 1pm that day. I note that on a daily basis, I would receive anywhere up to approximately 50 emails per day.

46. I do not have a recollection of having read version 2 of the Project report. I may have, although it may have only been a cursory look. I say that because the email Justin sent enclosing the second draft of the report did not indicate that anyone had had major issues and described the nature of the changes that he had made. It is likely that if I looked at anything, it was only those areas of the report that he had indicated he had made changes to.

47. The less than 24-hour turn around that Justin was asking for was, in the practice of these things, consistent with there not having been any major changes made to the draft report as a result of feedback previously received. I would not have needed to read the second version either at all or carefully at least, to have had the state of mind that the choice should be offered to the QPS to decide how to proceed. Hence, even though I cannot recall doing so, I may have said to Justin Howes words to the effect that the QPS should be given the options.

48. On 12 January 2018, Justin Howes sent me an email from his personal email account asking me to forward to him the Project Report to convert to an Options Paper. I do not recall now why Justin Howes was at home that day, but he referred in the email to being "exhausted" and alluded to not getting any sleep the previous night (refer to **PB04** of my statement dated 21 September 2022). The entry in the leave calendar is that Justin was sick on this day.

49. Back in 2018, we did not have any remote access to the work desktop or external access to any work folders. We did not have the facilities to work from home, unless we used our own personal computers and sent documents to our own personal email address. Whilst we generally would not work from home, there were occasions where sometimes we could complete some work from our personal computers at home. There had been previous occasions when Justin (and other staff) would email from a personal email address if they were doing work from home on their personal computer.

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50. On 12 January 2018, I assumed (and likely understood) that Justin was working from home on his personal computer, which is why he emailed from his personal email account. I can see from the email correspondence that I forwarded the attachment from Justin's previous email to everyone. It doesn't look like I went into the general accessible folder to access the document (which is where the feedback was saved).

51. I do not recall any specific discussions with either Cathie Allen or Justin Howes about preparing the Options Paper. Back in 2018, I had regular meetings with both Cathie and Justin concerning lots of different issues such as management, staffing, daily running and functioning of the laboratory, recruitment and contracts. Cathie and I would have meetings together at least once a week. Justin, Cathie and I would also have meetings together as well, but not as often as my one-on-one meetings with Cathie. Justin and I would discuss things with each other on a daily basis as our offices are next door to each other.

52. Project #184 and the Options Paper wasn't as an important issue to me at the time, as it was to Justin Howes, which I think explains why I don't have a recollection of discussions surrounding it at the time. He was the author and the driver of the project. As I have said, I accept that there most likely was a discussion about preparing an Options Paper, however I do not have an independent recollection of that now.

53. Back in 2017 and 2018, Project # 184 was only one of many different projects which were running simultaneously within the laboratory. The Analytical team have the majority of these projects as they handle the scientific, hands-on, laboratory experiments. The February 2018 minutes reflect 15 projects which were running simultaneously in that period. I also note from email correspondence, I was also involved with the Forensic Services Commonwealth Games Committee which had planning activities on or around that time, as well as undertaking STRmix training, all of which added to busyness of my part-time working days.

54. In any event, I had no involvement at the time in drafting the Options Paper or the information contained within it. I accept that I would have known at the time I learned

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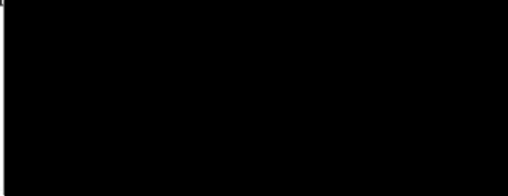

that the Options Paper had been presented to QPS and it had agreed to Option 2 that I, as one of the management team, had not signed off on a project report for Project #184. I do not now remember whether that occurred to me at that time, or if it did, what I had been told or what I thought was the reason for that. I do not recall whether the preparation of an Options Paper was in lieu of completing Project #184, or any discussions about not proceeding with Project #184.

55. On 19 January 2018, a draft Options Paper was emailed to me by Justin Howes (refer to **PB05** of my statement dated 21 September 2022). I could not have seen this email or the attachment until I returned to work on 22 January 2018, as I did not have external access to work emails at that time.

56. When I returned to work on 22 January 2018, I would have had to catch up on a large number of emails which were sent to me over the period whilst I was on leave. I am aware that on this date, a subsequent version of the Options Paper was emailed to me at 3:43pm. As this was the first day of school for my child, I had already left work on this day to do the school pick up.

57. I have no recollection of reviewing the Options Paper before it was presented to QPS, which I understand to have been on 30 January 2018. It is possible that I may have read it at the time, however it is equally possible that I had not read it then. It is possible that I may have simply assumed that the Options Paper contained similar information as the Project Report and that it presented the options for QPS. I did not reply to either of the emails of 19 and 22 January 2018 enclosing the then drafts.

58. I was not present at the meeting with QPS when Cathie Allen and Paul Csoban presented the Options Paper and I have no knowledge of what was discussed during that meeting.

59. After QPS made a decision on the Options Paper, Cathie Allen sent an email to Justin and I on 5 February 2018 advising of the decision by QPS, and asking whether there was any issue with circulating the Options Paper to the Management Team (refer to **PB08** of my statement dated 21 September 2022). I had no issues with providing the

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Options Paper to the Management Team because my view was they should know what had been done. They were already aware from the meeting on 1 February 2018 that it was being done. It drew from the draft report that had been sent to them previously. I did not know anyone had negative feedback about the draft report.

60. I did not know at that time that any of the management team had any difficulty with the draft report and so did not have any reason to think that the Options Paper would cause any concern. I neither remember nor is it recorded in the minutes of the meeting that anyone in the management team meeting on 1 February 2018 had an issue with an Options Paper being provided to QPS, drawing from the report.

61. I have been asked why I wrote "*It is QPS decision (so to speak)*" in my response to an email by Cathie Allen. I don't remember what I was thinking when sending that email however it was my view then as it still is now that while it involved laboratory processes it was a decision that needed to be made by QPS, which would explain why I said that

62. I accept that the Options Paper did not include the risks and benefits of all options, or convey the significant benefit of other data, apart from the percentage that might be uploaded to NCIDD. I did not draft the Options Paper and it does not appear that I was a formal reviewer of it. When and if I read it, I would have done so from the perspective of my team's responsibilities. It is hard to say when I cannot remember the circumstances in which I looked at the document, whenever that was, but in any case I may not have noticed that it emphasised the limited data about uploads to the NCIDD rather than the other data of successes.

63. In relation to the change that was brought about from the Options Paper, for the Evidence Recovery and Quality team specifically, it meant a reduction in micro-conning as a matter of routine for every sample. Whilst it is accepted that the micro-conning process is quite a manual process, staff had been undertaking this process as a matter of routine since 2013 and it was only a small part of their daily rostered tasks even as at January 2018.

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64. The change from Profiler Plus to PP21 for the testing of priority 3 samples became necessary because the Profiler Plus kit was being discontinued. In January 2018, we were coming close to exhausting our Profiler Plus kits, which meant that a switch to PP21 for priority 3 testing was imminent. Staff were, however, already using PP21 for testing priority 1 and 2 samples. This meant they were already trained in using PP21 and there were SOPs in place for that testing procedure.

65. The change to PP21 for testing priority 3 samples would only have had a small impact on the turn around time for my team, which would have been easily absorbed as by processing all samples in the same profiling kit, processes became more streamlined. It would have resulted in a slightly longer time to do a quality check (i.e. a capillary electrophoresis check) and plate reading on the DNA profiles before being released for interpretation. The latter, however, is a task undertaken by both teams and so did not only impact on my team.

66. The change would have had a greater impact on the Forensic Reporting and Intelligence Team (under Justin Howes), where the DNA profile interpretation process occurs. There was a greater backlog of work within that team at the time and this change would have made for more efficiencies in the team and assisted with reducing their turn around time.

67. The change to PP21 testing for priority 3 samples occurred around the end of January 2018 (when the Profiler Plus kits were exhausted). The management of this change within ERQ would have been to update the workflows and SOPs and request changes to the Forensic Register (as per my feedback to the Project #184 report version 1).

68. In November 2018, after the changes had been implemented, Inspector Neville raised an issue with Priority 1 samples not being micro-conned. I understood that this was brought to Cathie's attention via an FYI email to me. My understanding was that the outcome of these discussions was to automatically micro-con Priority 1 samples and provide additional wording to QPS for results within that range.

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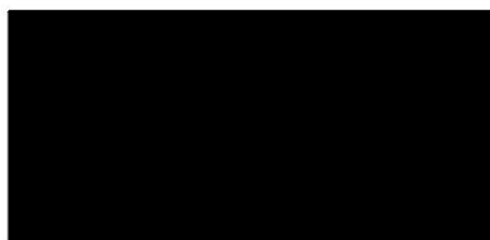

69. The change for the Analytical team (as an outcome of these discussions between Cathie and QPS) was for Priority 1 samples to be automatically micro-conned. This was a process change that was implemented quickly and easily. The wording changes were done by Justin Howes, with the reporting senior scientists. The decision of whether to micro-con priority 2 and 3 samples could be requested by FSS DNA staff when interpreting results, or requested by the individual investigating officer (refer to **PB76** of my statement dated 21 September 2022).

THE SHANDEE BLACKBURN CASE

70. The case file for the Blackburn murder has two OQIs printed on the file, reported as 34043 Positive Extraction Controls with low DNA yields, identified on 22 March 2013, and 34817 Incorrect conditions used for Capillary Electrophoresis, identified on 8 July 2013. Whilst these documents have my name mentioned as the approver, I was not in fact the approver. I was on maternity leave at the time and Amanda Reeves was acting in my position. Quality Information System (QIS) Records indicate that Amanda Reeves was the approver of both of these OQIs; see exhibit **PB130** attached to this statement.

71. In February 2022, I received a request from Cathie Allen to volume check a number of samples relating to the Blackburn case (Operation Zimzala). I allocated this task to Luke Ryan and Sharon Johnstone to complete.

THE UPDATE PAPER

72. The Update Paper was authored by Justin Howes and Cathie Allen. To my recollection, the first mention in relation to providing an Update Paper, was a request by Cathie Allen to extract data from BDNA. I cannot recall now what the specific trigger was behind Cathie's request for the data extraction at that point. I may or may not have been privy to the specific reasoning or purpose for the request at the time.

73. I have searched through some of my work documents to find the catalyst for the request for the data extraction by Cathie. I did find that on 11 November 2021, a

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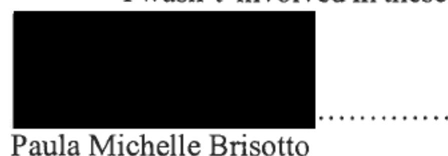
Forensic DNA Analysis Management Team Operational Focus Meeting took place. I was present for this meeting with Justin Howes (acting Managing Scientist at the time and Chair of the meeting), Sharon Johnstone, Allison Lloyd, Adrian Pippia, Kylie Rika, Luke Ryan and Kirsten Scott. Towards the end of this meeting, Kylie Rika started discussion under the agenda item 'Other Business" about the DIFP process.

74. From the minutes of this meeting, there appears to have been a brief discussion about the DIFP process. The minutes from this part of the meeting are as follows:

> ***"DNA Insufficient for Processing (DIFP) process***
> *KDR collecting samples where better results obtained after case manager requested concentration, including profiles for NCIDD. General discussion ensued that this possibility was communicated and accepted by QPS, and that they could request processing any time and that the case manager may rework if case circumstances indicate worthwhile. Value for DIFP determined from PCR (PP21 validation); values may be different with VFP which is more sensitive.*
>
> *Suggestion from LBR that may be worthwhile if moving to VFP that we profile above this value and then after collecting enough data (eg. last data was a year of data), review the findings to see if a threshold could be determined.*
>
> *KDS mentioned if collecting data, need to balance with the number that do not eventuate with profiles (as many get requested by QPS monthly for reactivation)."*

75. There were no actions as a result of this discussion. Whilst, I do not have an independent recollection of this discussion now, I also don't recall there being any contentious discussions arising from this meeting. I do not recall contributing to the discussion.

76. Around 16 and 17 December 2021, I was sent two emails from Cathie Allen which were sent to me as an 'FYI' concerning Operation Amunet. Cathie had been discussing a number of issues surrounding Operation Amunet with Inspector Neville. I wasn't involved in these discussions with Cathie Allen or the QPS, beyond receiving

............

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a forwarded 'FYI' email. There was nothing for me to respond to or action at that time.

77. These are the only email discussions I could find which occurred in the lead up to the data extraction request at the beginning of 2022.

78. On 16 February 2022 at 4:09pm, Justin Howes sent an email to myself and Cathie Allen about retrieving data from BDNA (refer to **PB11** of my statement dated 21 September 2022). I do not have a great recollection of what prompted that email about gathering data. I have, however, searched my work calendar from that date and found that at 9:30am on 16 February 2022, there was a meeting held between Cathie Allen, Peter Culshaw, Justin Howes and myself. The request for a data extraction may have followed that meeting. On 18 February 2022 Cathie informed Justin and I that she had sent a quote to BDNA to request that data.

79. I have a recollection that around that time, Cathie Allen had asked me to create a timeline of how we had changed a number of our operations and procedures, including audits and projects, since 2009. It may be that at that same time Justin Howes was tasked with providing parameters for the data extraction from BDNA. I do not hold any records of this however.

80. On 25 February 2022, I received an email from Cathie Allen to Justin and myself, wanting to discuss an email from Inspector Neville about the testing thresholds. Inspector Neville's view, from the email sent to Cathie, was that the testing threshold should go to 0.006 ng/µL (refer to **PB13** of my statement dated 21 September 2022).

81. My recollection of this subsequent meeting was that Cathie Allen wanted Justin Howes and I to discuss the ideas put forward by Inspector Neville about lowering the threshold value. It is likely we agreed that we should not change the threshold value without first considering and assessing the data that had already been requested from BDNA. This is consistent with Cathie Allen's response to Inspector Neville which was sent by email on 3 or 4 March 2022.

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82. On 3 March 2022, Kylie Rika sent an email to me proposing to compile a list for case managers to consider further testing options of low quant samples. I responded to Kylie on the same day advising that a data grab had been requested from the Forensic Register and that we would use that information to determine the next steps moving forward. Such was consistent with my understanding. See exhibit **PB131** attached to this statement.

83. On 4 March 2022, Cathie Allen received the data from BDNA and forwarded this data to Justin and myself. On that same date, Justin Howes replied that he would get started, presumably on the assessment of the data.

84. On 15 March 2022, Cathie Allen sent me an email stating that she would be drafting the Update Paper with Justin Howes. I had no involvement in drafting the update paper. My only involvement was to review the Update Paper.

85. Two separate papers were prepared. One was the Update Paper prepared by Justin, and the second was the Executive Briefing drafted by Cathie Allen. My understanding was that the Update Paper was not sent to QPS, only the Executive Briefing. I was not involved in the provision of the Executive Briefing to QPS.

86. Version 1 of the Update Paper was in its draft stage and had not yet undergone a technical review. The technical review is when all the data in a report is double checked by a second person. This usually occurs before a report goes to the Management Team for review.

87. I understood that Lara Keller directed that the Update Paper was not to progress any further at that stage. Cathie Allen informed us of Lara Keller's decision in an email in early April 2022.

88. On 11 May 2022, Kylie Rika sent an email to me asking to let the Management Team know that data was requested from the Forensic Register and that Lara Keller did not want work to progress further at that point. I responded to Kylie Rika on the same day to advise that I was happy for the Management Team to be advised of the Forensic

Register data request. I said that the DIFP process would be assessed as part of the DNA review and it was reasonable to wait to see what those recommendations were, to ensure any data interpretation is appropriate. I suggested that these issues be mentioned at the Management Meeting the next day. See exhibit **PB132** attached to this statement.

89. On 12 May 2022, during a regularly scheduled Management Team meeting, the information was provided that data had been requested and received from BDNA, however was not progressing as per Executive Director advice pending the outcome of the DNA Review. At this stage, as far as I was aware, the Management Team were not aware of the draft Update Report as this had been put on hold since early April. I do not recall any questions or comments being made during the meeting.

90. On 19 May 2022, I recall there was a MS Teams meeting held between QPS and FSS, which was a bi-monthly meeting attended by Cathie Allen and Lara Keller. I was in attendance as a guest after undertaking a short period in the Managing Scientist position. I did not regularly attend these meetings. During this meeting, the success rates and threshold levels were mentioned as an agenda item. To the best of my recollection, there was nothing else discussed on this topic beyond what is reflected in the minutes for the meeting (refer to **PB20** of my statement dated 21 September 2022).

91. On 2 June 2022, I sent an email to Cathie Allen with some of the information I had found on the microconning changes to workflow and SOPs since 2012. I believe this was in response to an earlier request from Cathie seeking this information.

92. On 3 June 2022, I was sent an 'FYI' email from Cathie Allen advising that Lara Keller wanted the final version of the Executive Briefing to be sent to QPS. That's when progress continued again on the Update Report and the Executive Briefing. A technical review was then undertaken by Allan McNevin. Feedback from Justin and I was requested in relation to version 2 of the Executive Briefing on 9 June 2022 (refer to **PB19** of my statement dated 21 September 2022).

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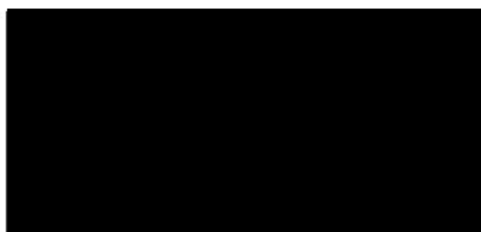
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93. I provided feedback to Cathie in relation to version 2 of the Executive Briefing. On 20th June 2022, I received an email from Cathie advising that she had updated the Executive Briefing to take into account most feedback. There were changes between version 2 from the final version which was provided to QPS (for example the 'Next Steps' paragraph at the end). I did not review the final version of the Executive Briefing before it was provided to QPS.

94. I understand that the Executive Briefing was provided to QPS by Lara Keller on 24 June 2022. My view is that the Executive Briefing provided to QPS did not place undue emphasis on NCIDD as opposed to comparisons of individual reference samples. It seems to be providing initial data and considerations to commence discussions with QPS, which is directly listed in the next steps in the Executive Briefing.

CHANGES MADE ON 6 JUNE 2022

95. On 6 June 2022, the Premier announced a decision that changed the process for testing samples within the DIFP range. Samples within the DIFP range were no longer to be reported as DIFP, but were to be processed straight to amplification. This meant that they were not first microconcentrated before amplification.

96. My view is that it was a direction we were required to follow. I recall my opinion at the time, or shortly after, being that there were pros and cons to the process selected. The cons being samples were not concentrated prior to amplification, and further reworking may be required with some of the DNA extract consumed during the first amplification. The pros being that direct to amplification allowed the reporting scientist to assess the DNA profile obtained and determine, based on the actual DNA profile, the best rework strategy for that sample (which is more limited if basing it on the quantitation value alone). I also believed that, while this was a direction we were required to follow, it provided the opportunity to collect data for samples that went direct to amplification within that quantitation range, so an assessment could be made as to suitable reworking strategies for future workflows.

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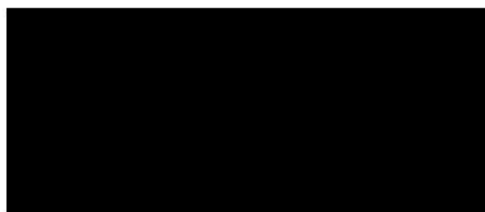....

97. I was not involved in the consultation that occurred between Lara Keller and Shaun Drummond which lead to this decision. There was no consultation between myself and Lara Keller. I understand that Lara Keller may have consulted with Cathie Allen.

98. I recall that on 2 June 2022, I sent an email to Cathie Allen with information I had found on the micro-conning changes to workflow and SOPs since 2012. I believe this was in response to an earlier request from Cathie seeking this information.

99. On 6 June 2022 there was a leadership meeting held between 11:30am – 12:30am with Cathie Allen, myself, Justin Howes and Peter Culshaw. This was one of our regular leadership meetings which was scheduled in advance. I do not have any notes from this meeting but I believe it would have been a general catch up.

100. I recall there was a later meeting held via MS Teams on 6 June 2022 between Lara Keller and the whole of the Forensic DNA Analysis Team. During this meeting any comments or questions were addressed by Lara Keller (refer to **PB31** of my statement dated 21 September 2022). There were also emails that day where staff were sending around the news articles and other media announcements.

101. On 7 June 2022, there were a number of emails sent between Cathie, Justin and I about the standard operating procedures ("SOPs"). Justin sent an email on 7 June 2022 advising of the following:

> *"Hi, this is against the PDA SOP and will add the same to CM and Release of Results:*
> *Workflow arrangements for samples as of 6 June, 2022:*
> *- samples will not have DIFP added to results in the quant range 0.001-0.0088ng/uL. These will be amplified after Quant. This applies to P2 and P3 samples.*
> *- case managers can assess samples for rework which could include a microcon after the first amplification. This does not apply to P3 samples which are processed without rework as per standard workflow arrangements.*

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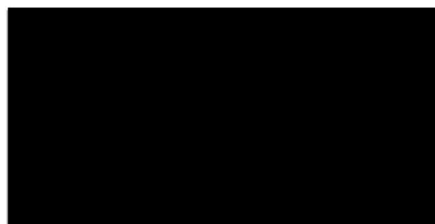
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- samples currently reported as DIFP that are requested to be restarted by QPS will undergo a microcon procedure.
- no change to the P1 workflow where samples in the quant range 0.001-0.0088ng/uL will undergo a microcon prior to amplification.

I think that captures what we will be doing.
Justin"

102. I understand that a Management Team meeting was held on 16 June 2022, however I was not present for this meeting and the minutes do not show the discussion which took place in my absence. On the afternoon of 15 June 2022, I tested positive for COVID-19 and so left work from that point. I didn't return to work until 23rd June 2022, however was doing some work from home during the latter part of this period.

103. In August 2022 there were some discussions held about the data (initially between Kylie Rika and Justin Howes, and then with the leadership team). As a result of these discussions, Cathie Allen spoke to Lara Keller, who advised that the Executive Briefing could be provided to the Management Team. On 28 September 2022, Helen Gregg sent the Executive Briefing to the Management Team, advising Lara Keller had provided the report to Superintendent McNab previously, and that it was on hold pending the outcome of the Commission of Inquiry.

CHANGES MADE ON 19 AUGUST 2022

104. On 19 August 2022, a directive from the DG was issued, advising that the Microcon concentration process was to recommence for certain samples. The directive was contained in a memorandum from the Acting Director General Dr David Rosengren as follows:

"All priority 1 and priority 2 samples with a quantitation result between 0.001 ng/uL (LOD) and 0.0088ng/uL, should be concentrated down to a volume of 35uL and undergo one amplification process.

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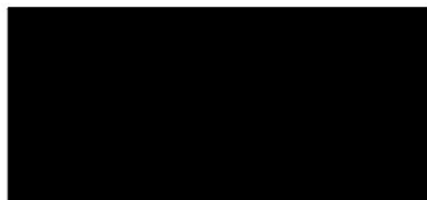
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If further amplification is considered beneficial, and if this process will exhaust the remaining sample volume, then written approval must be obtained from the Queensland Police Service (QPS) prior to that process being initiated."

105. At 10.51am on that date, prior to the Directive, Justin and I received an email from Cathie with the subject line 'Peer review please' which requested that I review her email below. The email was said to include parameters from the spreadsheet provided by BDNA for data extract for the follow up report. I don't recall looking at this when I received it.

106. I believe I may have received a telephone call from someone, possibly either Helen Gregg or Alison Slade, asking me to attend an urgent meeting. Shortly after, at around 11.22am, I received a MS Teams meeting invitation from Megan Fairweather to attend a discussion on Microcon between 11:30 – 12:00pm with Cathie, Justin, Helen and Megan Fairweather.

107. At 11.23am, Justin, Cathie and I received an email from Helen Gregg attaching an updated memorandum from the DG. Helen did not provide any instructions in the email. I had not seen this document before that point, and (refer to **PB41** of my statement dated 21 September 2022) without the information in the memo, I would not have known what Megan was talking about regarding consumption of samples.

108. At 11.30am, I attended the MS Teams meeting with Helen, Megan, Cathie and Justin. During this meeting, I recall some oral information being provided by Megan along the lines of QPS requesting to preserve samples for future testing, or something to that effect. I do not recall Megan telling me who this request had come from; my impression was formed that it was not for us to know, it was just QPS.

109. Megan led the discussion. The focus of the discussion was to seek advice from Cathie, myself and Justin about the process of preserving samples, as requested by QPS and complying with the memorandum. We all viewed the memorandum as a direction. I understood the memorandum was not contrary to QPS request. It discussed the prospect of reverting back to the 2018 procedure prior to the Options Paper – auto-

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microcon concentration of samples to 35mL. That was the standard operating process in place at the time.

110. There was further discussion about the additional amplification process and leaving enough sample behind for external testing. My understanding was that QPS had provided feedback on the memorandum, that their preference was to not consume all of the sample. Everyone was involved in this discussion about sample consumption. A second amplification would consume the sample and it was discussed that we needed to determine what the minimum volume required to retain for QPS was.

111. I don't recall anyone asking for options, however I do recall there was a short timeframe for providing a response, particularly considering the meeting was titled as 'urgent' and Helen Gregg followed up fairly quickly asking for our thoughts. The action required of me, and Justin, was to find out how much of the sample we would need to preserve for testing at another laboratory. This was essentially in relation to circumstances where we do external transfers of testing.

112. I would expect Justin to have more knowledge about these matters because i) his team orders the reworks, ii) his team and Justin are involved in any discussions/contact with QPS in relation to external testing and iii) Justin is a member of the Biology Specialist Advisory Group (BSAG) (members are heads of laboratories across different jurisdictions). Justin inputs into a spreadsheet which lists data on processing and/or any other information provided by and shared with other jurisdictions.

113. At 11:58am, I received an email from Helen attaching a second amplification document (refer to **PB43 and PB44** of my statement dated 21 September 2022) and requesting my thoughts. There were further emails exchanged between Justin, Cathie, , Helen, Megan and I about the BSAG spreadsheet and volume required to be retained for QPS (refer to **PB46** of my statement dated 21 September 2022).

114. At 12:03pm, Cathie sent an email to Megan, Justin, Helen and me as follows:

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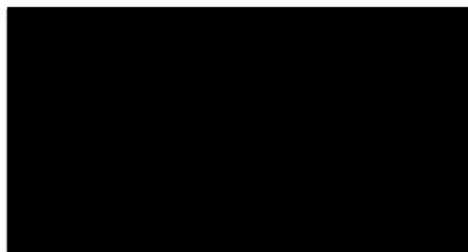

"Hi Megan

They can opt to –

- *do nothing, review other samples in the case, see if other items are available for testing, ask for other samples to be concentrated & wait for new technology*
- *authorise second amp and accept the risk (which would be documented)*
- *see what other technologies are available to them and undertake that at a financial cost to them*

Cheers

Cathie"

115. At 12:03pm, Justin sent an email to Megan, Helen, Cathie and me as follows:

"Hi, the consultation was mentioned to be after the auto-mic and amp, which doesn't leave enough volume for QPS to look into other labs except for Y-chromosome testing (YFP in spreadsheet) where only two labs are potentials.
Justin"

116. There were a number of emails exchanged between the group that afternoon which are referred to in exhibits **PB43, PB48, PB49, PB51, PB52** and **PB53** of my statement dated 21 September 2022. After options were provided, a video call via MS Teams was held with Helen which only lasted for 10 or 11 minutes.

117. I recall Helen advising that a DG Direction had been provided and we were to adhere to the DG Directive to concentrate the samples according to the pre-2018 procedure as per the memorandum. It was further decided that advice needed to be sought from ESR. The response from ESR gave the volume required for their testing, and Helen asked if the volume remaining after micrcon and first amplification was sufficient, which I believe we all agreed seemed to be suitable. The memorandum was sent to all staff after 3pm, and I then followed up with an email to the Analytical team with workflow instructions.

118. *Explain the effects on the Analytical Team, if any, of the change of process on 6 June 2022, whereby samples with a quantification value between 0.001uL/ng and*

0.0088µL/ng were to be amplified, analysed, and profiled without initial concentration

a. Immediately after the change of 6 June 2022, the Analytical team would manually change the "*technique*" on the quant transition page of the Forensic Register to STR amplification in order to progress the sample to amplification.

b. A Forensic Register enhancement (change) was requested, and shortly after the Forensic Register changes were in place, all samples above 0.001ng/µL would progress to amplification in PP21. The Analytical team were no longer validating '*DIFP*' results and had ceased doing so for any sample processed after 6 June 2022.

c. This change meant a slight increase in the number of amplifications performed per week.

d. On review of the records, I understand that there were about 100 samples per week in 2021 recorded as '*DIFP*'. This would equate to approximately one and a half amplification batches over a week, which is not a significant increase for analytical batch processing, where up to 90 samples can be amplified per batch.

e. While this would have had a slight flow on effect to the task of interpreting DNA profiles using the GeneMapper ID-X software, this would have only equated to one and a half batches to read over a week, however as outlined in paragraph 65, this is a task shared across the Analytical , Evidence Recovery and Reporting Teams.

119. *Explain the effects on the Analytical Team, if any, of the change in process on 19 August 2022, whereby Priority 1 and Priority 2 samples with a quantification value between 0.001µL/ng and 0.0088µL/ng were to be concentrated to a volume of 35µL and amplified once. Explain any concerns you had with this change*

a. Priority 1 samples within the '*DIFP*' range have been concentrated since 2018

b. On review of the records, I understand that the approximate number of samples micro-conned since August 2022 (around 7 weeks' worth) is 100. This would include samples within the '*DIFP*' range, and also samples retrospectively

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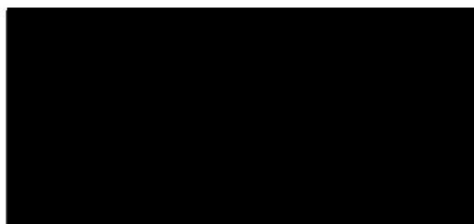


requested for microcon after 19 August 2022 and as per the memorandum from the A/DG..

c. I believe that this means that from 19 August 2022 onwards, and including the retrospective microcon samples also requested, the Analytical team would have been processing approximately 9 batches of microcons per week.

d. This would have been suitably managed by the Analytical team with no additional resourcing required after 19 August 2022. Ergonomic considerations would have been factored into the rostering, so Analytical staff would perform at most one microcon batch per week.

120. *Explain any concerns you have with these changes*

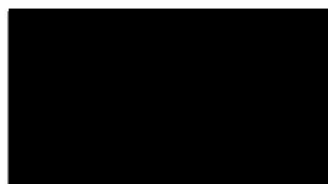
a. I have no personal concerns with the decision made on 19 August 2022.

b. Operationally, my concern at the time was to ensure Forensic Register functionality was in place for the changes so that staff did not have to manually select samples for different processing based on the quantification value, as this would introduce error.

c. Ergonomically, my concern was to ensure staff were able to manage the retrospective microconning required. This was discussed with some Analytical staff, and suitably managed with rostering of tasks.

121. On 7 September 2022, Kylie Rika sent an email to Lara Keller, Justin Howes, Cathie Allen and me, requesting to see the data analysis/outcomes of the 4 years' worth of DIFP data obtained from BDNA. Cathie then included me and Justin in a response to Lara asking whether staff could be provided with the follow-up report.

122. Lara Keller advised on 15 September 2022 that this could be provided to staff. I then asked Lara Keller whether staff could be provided with the Executive Briefing or the full Update Report, the latter which was unreviewed. Lara responded with the email and document she provided to the QPS, which was the Executive Briefing. See exhibit **PB133** attached to this statement.



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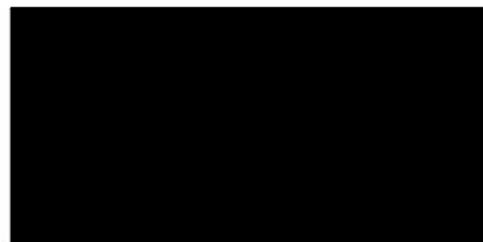
Paula Michelle Brisotto



123. On 28 September 2022, Helen Gregg sent an email to the Management Team attaching the Assessment of Low Quantification DNA Samples (referred above as the Executive Briefing)that had been provided to QPS, advising the paper was for information only, and is on hold pending the outcomes of the Commission of Inquiry. See exhibit **PB134** attached to this statement.

Data Analysis of Modified Sexual Assault Process for Zero Spermatazoa Detected at Evidence Recovery

124. In May 2017, I undertook a data assessment and drafted a report titled "Data Analysis of modified sexual assault process for zero spermatozoa detected at Evidence Recovery". This report was simply an analysis of data for 738 samples, to assess the difference in the pre and post August 2016 modified process for zero spermatozoa detected at Evidence Recovery. The purpose of the data analysis was to determine what, if any, impact this may have had on the DNA results report for the case. The report did not contain any recommendations that required endorsement or approval as it was not a change management process. It was simply an analysis of data in relation to 738 samples.

125. On 30 May 2017 I sent my draft report to Kylie Rika, Luke Ryan and Matthew Hunt for feedback. On 9 June 2017, Kylie's feedback was sent to me by email, attaching a track changes version of the draft report. Kylie's email to me was as follows (see exhibit **PB135** attached to this statement):

> *"Thanks Paula.*
> *I think the report is fine. I have added some more feedback in purple. For the purposes of this data analysis – and its scope, the report is fine. I am still curious as to why we are having a small set of samples where we are seeing 0sp to 2+sp. This difference is too big (even though it only relates to a small number of samples). Perhaps we need something in the report to highlight this and what we seek to do to investigate??*
> *Nice work Paula* 😊

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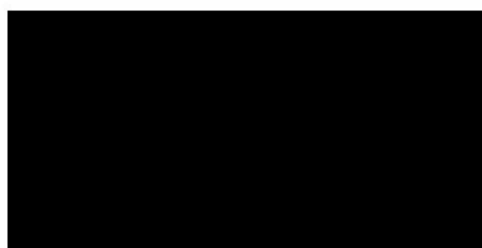
Paula Michelle Brisotto



Thanks

Kylie Rika"

126. My view of Kylie's feedback was that she was accepting of the report, and in agreement that the data analysis and report was in scope. Her additional comment in the email referred to the small subset of samples with a difference in the observation of spermatozoa on the microscopy slide. While she refers to mentioning in the report about highlighting this and what we seek to investigate, within the tracked changes, she confirmed Project #181 was looking into possible causes of the differences. I took this to mean she agreed the focus of this data assessment was not to perform an investigation, rather this was the focus of Project #181.

127. In relation to the data analysis for sexual assault samples, the feedback from Matthew, in my view, was also in support of the report. A particular comment is below:

"In many instances we have found that this issue is mitigated by the common practice of submitting multiple swabs within a typical SAIK, thus increasing the chances of detecting semen. The fact that this data analysis has found that the methods in use prior to August 2016 would have had in only a relatively limited impact on the particular reported results for these SAIKS should be reassuring, however we should continue to strive to eliminate impacts of this type for all cases, and seek to improve the sensitivity of our methods, including by selecting the most effective point in the process to conduct microscopy. …. "

128. The draft report went through two rounds of feedback and a number of amendments were made. I sent the draft report and the feedback to Justin Howes on 26 May 2017, however I cannot locate now, or recall, whether any feedback was provided from him. At some point, I had a meeting with Cathie Allen to discuss the draft report and the feedback received. On 15 August 2017, I sent an email to Justin Howes again requesting his feedback. My email to Justin Howes was as follows (see exhibit **PB136** attached to this statement):

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Paula Michelle Brisotto

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"Hi Justin,

I've had a meeting with Cathie about the feedback received and where to from here.

We are on the second round of feedback, and both Matt, Kylie and Luke have provided theirs. From here, Cathie has requested your involvement, so we can try and take on board some feedback, while trying to keep the data analysis within scope. I am hoping from your experience with sexual assault examination and interpretations, you can provide some wording within the document, so we can all get to a point where we are happy with the content, the assessment and the summary. I think I am too close/getting fatigued with this, and I would like a fresh set of eyes/approach to looking at this report.

Please find attached:

1 – Kylie's feedback

2 – Matt's feedback

3 – my updates from Matt's feedback.

Unfortunately, I didn't get to spend much time doing this today. If you are able to have a look over these documents, and provide wording suggestions/improvements or alternative words, please have at it.

I have kept in 'systemic failure', as I still feel that this was the concern on my return, and is an evaluation of the data – similar to what we did with the MPII investigation, with the outcome not showing a systemic failure of the instrument.

I am also not sure if the scope is clear, and if the assessment of the case as a whole (e.g. submit any NFA samples or read diff slides if DNA profile indicates male in sperm fraction etc) is clear enough.....

Many many thanks,

Paula"

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Paula Michelle Brisotto

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129. At the time of drafting this report, Project #181 was already in progress (initiated in May 2016 whilst I was on maternity leave). This data assessment intended to perform data analysis on samples submitted using a modified workflow (implemented in August 2016) whereby samples which had zero spermatozoa on evidence recovery generated microscopy slides would still be submitted for DNA extraction (and a subsequent microscopy slide prepared during the DNA extraction). Specifically, this assessment would compare the results of the microscopy slides generated within evidence recovery and from the DNA extraction.

130. The data assessment overlapped with the ongoing work of Project #181. During this time, the Project #181 expanded in terms of scope and scale of the investigation, and therefore I considered that Project #181 (which included project team members from both evidence recovery and reporting teams) would be the most appropriate body of work to continue to assess the relevant workflows and make recommendations to the management Team based on experiments and results. This was particularly relevant given the direction of Project #181 indicated it was unlikely to return to the workflow which this report was analysing, therefore any conclusions or assessments made would have limited usefulness.

131. It also appears that in November 2017, I attempted to create a Summary and Timeline document for the data assessment. In January 2018, it appears I started drafting a simplified version of the data analysis report. Both documents are incomplete and labelled 'draft'.

132. On 3 July 2020, Kylie Rika sent an email to Allan McNevin, Chelsea Savage, Matthew Hunt and Emma Caunt, and copied in myself. Kylie's email was in relation to feedback for the Project #181 report and suggested that the body of work from my draft data report be included in Project #181. I responded that the data assessment was not part of Project #181 and so I preferred for it to remain separate as it had not been completed. I told Kylie that if the report were to proceed to completion, it would be a standalone document. Kylie replied to this email to say "no worries".

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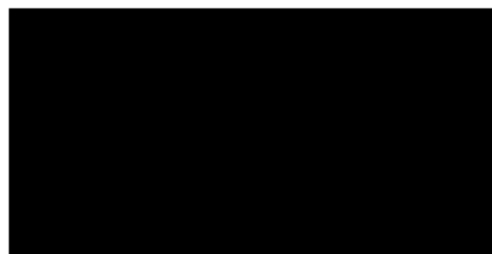

133. Project #181 was then approved and endorsed by the Management in August 2020. After the completion of Project #181 was completed, the project's recommendations were implemented, which resulted in a change in the procedures relating to testing for seminal fluid and spermatozoa testing. After this change in procedure following the implementation of Project #181, there was no real outcome to be achieved by progressing any further with the 2017 draft report.

THE VALIDATION AND IMPLEMENTATION OF 3500

134. Emma Caunt's evidence is that in 2018, following the validation of the 3500s, the peak heights were larger and there were issues with the pull-up which affected interpretation. Emma alleges that she raised this issue with me at the time and examples were provided to me concerning this issue. I have no recollection of this issue being raised with me alone. I have searched through my emails and cannot find any email correspondence from Emma, providing me with examples surrounding this issue. As I do not know what examples were provided to me, I am unable to comment on this now.

135. In 2018, the 3500's were still being validated. Emma Caunt was a project officer for the projects relating to the assessment of casework PP21 samples on the 3500, and in that capacity, was involved in feedback during the course of the assessment. If there were pull-up issues in 2018, it would have been before the implementation of the 3500 instrument in February 2021. There were a number of projects undertaken on 3500 for casework samples, all bought together in a report by Sharon Johnstone, signed by the Management Team in late 2019. I do not recall anything specifically raised to me, as I believe all of management team, including the project staff, were looking at any issues raised as part of the project.

136. The 3500 for PP21 casework samples was implemented in February 2021. I am unable to locate any correspondence from Emma concerning issues with pull-up post implementation of PP21. I have no recollection of Emma bringing an issue concerning the pull-up to my attention, post implementation in 2021.

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Paula Michelle Brisotto

137. Generally, if someone asks about an increase in pull-up, or some other issue relating to the analytical instruments or processing, it is referred to the Senior Scientist managing the Analytical Team, as they oversee those processes. Part of the CE Quality check role within the Analytical Team is to assess artifacts during the capillary electrophoresis process, so if increased pull-up is observed, they will assess this and may do a spectral calibration, change the capillary, or look at the reagents.

138. I cannot recall now being made aware of specific issues surrounding an increase in pull-up above what was observed during the project verification and on implementation of PP21. I have since been advised by the Analytical Team staff that since the implementation of the 3500's, they have increased how often they do spectral calibrations in response to pull-up observed. What I have been advised is that spectral calibrations used to be done once a month on the previous capillary electrophoresis instrument, and they are now performed weekly on the 3500 instruments.

139. I am aware of pull-up and other interpretational issues were raised in a Profile Interpretation Meeting held with reporting staff and case managers, of which the reporting senior scientists managed and addressed actions. I do not believe a meeting has been held for over 12 months. I was also aware of an initial request for a project submitted by Thomas Nurthen and Adrian Pippia in June this year where they were requesting to assess the performance of an Analytical threshold for PowerPlex 21 samples, in response to "*consistent with the observations in Project #186, consistent high level pull up regularly observed in casework PP21 samples*". The request was not directed to me; however I was included as a CC in an email when follow-up on a decision from the Reporting managers was being sought. From this email correspondence, it appears the decision from the reporting managers was to hold this project at this time.

QIASYMPHONY (PROJECT #192)

140. Project Report #192, related to the Validation of QIAsymphony SP for Bone Extraction. This Project received a lot of feedback from line managers at the time which was addressed and dealt with in the report. This report was endorsed by the

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Management Team in early April 2018 and approved by Cathie Allen on 10 April 2018.

141. Rhys Parry's evidence is that he raised issues with me around the time, concerning the validation and experimental design. I have no recollection now of conversations with Rhys Parry around this back then, however from email communication to Helen Gregg in April 2018, it appears I was seeking advice on an appropriate number of samples for this experiment, which may have been a result of a discussion with Rhys.

142. On 30 April 2018, Rhys Parry sent an email to me attaching a Project Proposal #192 (Supplemental) titled, Comparison of Organic (phenyl-chloroform) and QIAsymphony SP Bone Extraction Methods. Rhys Parry was the author of this project proposal. I forwarded Rhys' Project Proposal to Justin Howes on 1 May 2018. I cannot recall exactly why I forwarded this, however as I have no communication or recollection of requesting this of Rhys, it may be that Justin was following up on this, hence why it was forwarded.

143. During 2018, there were various discussions with Helen Gregg, Justin Howes, Luke Ryan, Kirsten Scott and myself about the question of repeatability and reproducibility. In September 2018, Justin Howes also sought advice from Dr Kaye Ballantyne, a Senior Research & Development Officer within the Office of the Chief Forensic Scientist for the Victoria Police, on how to best statistically compare data in repeatability/reproducibility/sensitivity etc. experiments.

144. In around April or May 2018, the PP21 Suppression issue first arose. This resulted in the eventual development of Project #201. The PP21 Suppression was a significant issue within the laboratory at the time and took priority over other projects. The issue was, essentially, a problem with the buffer which had resulted from a change to PP21 by the manufacturer. We had not been notified of the buffer change by the manufacturer, and this problem was first identified by the DNA profiles appearing suppressed at some loci, resulting in interpretational issues. During the course of assessing the issue, processing was ceased on the QIAsymphony instruments while the investigation was underway. An adverse event investigation was launched as a

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Paula Michelle Brisotto

result, and an OQI was created in June to record the investigation of the PP21 Suppression issue.

145. Once the root cause of the issue was identified as a buffer change, Project #201 was initiated in September 2018 to verify the new buffer. This investigation and subsequent project was a lengthy process which was not finalised until January 2019. It involved significant testing and experimentations to identify the cause of the issue, which was not known to us at the time to be a result of a manufacturing change.

146. The QIAsymphony instruments could not be used until the PP21 Suppression issue was resolved. As such, supplementary testing for Project #192 (which was utilising the QIAsymphony instruments) could not progress any further until the PP21 Suppression issue was rectified. The Minor Change Register records that the reimplementation of QIAsymphony instruments occurred on 4 February 2019.

147. Following the reimplementation of QIAsymphony, in April 2019, a Project Proposal for further Repeatability and Reproducibility testing on Project #192, was put forward by Luke Ryan. This proposal was approved by Cathie Allen on 5 April 2019.

148. On 23 March 2020, Project Report #192 Validation of QIAsymphony SP for Bone Extraction, Supplementary Repeatability and Reproducibility was endorsed by the management team. It was approved by Cathie Allen on 24 March 2020.

149. Specifically in relation to Project #185, additional experiments were proposed and sent to the Management team for feedback. All of the management team endorsed the original proposal, and additionally endorsed the updated experiments (which were in relation to the testing for repeatability and reproducibility). This resulted in a change to the experimental design for this project. I do not have a recollection now about any specific discussions with Rhys Parry around these issues with Project # 185, as I believe this was directed to Justin Howes.

150. Another example is Project #175, which also had feedback from Thomas Nurthen and Rhys Parry. This feedback resulted in a modification to the experiments which were

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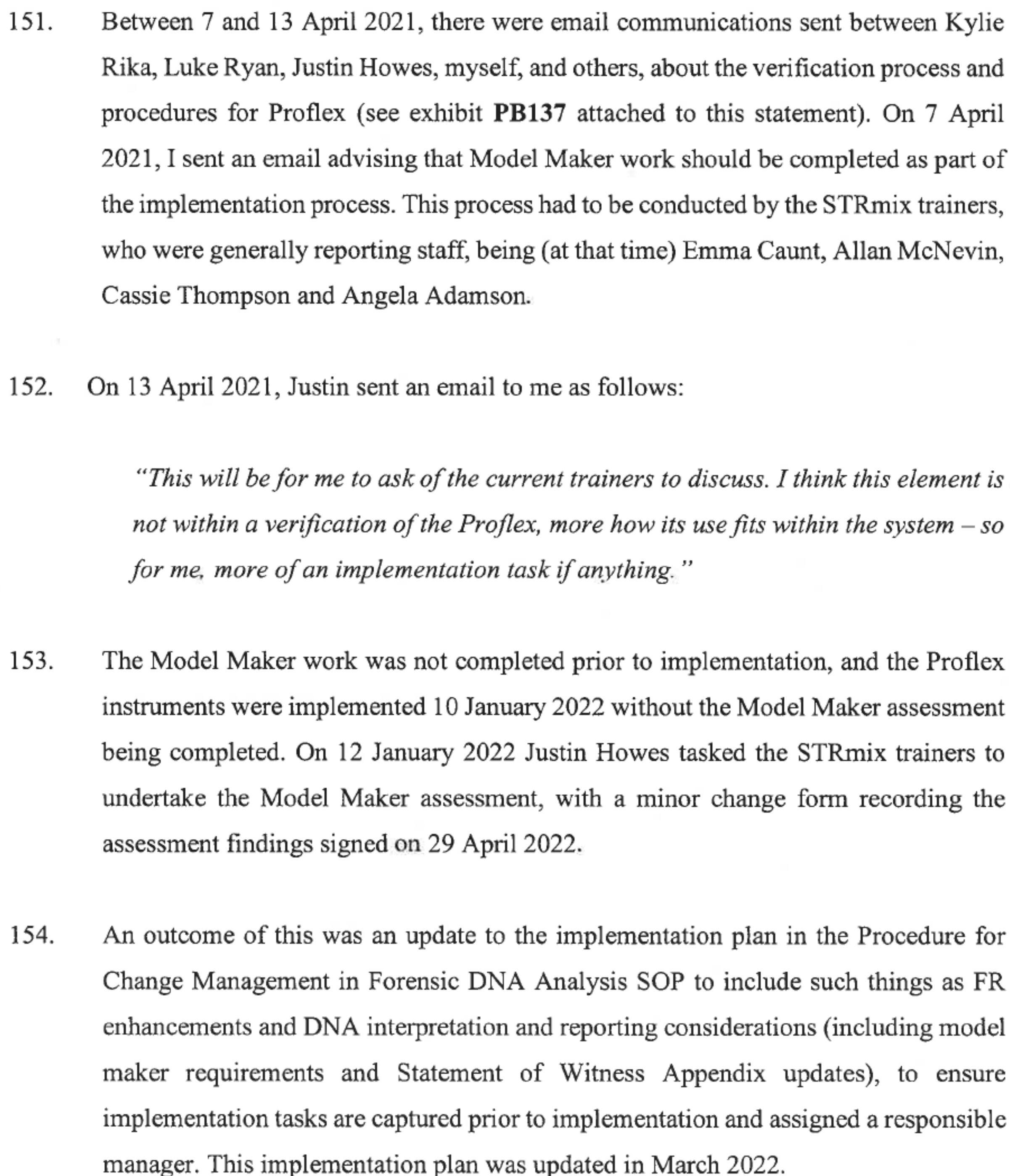

agreed to by the management team and incorporated in the project. This was, based on the dates, at the same time as Project #185 feedback.

VERIFICATION OF PROFLEX FOR PP21

151. Between 7 and 13 April 2021, there were email communications sent between Kylie Rika, Luke Ryan, Justin Howes, myself, and others, about the verification process and procedures for Proflex (see exhibit **PB137** attached to this statement). On 7 April 2021, I sent an email advising that Model Maker work should be completed as part of the implementation process. This process had to be conducted by the STRmix trainers, who were generally reporting staff, being (at that time) Emma Caunt, Allan McNevin, Cassie Thompson and Angela Adamson.

152. On 13 April 2021, Justin sent an email to me as follows:

> *"This will be for me to ask of the current trainers to discuss. I think this element is not within a verification of the Proflex, more how its use fits within the system – so for me, more of an implementation task if anything."*

153. The Model Maker work was not completed prior to implementation, and the Proflex instruments were implemented 10 January 2022 without the Model Maker assessment being completed. On 12 January 2022 Justin Howes tasked the STRmix trainers to undertake the Model Maker assessment, with a minor change form recording the assessment findings signed on 29 April 2022.

154. An outcome of this was an update to the implementation plan in the Procedure for Change Management in Forensic DNA Analysis SOP to include such things as FR enhancements and DNA interpretation and reporting considerations (including model maker requirements and Statement of Witness Appendix updates), to ensure implementation tasks are captured prior to implementation and assigned a responsible manager. This implementation plan was updated in March 2022.

ASSISTANCE AT THE MORTUARY AND CORONIAL ID MEETINGS

155. Generally, the Supervisor of the Evidence Recovery Team is the point of contact for samples requiring examination, including coronial samples and assistance to pathologists for selection of post-mortem samples. Allison Lloyd, who has been in the Evidence Recovery supervising Scientist position since late last year, would respond to these requests.

156. At times, there are requests made from pathologists to assist with sample selection at the mortuary. If assistance can be provided through viewing photographs, instead of physically attending the mortuary, then this would occur, as a risk management procedure.

157. My understanding is that it was not the case that reporting scientists were prohibited from attending the mortuary to assist pathologists, but rather it was a task best suited to the Evidence Recovery Supervisor to coordinate samples that may be forthcoming, and there were procedures put in place from an efficiency perspective, as well as a risk management perspective.

158. Scientists who have achieved competency in examination of bones and teeth would be suitable to provide advice on sample selection. The Senior Scientists of the Evidence Recovery team, both Allison Lloyd and Allan McNevin, are trained Reporting Scientists. Allison Lloyd, the current supervising scientist, is also trained in bone examination and sample selection, and has assisted on many DVIs and regularly assists pathologists in her current role.

159. My understanding is the Coronial ID meetings are a status update to advise of potential cases that may require examination and may also contain updates regarding active cases. I have not attended a Coronial ID meeting. Allison Lloyd, who has been in the Evidence Recovery supervising Scientist position since late last year, has never attended a meeting. Generally, the Scientific Services Liaison Unit directly contacted the allocated reporting scientist once a case had been allocated to obtain a status update.

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Paula Michelle Brisotto

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160. The Coronial ID meetings have not been held for some time, at least for two years. It appears from the minutes that this may be due to COVID-19. The 'minutes' are sent out to the Evidence Recovery supervising scientist weekly, with updates about cases prepared by the liaison unit. These minutes are saved on the network and are accessible by all Forensic DNA Analysis staff.

161. For any allocated casefile, SSLU (the liaison unit) would contact the allocated reporting scientist directly to provide status updates. To my knowledge, Allison has not inputted information into the minutes, and status updates on cases in progress is obtained from the allocated Reporting Scientist. Otherwise, the minutes are for information only.

162. These are tasks which are undertaken by the Forensic Reporting and Intelligence team (Justin Howes' team) so I do not have any involvement or management over this process after the items are examined in the Evidence Recovery Team. I have never been to a meeting myself, and received only some minutes back in 2020 (when I was included with Allan McNevin). The minutes went to Allan as he was the supervising scientist of the Evidence Recovery team (and later to Allison, when she took over that role).

163. Generally, I may be included in communication when a coronial sample is requiring DNA testing, however this is generally a CC or as part of a group email (including relevant management team members and the allocated reporter), so there is overall awareness of samples being received. This is outside of the Coronial ID meetings though.

GENERAL MANAGEMENT AND HR ISSUES

164. Quality is a central component of all the work we conduct. We have an overarching quality management system in place, and a dedicated quality senior scientist. We hold NATA accreditation against ISO 17025, which is re-assessed at least every 2 years.

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Paula Michelle Brisotto

There are many levels of quality controls and checks in place to ensure the very high quality of the work produced.

165. My view is that Turn Around Time (TAT) for sample processing is important, but not at the expense of quality. Staff routinely receive requests from clients regarding TATs for sample processing (e.g. TATs for issue of statements for upcoming scheduled court dates). Samples are not reported unless all quality controls and systems have been passed, regardless of the request for specific TATs.

166. TAT is also important in terms of public safety, and this is particularly the case for priority 1 cases where there may be an ongoing public safety risk. In these cases the QPS request short TATs to assist the investigation, and to mitigate the public safety risk. We often also receive positive feedback from the QPS regarding the short TAT for priority 1 cases, and I perceive this to be a compliment regarding both the quality of the results and the fast TAT.

167. In numerous working for Queensland feedback surveys from staff, performance management has been raised as an ongoing issue. The management team have tried to determine how best to action this, and it became apparent until relevant KPIs are available, performance cannot be measured as there is no expectation what targets staff are expected to achieve. This was put forward as a top 3 priority during the work with Tess Brooks (1st Call Consulting) and was a top 3 initiative in the Strategy focussed Management meeting in 2021.

168. Work was undertaken with all management team members to create a spreadsheet of KPI's that could be put into the Forensic Register to measure time taken from end to end and between processes. According to meeting minutes from 02 June 2021, 'accountability' and 'transparency' are points of great interest to staff. I believe this KPI spreadsheet was submitted to BDNA for a quote earlier in 2022.

169. Career Success Plans (CSPs) are similar to individual development plans and are designed to record conversations relating to both individual goals and team-based outcomes.

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Paula Michelle Brisotto

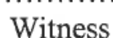
170. I cannot comment on how often CSP's are done within the reporting teams, I can only comment on how often they are done in the Evidence Recovery and Quality Team. A CSP cycle is generally every 12 months, with a six-month review. Line managers within the Evidence Recovery and Quality Team are up to date on CSPs for their staff, and have these regularly with team members.

171. In relation to the professional development of scientists within the laboratory, there is a Queensland Health policy in place, which provides for a professional development allowance and professional development leave. All health practitioner (HP) staff have access to this, as they are paid an allowance for professional development directly in their pay. They have access to Professional Development leave, which to my knowledge, no staff has been unreasonably refused any attendance. I cannot myself think of any time I have not supported staff accessing Professional Development Leave.

172. I do not agree with Emma Caunt's allegation that I did not value her opinion or include her when making decisions within the laboratory. While Emma is not within the Evidence Recovery and Quality Team that I oversee, I have found a number of emails where Emma's opinion is sought. I cannot comment on how she feels about her opinions not being valued as that is how she feels, however from my perspective and based on my emails, her opinion/input was sought because it is valued.

173. Kylie Rika refers to an issue which arose during a meeting with Cathie Allen and others on 7 December 2017. Kylie states that she was upset at the way Cathie spoke to her during the meeting, and that she subsequently spoke to me about it. This is not unusual, in that Kylie would talk to me if she was upset or had any questions or concerns and I would offer support and suggestions where I could, as I would do with any staff member.

174. I do not now have a recollection of the specifics of this conversation with Kylie on 7 December 2017. Kylie alleges that my advice to her was to stay calm, and to let Cathie



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Allen carry on acting inappropriately as it was out of her control. In my view, it does not sound like something I would say in response to a staff member who was upset.

175. I do recall at a point in time discussing 'modelling behaviour' with Kylie Rika, however I cannot recall if this related to the conversation with her and/or Workplace Edge on or around December 2017.

176. In December 2017, I undertook a short period acting as Team Leader within the Forensic Reporting and Intelligence Team while Justin Howes was on leave. When I finished acting in this role, I prepared a 'FRIT handover' document for Justin Howes to summarise what had occurred whilst I was acting in this position. Within this FRIT handover, I made the following notes:

> *"HR – feedback from Management meeting 07/12/2017 – KDR and TEN upset by some comments within meeting in relation to Y-filer project. KDS commented re: length of time around Y project. Discussed feedback with KDS, and email sent to KDR. All ok.*
>
> *- In same meeting, RSI raised from KDR – upset by CJA question regarding if any enhancements in VSTS (tone, manner etc). Talked to KDR about this for some time. Also spoke to CJA.*
>
> - *15/12/2017 – issue raised to Workplace Edge (Allan Holz) via email. Discussion with myself, and then Kylie. Issue seems resolved at present."*

177. Whilst I have reflected this event in my notes within the FRIT handover, I have no independent recollection of my subsequent conversations with Cathie Allen or Allan Holz.

178. Given the interactions that happened post my chat with Kylie, it seems unlikely I would have said to 'stay calm and accept inappropriate behaviour', especially in light of my follow-up with Cathie and conversations with Workplace Edge as per the handover. Using the wording "issue seems resolved" indicates there was a satisfactory outcome and no further follow up was required at that time.

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Paula Michelle Brisotto

TAKEN AND DECLARED before me at Brisbane in the State of Queensland this 17th day of October 2022.

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Paula Michelle Brisotto

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Witness Caitlin Fletcher

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Paula Michelle Brisotto Witness

EXHIBIT INDEX

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PB129

Fletcher, Caitlin 67002

From: Paula Brisotto
Sent: Monday, 16 August 2021 4:04 PM
To: Luke Ryan
Subject: Re: Priority 1 cases - and

Great email! Thanks Luke 😀

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From: Luke Ryan <
Sent: Monday, August 16, 2021 3:46:02 PM
To: Abigail Ryan < Adam Kaity < Adrian Pippia < Alanna Darmanin < Alicia Quartermain < Allan McNevin < Allison Lloyd < Amy Cheng < Angela Adamson < Angelina Keller < Anne Finch < Belinda Andersen < Biljana Micic < Cassandra James < Cathie Allen < Cecilia Flanagan < Chantal Angus < Cindy Chang < Claire Gallagher < Deborah Nicoletti < Emma Caunt < FSS.FDNA.Admin < Generosa Lundie < Helen Williams < Ingrid Moeller < Jacqui Wilson < Janine Seymour-Murray < Josie Entwistle < Julie Brooks < Justin Howes < Kerry-Anne Lancaster <Kerry- Kevin Avdic < Kim Estreich < Kirsten Scott < Kristina Morton < Kylie Rika < Lai-Wan Le <Lai- Lisa Farrelly < Luke Ryan < Madison GULLIVER < Maria Aguilera < Matthew Hunt < Megan Mathieson < Melissa Cipollone < Michael Goodrich < Michael Hart < Michelle Margetts < Naomi French < Paula Brisotto < Penelope Taylor < Phillip McIndoe < Pierre Acedo < Rhys Parry < Ryu Eba < Sandra McKean < Sharelle Nydam < Sharon Byrne < Sharon Johnstone < Suzanne Sanderson < Tara Prowse < Tegan Dwyer < Thomas Nurthen < Valerie Caldwell < Vicki Pendlebury-Jones < Wendy Harmer < Yvonne Connolly <
Subject: Priority 1 cases - and

Afternoon All

I wanted provide a summary of the fantastic work we did for the two most recent P1 cases: and As always these TATs are incredibly fast and provide vital support to investigators and scientific officers running these jobs. When I have met with external reps in the past they have been genuinely surprised we turn around casework samples in 12-14 hours and have told me these would be some of the fastest TATs in the world.

Great effort from everyone, even if you didn't have hands on these samples, you all make this possible.

For [redacted] (timeline relates to [redacted] – total time from P1 extraction start to Link Report: **7 hours and 55 minutes.**

- Items authorised as P1 Wednesday 11/08/2021 1444hrs
- DNA Extraction completed: 0842hrs Thursday 12/08/2021
- Quant completed: 1123hrs Thursday 12/08/2021
- Amp completed: 1223hrs Thursday 12/08/2021
- CE completed: 1452hrs Thursday 12/08/2021
- CEQ completed: 1514hrs Thursday 12/08/2021
- Plate Reading completed: 1552hrs Thursday 12/08/2021
- PDA complete and reviewed: 1611hrs Thursday 12/08/2021
- NCIDD load complete and Link reported: 1637hrs Thursday 12/08/2021

For [redacted] (timeline relates to [redacted] – total time from P1 notification to NCIDD load was: **4 days and 5 hours, this does include the 2 day weekend and a EXTN investigation.**

- Items authorised as P1 Thursday 12/08/2021 0803hrs.
- Items were already in process and completed Integrated QIAsymphony Extraction 1452hrs in Thursday 12/08/2021
- Quant completed: 1554hrs Thursday 12/08/2021
- Amp completed: 0712hrs Friday 13/08/2021
- CE completed: 1018 hrs Friday 13/08/2021
- CEQ check completed: 1528hrs Friday 13/08/2021 (5 hour delay because an EXTN had peaks and during this 5 hours a re-CE and reamp/CE was conducted before the original CE plate could be released).
- Plate reading completed: 1547hrs Friday 13/08/2021.
- PDA completed and reviewed: 1045hrs Monday 16/08/2021
- NCIDD load completed: 1359hrs Monday 16/08/2021.

Thanks
Luke

Luke Ryan
A/Team Leader – Evidence Recovery & Quality
Forensic DNA Analysis, Forensic and Scientific Services
Prevention Division, Queensland Health
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a 39 Kessels Rd, Coopers Plains, QLD 4108
e [redacted] **w** www.health.qld.gov.au/healthsupport/businesses/forensic-and-scientific-services

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PB130

34043 - Positive Extraction Controls with low DNA yields

Print Report | History

General | Investigation | Action | Tasks | Follow-up and Approval | Associations | Records | Workflow

Event	Event Description	Event Date	Updated By
Approval	OQI Closed Approved	16/09/2013 13:43:49	Amanda REEVES
Follow-up	OQI submitted for Approval	06/05/2013 16:38:23	Allan MCNEVIN
Follow-up	OQI Action complete and submitted for Follow-up	06/05/2013 16:38:14	Allan MCNEVIN
Action	OQI actioned	06/05/2013 16:38:14	Allan MCNEVIN
Action	OQI investigation complete and submitted for Action	06/05/2013 16:36:51	Allan MCNEVIN
Investigation	OQI investigated	24/04/2013 10:55:47	Allan MCNEVIN
Assignment Accepted	Assignment was accepted	26/03/2013 09:56:07	Allan MCNEVIN
Assignment	New OQI created awaiting acceptance	26/03/2013 09:54:36	Allan MCNEVIN

Last Modified at 16/09/2013 1:43 PM by Amanda REEVES, Created on 26/03/2013 9:54 AM by Allan MCNEVIN

CISSU (07) 3000 9333

34817 - Incorrect conditions used for Capillary Electrophoresis

Print Report | History

General | Investigation | Action | Tasks | Follow-up and Approval | Associations | Records | Workflow

Event	Event Description	Event Date	Updated By
Approval	OQI Closed Approved	01/11/2013 15:04:51	Amanda REEVES
Follow-up	OQI submitted for Approval	26/09/2013 15:47:13	Allan MCNEVIN
Follow-up	OQI Action complete and submitted for Follow-up	26/09/2013 15:46:57	Allan MCNEVIN
Action	OQI actioned	06/08/2013 10:09:29	Allan MCNEVIN
Action	OQI investigation complete and submitted for Action	06/08/2013 09:53:40	Allan MCNEVIN
Investigation	OQI investigated	12/07/2013 10:55:33	Allan MCNEVIN
Assignment Accepted	Assignment was accepted	12/07/2013 10:55:23	Allan MCNEVIN
Assignment	New OQI created awaiting acceptance	09/07/2013 13:21:26	Allan MCNEVIN

Last Modified at 1/11/2013 3:04 PM by Amanda REEVES, Created on 9/07/2013 1:21 PM by Allan MCNEVIN

PB131

Fletcher, Caitlin 67002

From: Paula Brisotto <[redacted]
Sent: Thursday, 3 March 2022 2:08 PM
To: Kylie Rika
Subject: RE: Testing restarted process improvement

Thanks for the extra information Kylie.

A data grab has been requested from the FR which may have information in it that could be used to inform next steps for this. Once this data is received, we will know more about what we can assess from it.

I think after this is done and depending on what can be determined, it would be a good time for you, Sharon and Justin to discuss the benefits of a list that FRIT will manage and assess for these reworks.

Thanks,
Paula

From: Kylie Rika <[redacted]
Sent: Thursday, 3 March 2022 1:10 PM
To: Paula Brisotto <[redacted]
Subject: RE: Testing restarted process improvement

Hi Paula,

I am thinking that they go onto a list for a CMer to consider any RW option. A CMer may want to consider a re-quant first for example. Or if the quant is just under 0.008 then try amp at max etc….

So I'm proposing they go to a list for a CMer to consider any testing option not just mic to 30 or mic to full.

Thanks
Kylie

From: Paula Brisotto <[redacted]
Sent: Thursday, 3 March 2022 11:55 AM
To: Kylie Rika <[redacted]
Subject: RE: Testing restarted process improvement

Hey Kylie,

Sorry for following up as I realise this is a crazy week. Are you able to provide more info on the below?

Thanks,
Paula

From: Paula Brisotto
Sent: Monday, 28 February 2022 10:31 AM
To: Kylie Rika <[redacted]
Subject: RE: Testing restarted process improvement

Hi Kylie,

In order to help determine next steps, can I clarify if the assessment by case managers is to determine if a full microcon or microcon to 30 is required?

Thanks
Paula

From: Kylie Rika <[redacted]
Sent: Tuesday, 22 February 2022 2:27 PM
To: Paula Brisotto <[redacted]
Subject: No, I don't support this: Testing restarted process improvement

Hi Paula

I would like ALL (internal and QPS) initiated further processing requests to go onto a list that CMers can assess and address.

Thanks
Kylie

PB132

Fletcher, Caitlin 67002

From: Kylie Rika <[redacted]>
Sent: Wednesday, 11 May 2022 2:30 PM
To: Paula Brisotto
Subject: RE: Testing restarted process improvement

Thanks Paula,

All of that sounds perfect! I just wanted to ensure all of mgmt. team were aware so that when I get questions from staff I am not speaking out of school. (I still have staff querying if we can review the DIFP process and quant ranges).

Kylie

From: Paula Brisotto <[redacted]>
Sent: Wednesday, 11 May 2022 2:22 PM
To: Kylie Rika <[redacted]>
Subject: RE: Testing restarted process improvement

Hi Kylie,

Happy to mention data was requested from the FR. I have spoken to Lara, and it seems clear from the TOR the DIFP process will be assessed as part of the DNA review, which is as expected. I think it reasonable we would wait and see the recommendations from the review to ensure any data interpretation is appropriate.

We have a meeting tomorrow, and can mention there?

Thanks,
Paula

From: Kylie Rika <[redacted]>
Sent: Wednesday, 11 May 2022 11:33 AM
To: Paula Brisotto <[redacted]>
Subject: RE: Testing restarted process improvement

Hi Paula

Are we able to please let all of mgmt. team know that data was requested from the FR and further, at this time Lara does not want any work on it to be progressed? I think it would be good for the mgmt. team to be aware of this given some of the content of the terms of reference of the upcoming review.

Thanks
Kylie

From: Paula Brisotto <[redacted]>
Sent: Friday, 29 April 2022 9:59 AM
To: Kylie Rika <[redacted]>
Subject: RE: Testing restarted process improvement

Hi Kylie,

The data requested from the FR covers all DIFP and NDNAD samples and requested reworks since the process was implemented, which I think equates to ~4 years' worth of data. This will provide a much more comprehensive assessment I think. It may be that the spreadsheet you provided is not needed, as this is duplicating the data - given the FR data grab covers all samples, not just the small subset currently recorded.

We had been advised by Lara that, given the review of Forensic DNA Analysis was mentioned in parliament, the reassessment and any findings/options moving forward would not be progressed at this time. Lara has communicated this with Supt McNab which was understood by the Supt. Lara has not yet advised this can be progressed, and I will raise this in my next catch-up with her if there are any updates.

Thanks,
Paula

From: Kylie Rika <[redacted]
Sent: Thursday, 28 April 2022 2:51 PM
To: Paula Brisotto <[redacted]
Subject: RE: Testing restarted process improvement

Hi Paula

I am just wondering if the data grab from FR has been received yet? Depending on the search parameters that were requested, I am wondering if we could possibly also use the data in a post implementation review of the DIFP process. From the mgmt. meeting on the 11 Nov 2021, I raised the following:

DNA Insufficient for Processing (DIFP) process

KDR collecting samples where better results obtained after case manager requested concentration, including profiles for NCIDD. General discussion ensued that this possibility was communicated and accepted by QPS, and that they could request processing any time and that the case manager may rework if case circumstances indicate worthwhile. Value for DIFP determined from PCR (PP21 validation); values may be different with VFP which is more sensitive.

Suggestion from LBR that may be worthwhile if moving to VFP that we profile above this value and then after collecting enough data (eg. last data was a year of data), review the findings to see if a threshold could be determined.

KDS mentioned if collecting data, need to balance with the number that do not eventuate with profiles (as many get requested by QPS monthly for reactivation).

I have attached the collection of samples so far.

This s/sheet was set up so that instead of staff emailing me or Adrian (at the time) with samples they wanted to bring to our attention (as examples of DIFP that then ended up in a good result), they could just add to this s/sheet.

I realise this s/sheet is not a balanced collection so we cannot derive any trends etc., but some of the info in it has made me think, we really need to review this process and the quant ranges used to drive DIFP.

I am aware of a lot more examples that people have in their large cases that they haven't yet had a chance to add to the s/sheet.

Happy to discuss further in person if you like.

Thanks

Kylie

From: Paula Brisotto <[redacted]
Sent: Thursday, 3 March 2022 2:08 PM
To: Kylie Rika <[redacted]
Subject: RE: Testing restarted process improvement

Thanks for the extra information Kylie.

A data grab has been requested from the FR which may have information in it that could be used to inform next steps for this. Once this data is received, we will know more about what we can assess from it.

I think after this is done and depending on what can be determined, it would be a good time for you, Sharon and Justin to discuss the benefits of a list that FRIT will manage and assess for these reworks.

Thanks,
Paula

From: Kylie Rika <[redacted]
Sent: Thursday, 3 March 2022 1:10 PM
To: Paula Brisotto <[redacted]
Subject: RE: Testing restarted process improvement

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So I'm proposing they go to a list for a CMer to consider any testing option not just mic to 30 or mic to full.

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Kylie

From: Paula Brisotto <[redacted]
Sent: Thursday, 3 March 2022 11:55 AM
To: Kylie Rika <[redacted]
Subject: RE: Testing restarted process improvement

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Thanks,
Paula

From: Paula Brisotto
Sent: Monday, 28 February 2022 10:31 AM
To: Kylie Rika <[redacted]
Subject: RE: Testing restarted process improvement

Hi Kylie,

In order to help determine next steps, can I clarify if the assessment by case managers is to determine if a full microcon or microcon to 30 is required?

Thanks
Paula

From: Kylie Rika <[redacted]
Sent: Tuesday, 22 February 2022 2:27 PM
To: Paula Brisotto <[redacted]
Subject: No, I don't support this: Testing restarted process improvement

Hi Paula

I would like ALL (internal and QPS) initiated further processing requests to go onto a list that CMers can assess and address.

Thanks
Kylie

PB133

Fletcher, Caitlin 67002

From:	Lara Keller <
Sent:	Tuesday, 27 September 2022 6:14 AM
To:	Paula Brisotto
Subject:	FW: Assessment of low quantification value DNA samples
Attachments:	Assessment of Low Quant DNA Samples_June 2022.pdf

---

From: Lara Keller
Sent: Friday, 24 June 2022 9:17 AM
To: McNab.BruceJ[OSC] <
Subject: Assessment of low quantification value DNA samples

Good morning Bruce

Kindly find attached follow up paper regarding DNA quantification values.

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

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PB134

Fletcher, Caitlin 67002

From:	Helen Gregg <
Sent:	Wednesday, 28 September 2022 8:17 AM
To:	Paula Brisotto; Kirsten Scott; Allison Lloyd; Sharon Johnstone; Belinda Andersen; Kylie Rika; Luke Ryan
Cc:	Matt Ford; Peter Culshaw; Lara Keller
Subject:	Asssessment of Low Quant DNA samples - additional paper
Attachments:	Assessment of Low Quant DNA Samples_June 2022.pdf

Good morning,

Please see attached paper. This was provided to Supt McNab by Lara earlier this year. This paper is for your information only, and is on hold pending the outcomes of the Commission of Inquiry.

Regards
Helen

Helen Gregg
Scientific Support Manager for Forensic DNA Analysis Commission of Inquiry

Forensic and Scientific Services, Queensland Health

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e w www.health.qld.gov.au/fss

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PB135

Fletcher, Caitlin 67002

From:	Kylie Rika <
Sent:	Friday, 9 June 2017 1:14 PM
To:	Paula Brisotto; Luke Ryan; Matthew Hunt
Subject:	RE: Data Analysis Report
Attachments:	Data Analysis report_draft1KDR2.doc
Follow Up Flag:	Follow up
Flag Status:	Flagged

Thanks Paula

I think the report is fine. I have added some more feedback in purple. For the purposes of this data analysis – and its scope, the report is fine. I am still curious as to why we are having a small set of samples where we are seeing 0sp to 2+sp. This difference is too big (even though it only relates to a small number of samples).

Perhaps we need something in the report to highlight this and what we seek to do to investigate??

Nice work Paula ☺

thanks

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

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

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From: Paula Brisotto
Sent: Tuesday, 30 May 2017 11:38 AM
To: Kylie Rika; Luke Ryan; Matthew Hunt
Subject: Data Analysis Report

Hi all,

As per our discussions, please find attached an updated draft of this report. Based on feedback, we are looking at a different approach where the report will go into further detail around the data in the results section.

I have taken the feedback I have received so far, and put it in the updated draft report. Please note I have only had a preliminary read over this (as I have been in FR training most of yesterday and this morning), and some of the wording needs to change and some paragraphs rearranged to make the document flow. It's a work in progress ☺

I have attached both the word doc and the spreadsheet, in case you need to refer back to the spreadsheet.

Thanks,
Paula

Paula Brisotto
Team Leader – Evidence Recovery and Quality Team, Forensic DNA Analysis, Police Services Stream
Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

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Data Analysis of modified sexual assault process for zero spermatozoa detected at Evidence Recovery

Paula Brisotto, Matthew Hunt, Kylie Rika, Luke Ryan

May 2017

Introduction

Prior to August 2016, exhibits which gave negative results for spermatozoa and seminal fluid were typically not submitted for DNA testing, using the differential lysis extraction protocol (depending on case circumstances and examination strategy these samples may still be submitted for differential lysis extraction or for cell extraction). In August 2016, the Evidence Recovery Team implemented a modified sample submission process for all samples whereby all samples screened for seminal fluid were submitted for DNA testing, using differential lysis extraction, irrespective of the presumptive screening results (i.e. even those samples for which spermatozoa were not located microscopically and P30 tests were negative were still submitted for DNA testing using a differential lysis extraction). The microscopy slides created during the differential lysis extraction were then read by Evidence Recovery Team scientists for final reporting of spermatozoa detection results.

This modification process was introduced in response to concerns that the initial microscopy conducted during ERT examinations may be detecting fewer spermatozoa than were seen by subsequent microscopy of slides produced after the differential lysis extraction process.

This data analysis examines the set of samples which had no spermatozoa or seminal fluid detected during the initial Evidence Recovery examination, and which were then submitted for differential lysis extraction. **The results from this data set will be used to assess the difference in the pre and post August 2016 examination and sample submission strategies based on the final DNA results and attempt to determine what, if any, impact this may have had on the DNA results reported for the case.** **– this sentence is important and is the purpose – so should be highlighted in some way.**

The results from this data set shouldn't be used to:

- extrapolate back to other cases not within this time period and prior to the modified process

- predict the effect on future cases

(as this data doesn't tell the whole story)

In assessing the potential implications for the DNA results reported, relevant aspects of case-management were taken into account, including presumptive screening test results, existing examination strategies for different sample types and other results within the case.

Queensland Government

Results

Since August 2016, the sample submission strategy was changed for samples which gave negative presumptive screening results for spermatozoa and seminal fluid (i.e. no spermatozoa observed on microscopy and P30 negative test). All samples which were tested for the presence of spermatozoa and seminal fluid were submitted for DNA extraction using the differential lysis protocol, regardless of the presumptive screen results.

During the period, 8 August 2016 to 28 March 2017, there were 738 samples for which the presumptive screening in Evidence Recovery did not identify spermatozoa during microscopy which were submitted for differential lysis extraction. For each of these 738 a microscopy slide was created during the Evidence Recovery examination (the Evidence Recovery slide), and a second slide was created during the differential lysis extraction (the Differential Lysis slide). Both slides were read by Evidence Recovery scientists.

The differences in the methods for creating the Evidence Recovery and Differential Lysis slides are a relevant context to the results of this data mining. Evidence Recovery slides are created by suspending the sample substrate (i.e. swab, scraping, material etc.) 200µL to 300µL of nanopure water. This suspension is then vortexed and agitated with a disposable pipette. One drop (using a disposable pipette) of the suspension is then spotted onto a microscopy slide. The Differential Lysis slides are created by taking 3µL from the male fraction (post separation from the female fraction) during the differential lysis protocol. The total volume for the male fraction when the Differential Lysis slide is created is approximately 50µL. It is expected that the Differential Lysis slide would be more sensitive (in terms of spermatozoa detection) for one main reason: the Differential Lysis slide is created by sampling 3µL from a total volume of 50µL of male fraction, therefore any spermatozoa present in the male fraction are at a higher concentration than the Evidence Recovery suspension which has a total volume of 200µL.

Table 1 Differential Lysis slide reads for the presence of sperm.

Original ER read	Diff Lysis Slide read	Number of samples	Percentage of Total
0 sperm	0 sperm	591	80.08
0 sperm	<+1 sperm	104	14.09
0 sperm	+1 sperm	36	4.88
0 sperm	+2 sperm	7	0.95

Of these 738 samples, no spermatozoa were observed on both the Evidence Recovery and Differential Lysis slides for 591 samples. This means that for 591 samples, either there were no spermatozoa present, or if they were present they were below the limit of detection for both the Differential Lysis and Evidence Recovery slide preparation techniques.

The remaining 147 slides, for which there were no spermatozoa observed on the Evidence Recovery slide, but where spermatozoa were observed on the Differential Lysis slide, **were assessed to determine the impact on final DNA results for that sample.** **– what about the value of seeing sperm period? For example, it could be highly informative to see sperm even in the absence of a usable DNA result. For example, you don't expect to see sperm at all on a 6 year old girls vaginal swab.**

Of the 7 samples for which no spermatozoa were located on the Evidence Recovery slide, but +2 spermatozoa were located on the Differential Lysis slide:

- 6 would have been submitted for differential lysis extraction pre-August 2016 based on a positive P30 result.
- The remaining sample was a vulval sample (from a SAIK. The vulval sample gave a 3P mixed DNA profile (not yet reported). The high vaginal and low vaginal samples had spermatozoa observed on the Evidence Recovery slides. The high vaginal sample gave a two person mixture which was conditioned on the complainant, and gave a remaining profile with >100 billion support for contribution from the suspect. The low vaginal sample gave a similar result to the high vaginal sample. Therefore failure to submit the vulval sample would not have altered the final result for the SAIK. – not really true – 3p could have given complainant and two male foreign DNA profiles – this could be quite informative compared to a 2p mix of complainant and one male profile.

For the 36 samples which gave no spermatozoa on the Evidence Recovery slide but +1 spermatozoa on the Differential Lysis slide:

- 19 would have been submitted for differential lysis extraction pre-August 2016 based on positive P30 results.
- Seven of these 36 samples would have been submitted for cell extraction rather than differential lysis extraction pre-August 2016. Submission of these seven samples for cell extraction rather than for differential lysis would not have altered the final results for these SAIKs because:
    - two gave single source profiles consistent with the suspect.
    - four gave either two/three person mixtures with >100 billion support for suspect contribution.
    - one sample (a perianal SAIK swab) gave a 2P mixture where the known contributor (SAIK complainant) and the suspect were represented. The vulval swab from this SAIK had +1 spermatozoa observed on the Evidence Recovery slide and gave a single source final result consistent with the suspect.

- The remaining ten of these 36 samples would not have been submitted for DNA testing (either by cell or differential lysis extraction protocols) pre-August 2016. Of these ten samples:
    - High vaginal sample (gave a two person mixture which was conditioned on the complainant, and gave a remaining profile with >100 billion support for contribution from the suspect. The second high vaginal, low vaginal, vulval and perianal samples all had spermatozoa detected on the Evidence Recovery slides. The low vaginal and vulval samples gave single source profiles which were consistent with the suspect. The second high vaginal sample gave a two person mixture which was conditioned on the complainant, and gave a remaining profile with >100 billion support for contribution from the suspect. Therefore failure to submit the first high vaginal sample would not have altered the final result for the SAIK.
    - Low vaginal sample (gave a complex final result which was not interpreted. The vulval and rectal samples from this SAIK had spermatozoa detected on the Evidence Recovery slide. The rectal swab gave a single source DNA result which was consistent with the suspect. The vulval gave a complex final result which was not interpreted. Given the results of the rectal sample, and vulval sample, failure to submit the low vaginal sample would not have altered the final DNA results for this SAIK.

    - Low vaginal sample (gave a complex final result which was not interpreted. The high vaginal sample from this SAIK was P30 positive and therefore would have been

submitted for differential lysis extraction pre-August 2016. This high vaginal swab gave a 2 person mixture with >100 billion support for contribution from the suspect. The perianal swab was also p30 positive and therefore would have also been submitted for a differential lysis extraction pre-August 2016. The perianal swab gave a single source profile consistent with the suspect. The left nipple sample from this SAIK was also submitted for testing and have a 3 person mixture with >100 billion support for contribution from the suspect. Therefore failure to submit the low vaginal sample would not have altered the final result for this SAIK.

- Low vaginal sample ([redacted] gave a final result which was not interpreted/ deconvoluted based on other results from the SAIK. The cervical, high vaginal and posterior fornix all gave 1+ spermatozoa on the Evidence Recovery slide and were submitted for differential lysis extraction (consistent with pre-August process). The cervical sample gave a two person mixture with >100 billion support for contribution from the suspect. Based on this other samples from this SAIK were not interpreted further. Therefore failure to submit the low vaginal sample would not have altered the final result for this SAIK.
- Low vaginal sample ([redacted] gave a complex final result which was not interpreted. The high vaginal and vulval samples from this SAIK gave >1+ spermatozoa on the Evidence Recovery slide. The vulval sample gave a complex final result which was not interpreted. The high vaginal gave a 2 person mixture, from which the complainant was excluded. The high vaginal mixture appears to be an 1:1 2 person mixture from two males. No suspect reference samples have been submitted, but if they were they could be compared to this mixture. Therefore failure to submit the low vaginal sample would not have altered the final result for this SAIK.
- Tapelift from inside crotch ([redacted] gave a complex result for the spermatozoa fraction which was not interpreted. The epithelial fraction also gave a complex result which was not interpreted. Therefore submission of this sample for cellular or differential lysis extraction would not have altered the final DNA result for this sample.
- A piece of fabric ([redacted] gave a single source profile matching the suspect for the spermatozoa fraction. The epithelial fraction gave a three person mixture with >100 billion support for contribution from the suspect. Submission of this sample for cell extraction would not have altered the final result for this sample (i.e. suspect DNA located), albeit from cells extraction rather than a spermatozoa fraction.
- Low vaginal sample ([redacted] gave a mixed DNA profile which indicates contribution from a male person, but has not been interpreted based on the high vaginal sample result. The high vaginal sample was P30 positive and therefore submitted for differential lysis and gave a two person mixture which was conditioned on the complainant, and gave a UKM1 remaining profile (n.b. reference sample for suspect does not have a final result). The vulval sample had spermatozoa observed on the Evidence Recovery slide and gave a mixed DNA profile with indications of contribution from a male person, but this result has not been interpreted based on the high vaginal sample result. Therefore based on the high vaginal sample result, failure to submit the low vaginal sample would not have altered the final result for this SAIK.
- High vaginal sample ([redacted] gave a two person mixture which was conditioned on the complainant and the remaining profile was UKM1 (n.b. offender is unknown). The low vaginal and vulval samples both had spermatozoa observed on the Evidence Recovery slide. The low vaginal gave a similar result to the high vaginal sample and was not interpreted further. The vulval sample was a three person mixture which was conditioned on the complainant, and the remaining profile was not suitable for NCIDD load. Therefore

based on the low vaginal samples result, failure to submit the high vaginal sample would not have altered the final result for this SAIK.

- **A sanitary pad ([redacted] gave a two person mixture with contribution from a male person (not interpreted further as yet, but apparent major is a male contribution). The high vaginal and rectal samples both had no spermatozoa observed on the Evidence Recovery slide and were P30 negative. The high vaginal sample gave a two person mixed DNA profile which was conditioned on the complainant, and the remaining profile was unsuitable for NCIDD. The rectal sample gave a single source profile which was consistent with the complainant. Therefore failure to submit the sanitary pad for DNA testing would have impacted on the final result of this SAIK, as the sanitary pad was the only sample which gave a profile with a male contribution.**

There were 104 samples which for which no spermatozoa were located on the Evidence Recovery slide, but >1+ spermatozoa were located on the Differential Lysis slide (i.e. less than 10 spermatozoa observed on the Differential Lysis slide). The results of these 104 samples should be considered within the context described previously, i.e. that it is expected that the Differential Lysis slides are more sensitive than the Evidence Recovery slide, and that an change in microscopy result from zero spermatozoa detected to between one and ten spermatozoa detected may be representative of this difference in sensitivity. Of these 104 samples:

- 46 would have been submitted for differential lysis extraction pre-August 2016 based on a positive P30 result or examination strategy.
- 39 would have been submitted for cell extraction (rather than differential lysis extraction) pre-August 2016. Of these 39 samples:
  - 17 samples gave final results which were complex unsuitable for comparison, partial unsuitable for comparison or no DNA detected. Therefore submission for cell extraction would be unlikely to alter the final result for these samples.
  - 8 samples gave final results which were single source and were consistent with an assumed known contributor. Therefore submission of these samples for cell extraction would be unlikely to have altered the final result.
  - Vaginal and anal swab ([redacted] gave a three person mixed profile which was conditioned on the complainant, and gave a remaining profile with >100 billion support for contribution from the suspect. Given that this sample would have been submitted for cell extraction pre-August 2016, it is likely that a similar result would have been obtained via a cell extraction.
  - Vulval sample ([redacted] gave a final DNA result which was not interpreted. The high vaginal and low vaginal samples from this SAIK had spermatozoa observed on the Evidence Recovery slide. The high vaginal gave a three person mixture, the low vaginal gave a two person mixture. Both mixtures were conditioned on the complainant, and gave a remaining profile with >100 billion support for contribution from the suspect. Therefore submission of the vulval sample for cell extraction would not have altered the final result for this SAIK.
  - Rectal sample ([redacted] gave a single source profile consistent with the suspect. The cervical, high vaginal, low vaginal, vulval and perianal samples from this SAIK all had spermatozoa observed on the Evidence Recovery slide and each sample gave a single source profile consistent with the suspect. Therefore submission of the rectal sample for cell extraction would not have altered the final result for this SAIK.

- Vulval and rectal samples ([redacted] and [redacted] gave three person mixtures which were conditioned on the complainant, and gave a remaining profile with >100 billion support for contribution from the suspect. Other samples in this SAIK (perianal and low vaginal) gave mixtures which were conditioned on the complainant, and gave remaining profiles with support for contribution from the suspect. It is possible that had the vulval and rectal samples been submitted for cell extraction they could have given a similar final result to that obtained from the differential lysis extraction.
- Vulval sample ([redacted] gave a partial profile consistent with the suspect. The high and low vaginal samples from this SAIK had spermatozoa observed on the Evidence Recovery slides. The high vaginal sample gave a single source profile consistent with the suspect. The low vaginal sample gave a two person mixture which was conditioned on the complainant, and gave a remaining profile with >100 billion support for contribution from the suspect. Therefore submission of the vulval sample for cell extraction would not have altered the final result for this SAIK.
- Two fabric samples ([redacted] and [redacted] gave two person mixtures for which no statistical interpretation was performed. A third scraping from the same fabric gave a single source profile from an UKF1 from the epithelial fraction. It is possible that had these two fabrics been submitted for cell extraction that the final result would not be different.
- Vulval sample ([redacted] gave a two person mixture which was conditioned on the complainant, and gave a remaining profile which was consistent with UKM1. The low vaginal sample gave a P30 positive result and was submitted for a differential lysis extraction and gave mixed DNA profile which was conditioned on the complainant and gave a remaining profile which is consistent with UKM1. Given the low vaginal sample result, and the possibility that the vulval sample would have given a similar result if submitted for a cell extraction, the final result for the SAIK is unlikely to be different if the vulval sample was submitted for cell extraction.
- Vulval sample ([redacted] gave a single source profile from UKM1. The high vaginal had spermatozoa observed on the Evidence Recovery slide and gave a mixed DNA profile with a male contributor (consistent with UKM1 although not reported). Given the high vaginal result and the possibility that the vulval sample would have given a similar result if submitted for cell extraction, the final result for the SAIK is unlikely to be different if the vulval sample was submitted for cell extraction.
- Mouth sample ([redacted] gave a single source female profile (likely the complainant but FTA does not yet have a final result). The high vaginal sample from the SAIK had spermatozoa observed on the Evidence Recovery slide and gave a mixed DNA profile with a major male contributor. Therefore given the high vaginal sample result and submission of the mouth sample for cell extraction would not have altered the final result for the SAIK.

- 19 samples would not have been submitted for DNA extraction (either cell or differential lysis extraction). Of these 19 samples:
  - 8 samples gave complex unsuitable, partial unsuitable or no DNA detected final results. Failure to submit these samples for DNA extraction would not have altered the final result.
  - 5 samples gave single source profiles from an assumed known contributor. Failure to submit these samples for DNA extraction would not have altered the final result.
  - Low vaginal sample ([redacted] gave a mixed profile with major contribution from the complainant (which was not interpreted or reported). The high vaginal sample from the SAIK gave a P30 positive result and spermatozoa were detected on the vulval sample on

the Evidence Recovery slide. The vulval sample gave a two person mixture which was conditioned on the complainant and gave a remaining profile UKM1 which was loaded to NCIDD. Therefore given the vulval result, and the low vaginal result, failure to submit the low vaginal sample for testing would not have altered the final result for this SAIK.

- Endocervix sample ([redacted] gave two person mixture which was conditioned on the complainant and gave a remaining profile with >100 billion support for contribution from the suspect (this result was the same as for the perianal sample and was not reported via EXH). Spermatozoa were detected on the Evidence Recovery slides for the high vaginal 2, low vaginal, vulval, and perianal samples. The high vaginal gave a similar result to the perianal and was not reported via EXH. The low vaginal and vulval samples both gave single source profiles consistent with the suspect. Given the results of the other samples for this case, and the fact that the endocervix sample was not reported via EXH, failure to submit the endocervix sample for testing would not have altered the final result of the SAIK.
- High vaginal sample ([redacted] gave a two person mixture which was conditioned on the complainant and gave a remaining male profile which was compared to two suspects for this case but both were excluded. The cervical sample for this case (which it should be noted had no spermatozoa detected on the Evidence Recovery or Differential Lysis slides) gave a similar result. The low vaginal sample gave a P30 positive result and gave a similar final result to the cervical and high vaginal. Spermatozoa were detected on the rectal sample on the Evidence Recovery slide, but gave a complex final result. Therefore given the results of the low vaginal sample, failure to submit the high vaginal sample for testing would not have altered the final result for this SAIK.
- High vaginal sample ([redacted] gave a two person mixture which was conditioned on the complainant and gave a remaining profile with >100 billion support for contribution from the suspect. The vulval had no spermatozoa detected on the Evidence Recovery slide, but which pre-August 2016 would have been submitted for cell extraction, gave a three person mixture which was conditioned on the complainant and gave a remaining profile with >100 billion support for contribution from the suspect. Given that the vulval sample may have given a similar result if submitted for cell extraction (rather than differential lysis) failure to submit the high vaginal sample for testing may not have altered the final result for this SAIK.
- High vaginal sample ([redacted] gave two person mixture which was conditioned on the complainant and the remaining profile was used to compare against nominated suspects. The low vaginal sample was P30 positive and gave a three person mixture which was also used to compare against suspects. Given the result of the low vaginal sample, failure to submit the high vaginal is not likely to have altered the final result for this SAIK.
- Fabric sample ([redacted] gave a two person mixture which had >100 billion support for contribution from the suspect. This was the only result for this sample, however there are a large number of exhibits in this case with >100 billion support for contribution from the suspect. Therefore although failure to submit this sample would have changed the final result of this sample, there are a number of other exhibits in this case linked to the suspect.

Discussion

The aim of this data analysis was to assess the 738 samples which had no spermatozoa or seminal fluid detected during the initial Evidence Recovery examination, and which were then submitted for differential

lysis extraction, and compare these to pre August 2016 examination and sample submission strategies to determine what, if any, impact this (what do you mean by “this”) may have had on the DNA results reported for the case as a whole.

738 samples has been considered a sufficiently large dataset for the purposes of drawing some general conclusions, although this relies on the particular cases processed during this period, and therefore sampling variability may show a greater or lesser impact by assessing another dataset. It was beyond the scope of this data analysis to assess slides other than those that were originally zero spermatozoa detected at examination, and were submitted for differential lysis extraction since 8 August 2016. I like this paragraph.

The focus of this data analysis has been largely from a whole case perspective and several results were considered not to be impacted upon because of other samples/ similar results within the case. Assessing results on a whole case basis is standard case management practice, and is a process utilised across all case and sample types. It is acknowledged that the impact on individual samples may be considered significant if semen is not observed at examination, the presumptive screening is also negative and no further action was taken for that sample. The risk if spermatozoa were consequently detected on the differential lysis slide and provided an interpretable DNA result, then potentially a valuable DNA profile for the case may not be obtained. Also don’t forget the value of seeing sperm regardless of obtaining a DNA profile or not. What this data analysis shows is that this risk is mitigated when considering the typical case submission as a whole including what the presump expansion explains about the meaning of no sp observed does not equal no sp present. The majority of SAIKs/sexual assault cases contain multiple swabs and items, which provide several opportunities to locate semen and subsequently obtain foreign DNA profile that may support an allegation of sexual assault.

Examination strategies are formulated to try and maximise the chances that even if one sample has no spermatozoa observed and the sample truly contains spermatozoa, then the DNA profile information can be obtained through other means. The presumptive screening for seminal fluid and examination strategies for submitting samples for differential lysis or cell extraction (including but not limited to: submission external swabs/swabs from minors for cell extraction; submitting all areas from an item if one obtains a positive sperm or presumptive result) and also the capacity of STRmix to interpret even mixtures of up to 3 contributors (and including conditioning) all contribute to minimising the overall case impact for a particular sample.

It is acknowledged the slide read at both examination and differential lysis is a detection step, and the sample used to make the slide is a very small amount from the prepared suspension (a drop and 3uL respectively), which is a representation of the spermatozoa that may be present in the sample. For very low levels of spermatozoa, if a second slide is prepared from the sample, lower or higher levels of spermatozoa may be observed, as is expected from sampling variability.

The aim of the differential lysis process is to attempt to separate any spermatozoa from any epithelial cells in order to aid in the interpretation of the DNA profiles obtained. While complete separation of the spermatozoa fractions and epithelial fractions is the ideal, this is not often the case, and carry-over of epithelial cells into the sperm fraction is common. The advantage of using STRmix for mixture interpretation helps mitigate the consequences of failing to obtain the ideal separation of spermatozoa and epithelial fractions, which is the aim for differential lysis. In cases where a sample undergoes a cell extraction and the sample does contain spermatozoa, it is reasonable to assume that this extraction process will extract any DNA present in the sample, including from any spermatozoa present. STRmix will similarly aid in the interpretation of any mixed DNA profiles obtained from this process. – yes but if

you submit through cells and get 4p mix – NFA, whereas you might have got 3pmix in sp frac and SS in epi – you can STRmix the 3pmix.

As described previously, there is a degree of concentration of spermatozoa in the differential lysis process, and the number of spermatozoa present to give a slide read of <+1 is very low (defined as 'very hard to find spermatozoa'), therefore to go from zero to <+1 after differential lysis may not be unexpected. Similarly a slide read of +1 ('hard to find spermatozoa') after differential lysis, following a zero slide read at examination may not be too concerning or necessarily need to be taken as symptomatic of a problem with the examination slide read process.

Where a zero sperm read has produced a +2 sperm read of the slide after differential lysis, then this is harder to rationalise, even allowing for some variation in the subsample taken for the slide, and the differential lysis concentrating step. In this data there were 7 samples of the 738 total which showed this degree of difference ie. Zero to +2 (easy to find spermatozoa) which equates to 0.95% of this sample set. 6 of these samples would have undergone differential lysis extraction based on the presumptive result, and therefore the DNA results would have been unchanged. The one sample remaining was a vulval swab, and would have been submitted for a cell extraction. One sample out of 7 that would have gone through cell extraction and possible comp unsuit result vs a diff lysis with poss 3p and usable result. Within this particular SAIK, the high vaginal and low vaginal swabs both had sperm observed and examination, and provided a DNA profile with a contribution >100 billion for the suspect. Given the reasons listed above, all samples where +2 spermatozoa were detected at differential lysis, the results for the case were not considered to be negatively impacted. Again, just finding suspects DNA may not be the only ideal "result". What about finding DNA that could implicate another person (ie. 3p with diff lysis vs 4p unsuit with cells extn).

Conclusions

Therefore in summary:

- Of the 738 total samples for which no spermatozoa were detected on the Evidence Recovery slide, 591 also had no spermatozoa detected on the Differential Lysis slide.
- 147 of the 738 samples had spermatozoa detected on the Differential Lysis slide (>1+, 1+ or 2+).
- Of these 147 slides, 1 sample (a sanitary pad gave a final result which would not have been obtained pre-August 2016. I.e. the decreased sensitivity of the Evidence Recovery slide (when compared to the Differential Lysis slide) resulted? would have resulted in the sanitary pad sample not being submitted for DNA testing pre-August 2016.

The results of the analysis of this data set have shown that the difference in sensitivity of the Evidence Recovery and Differential Lysis swabs, although acknowledged, has not resulted in a systemic failure (I don't think anyone was ever concerned with there being a systemic failure, rather it being the case that for a small set of samples we are seeing 0sp to 2+sp – why is this? This difference is too big (even though it only relates to a small number of samples) with regards to final reported results. There was one sample in the 738 sample data set which would not have been submitted for DNA testing pre-August 2016, and which gave 1+ spermatozoa on the Differential Lysis swab and a final DNA result consistent with the suspect. This was the only DNA result for this case. Pre-August 2016 this sample would have been reported to the QPS as "Semen not detected" and no further action taken. It should be noted that this presumptive EXH advised the QPS that "Spermatozoa were not observed…" rather than advising

that there were no spermatozoa present. If deemed critical, the QPS could request further processing of this sample.

Therefore, although some individual samples may be negatively impacted as a consequence of the sensitivity of the examination slide process, overall this is considered to be an acceptable risk as it occurs relatively infrequently (which is fine, but why is it happening – proj 181 aims to find out), and from a case perspective the risk is mitigated by the established practices of multiple sample submissions, examination submission and interpretation strategies. This paragraph extrapolates back to all cases which I don't think we can do for reasons previously mentioned.

The results of this study did not demonstrate a systemic failure in the examination of exhibits for seminal fluid. There is a failure in less than 1% of samples. This is a small rate but could have a big impact on the case overall. As long as QPS understand this and that they need to consider that "Spermatozoa were not observed…" does not mean there is no sperm and that about 1% of the time this could be a false negative and they could consider re-testing/further submissions etc… then that is OK. The examination processes described throughout this report, as well as the resulting DNA profile, the assessment of the whole case, and the ability to submit for processing any samples not actioned, aims to mitigate the risk that may arise when spermatozoa is not detected at the examination step. Continuous process improvements are imbedded in Forensic DNA Analysis and are part of our quality management system, and improvements to the examination of sexual assault process will continue, as they will with all processes within the unit, to ensure any risks are mitigated as much as practical. (???)

PB136

Fletcher, Caitlin 67002

From: Paula Brisotto <[redacted]>
Sent: Tuesday, 15 August 2017 1:28 PM
To: Justin Howes
Subject: Data analysis report
Attachments: Data Analysis report (2)KDR.doc; Data Analysis report_draft1 - LBR track changes_ MOH track changes.doc; Data Analysis report_draft1 - LBR_ MOH_PMB.doc

Hi Justin,

I've had a meeting with Cathie about the feedback received and where to from here.

We are on the second round of feedback, and both Matt, Kylie and Luke have provided theirs. From here, Cathie has requested your involvement, so we can try and take on board some feedback, while trying to keep the data analysis within scope. I am hoping from your experience with sexual assault examination and interpretations, you can provide some wording within the document, so we can all get to a point where we are happy with the content, the assessment and the summary. I think I am too close/getting fatigued with this, and I would like a fresh set of eyes/approach to looking at this report.

Please find attached:
1 – Kylie's feedback
2 – Matt's feedback
3 – my updates from Matt's feedback.

Unfortunately, I didn't get to spend much time doing this today. If you are able to have a look over these documents, and provide wording suggestions/improvements or alternative words, please have at it ☺

I have kept in 'systemic failure', as I still feel that this was the concern on my return, and is an evaluation of the data – similar to what we did with the MPII investigation, with the outcome not showing a systemic failure of the instrument.

I am also not sure if the scope is clear, and if the assessment of the case as a whole (e.g. submit any NFA samples or read diff slides if DNA profile indicates male in sperm fraction etc) is clear enough.....

Many many thanks,
Paula

Paula Brisotto
Team Leader – Evidence Recovery and Quality Team, Forensic DNA Analysis, Police Services Stream
Forensic & Scientific Services,
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PB137

Fletcher, Caitlin 67002

From: Justin Howes <[redacted]
Sent: Tuesday, 13 April 2021 11:34 AM
To: Kylie Rika; Paula Brisotto; Luke Ryan
Subject: RE: Proposal #199 - Verification of Proflex for PP21

Hi
Thanks for this Kylie. This will be for me to ask of the current trainers to discuss. I think this element is not within a verification of the Proflex, more how its use fits within the system – so for me, more of an implementation task if anything.

I will put some questions to the trainers for consideration and recommendation.

Thanks
Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

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

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

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From: Kylie Rika <[redacted]
Sent: Tuesday, 13 April 2021 11:00 AM
To: Paula Brisotto <[redacted] Luke Ryan <[redacted] Justin Howes <[redacted]
Subject: RE: Proposal #199 - Verification of Proflex for PP21

Hi all

Paula had a chat with me on Friday and here are some further thoughts:

Are we looking to validate just one Proflex then say that the rest are ok (if that validation is OK)? If yes, then maybe its OK to check the following on just the one proflex (I would be keen to get advice from our STRmix trainers):

Model Maker (peak height variance parameters)

Performance check using profiles that have been tested using the new thermal cyclers. Zane mentions two approaches for this below:

- If you still have the DNA extracts of the mixtures used during your STRmix validation you could re-amplify a sub-set of these (20-30 mixtures of varying complexity/template amount) using the new thermal cyclers, interpret the resulting profiles in STRmix, then compare the LRs assigned for true donors & non-contributors back to the original result.
- If these extracts are no longer available, you could prepare some new mixtures, interpret in STRmix, and examine sensitivity (for true donors) and specificity (for non-contributors) as a function of per contributor average peak height.

I would also be keen to see what the STRmix trainers think about this work as part of validation or at implementation stage.

Justin, do you want me to set up a meeting with the STRmix trainers or will you do that?

Thanks

Kylie

From: Kylie Rika
Sent: Wednesday, 7 April 2021 5:29 PM
To: Paula Brisotto <[redacted] Luke Ryan <[redacted] Justin Howes <[redacted]
Subject: RE: Proposal #199 - Verification of Proflex for PP21

Hi all

Please bear with me as I write down some thoughts:

With the introduction of STRmix, the question of when to conduct end to end whole system verification is a more crucial consideration than ever before given the way STRmix uses the variances.

In the old days we could get away with just intuitive assessment of the profile results after verifying a new instrument. We can't do that anymore with STRmix.

The advice from Zane Kerr (see attached) pretty much sums up why we need to re-run MM. Whether we do it now or prior to implementation doesn't matter but other than for BCP purposes, I can't see the benefit of not doing it as part of the verification. Is there a rush because the 9700s are about to die?

It's a shame all the STRmix trainers are away this week but I am interested in their feedback on MM now or at implementation.

Thanks
Kylie

From: Paula Brisotto <[redacted]
Sent: Wednesday, 7 April 2021 10:07 AM
To: Luke Ryan <[redacted] Kylie Rika <[redacted] Justin Howes <[redacted]
Subject: RE: Proposal #199 - Verification of Proflex for PP21

Hi all,

I am wondering if this question re: MM is more for an implementation phase, instead of the verification of the instruments?

My thoughts are - the instrument verification can proceed as per the experimental design (including updates as an outcome of the combined feedback), and MM can be part of the implementation stage, as required.

With respect to running MM on each Proflex, I do not believe this is necessary as we have never done this previously, and should all Proflex's be assessed as fit for purpose, then my thinking is it will not matter which instrument MM is run on…. This is my understanding at present, so if advice has changed, happy for this to be a further discussion wrt implementation for these and as part of future verifications.

I think given all of the STRmix trainers are currently on leave, this part of the implementation can be put to that group next week for input, with the verification to proceed as is (with reference to any requirements for STRmix as part of the implementation).

If this seems a good way forward, Justin can you coordinate this discussion with the STRmix trainers for feedback to management team?

Thanks,
Paula

From: Luke Ryan <[redacted]
Sent: Thursday, 1 April 2021 1:45 PM
To: Kylie Rika <[redacted]
Cc: Paula Brisotto <[redacted] Justin Howes <[redacted]
Subject: RE: Proposal #199 - Verification of Proflex for PP21

Hi Kylie
I sought your input on the proposed experiments because FRIT are the STRmix SMEs and better placed than me to design the STRmix experiments.

Given this external advice has the potential to change the way we validate/verify all instruments/techniques I'll refer this advice to JAH and PMB for further discussion with the Mgt Team.

Thanks
Luke

From: Kylie Rika <[redacted]
Sent: Thursday, 1 April 2021 1:26 PM
To: Luke Ryan <[redacted]
Cc: Paula Brisotto <[redacted] Justin Howes <[redacted]
Subject: RE: Proposal #199 - Verification of Proflex for PP21

Hi Luke

This is your project and I have done what was asked – to provide feedback. You further asked me to coordinate the STRmix advice as this would form part of my feedback. I have done that.

If the feedback is not in line with where you were hoping the project would go, then it is now an item for mgmt. team discussion/decision.

I have fulfilled my role as reviewer of the experimental design

Thanks
Kylie

From: Luke Ryan <
Sent: Thursday, 1 April 2021 1:00 PM
To: Kylie Rika <
Cc: Megan Mathieson < Generosa Lundie
< Paula Brisotto < Justin Howes
<
Subject: RE: Proposal #199 - Verification of Proflex for PP21

Hi Kylie
Excellent thanks. Do you support this advice – you didn't specify? If yes, as this may be a large body of work (i.e. potentially model maker runs for each new Proflex) I think this needs to go to Mgt Team for review. To enable this, can you please propose new experiments or modifications to existing experiments which you consider would satisfy this advice? Can you please be specific in your proposed experiments and include intent, experimental design and acceptance criteria so if approved it can be inserted directly into the Experimental Design. I will provide these experiments to the Mgt Team for discussion and feedback.

Thanks
Luke

From: Kylie Rika <
Sent: Thursday, 1 April 2021 12:31 PM
To: Luke Ryan <
Cc: Megan Mathieson < Generosa Lundie
<
Subject: RE: Proposal #199 - Verification of Proflex for PP21

Thanks Luke

Emma has access to the STRmix support site so I asked her to get some advice from them.

The advice is attached.

Thanks
Kylie

From: Luke Ryan <
Sent: Wednesday, 31 March 2021 3:09 PM
To: Kylie Rika <
Cc: Megan Mathieson < Generosa Lundie
<
Subject: RE: Proposal #199 - Verification of Proflex for PP21

Hi Kylie
I've put together responses for your feedback. I appreciate there is a lot of info so if any of this is unclear and you want to discuss let me know. The second revision of the Exp design will include a range of changes and will hopefully address your feedback.

Response – Validation vs Verification
We used the NATA 'General Accreditation Guidance – Validation and verification for quantitative and qualitative test methods" (January 2018) to determine whether a verification or validation was required. This NATA document is

based on ENSFI and other relevant standards. See Appendix 1 for decision tree (and below). When we worked through the workflow it could go through two pathways (see below, I have highlighted the pathways I thought were relevant). I have explained our reasoning for the two paths we took below.

Yellow path:

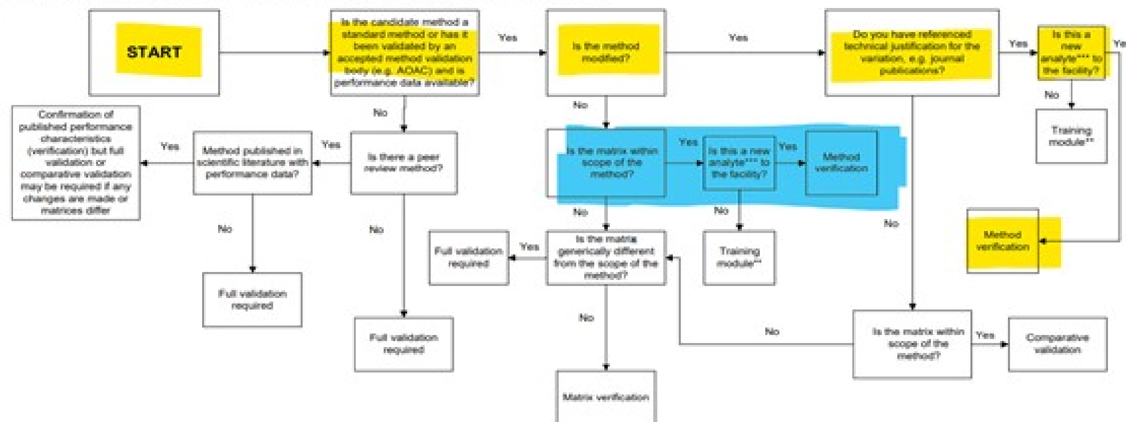
1. Is the Candidate method…: Yes - PCR amplification has been previously validated internally and by Promega using the same thermal cycling parameters as will be used on the Proflex albeit on the 9700. Proflex will be used with 9700 emulation mode which mimics the ramping/thermal cycling characteristics of the 9700.
2. Is the method modified: Yes – Proflex is a new instrument (or analyte – based on definition of analyte in the NATA doc). N.B. this is the point where the yellow and blue paths diverge. I think you could justify a yes/no answer for this.
3. Is this a new analyte to the facility – Yes, Proflex is the analyte being tested and it is new to the facility.

Blue Path

1. Is the method modified – based on my reading of the document I don't think the method is modified. Thermal cycling parameters are not modified. Reagents are not modified. Thermal cycling conditions are not modified based on use of 9700 emulation mode. This position is justified given the next question allows you to indicate the Proflex is new to the facility (i.e. having a new instrument doesn't necessarily mean the method is modified).
2. Is this a new analyte to the facility: Yes – Proflex are a new instrument

The Yellow and Blue paths both lead to a verification. Based on this assessment the testing of the Proflex was as a verification and not validation.
The Experimental Design will be updated to include more details on the 9700 emulation mode on the Proflex and how this is designed to replicate the thermal cycling conditions (specifically the ramp rates) on the 9700s which were used for development and validation of PP21.

Appendix 1. Method validation and verification decision tree



Response - From the ENSFI guidelines I note that for a new thermal cycler model, it is suggested that a number of samples previously profiled are repeated using the kit in question.
Staff samples which have been previously run in PP21 on the 9700s will be analysed. We can determine allele call concordance however I think it would be difficult to determine whether other observed variation (i.e. peak height difference) is due to the Proflex vs 9700 or extract variation amp to amp (as observed in VFP validation testing of mixing), STARlet variation in amp preparation, STARlet variation in CE prep and 3500xL CE variation. It is possible to look at macro variations, i.e. amplifying at 0.5 ng template and getting partial/XS results which would indicate critical failure.

Response - Sensitivity
Based on your and other feedback a range of DNA template inputs will be included in the Casework plate run on each Proflex. This will simulate "real" casework samples which have a range of input templates. This will enable us to assess amplification at a range of inputs.

Response - Repeatability and Reproductivity

These are requirements for validations and so were not included in this verification. The same casework amp and will be run on each Proflex, and results can be compared.

The data analysis and acceptance criteria are being expanded to included among other things comparison of results between Proflex instruments. This does provide a form of repeatability/reproducibility assessment.

Response - Homogeneity of heating block
This is assessed during the Proflex PMs, last conducted on 22-09-2020. A report for each Proflex is in the FR against each respective Proflex. Assessing block accuracy and uniformity using the t-POD probe is the most accurate method as it measures the temperature of each well. This is more accurate than using CE results block performance as it would be difficult to determine whether observed variation is due to the Proflex, extract variation amp to amp, STARlet variation in amp preparation, STARlet variation in CE prep and/or 3500xL CE variation.

FDNA and/or BTS do not have the t-POD device and therefore we cannot assess this ourselves.

Response - I also think we need to get advice from the STRmix support group to see if we need to do MM again etc..
Can you please coordinate this advice as this would form part of your feedback.

Response - I don't think we can rely just on intuitive qualitative comparisons, we need some form of statistical analysis. I suspect we may need to re-do b/line, stutter, assess locus efficiency (APH for each sample across each locus) etc
We are expanding on data analysis and acceptance criteria to include more quantitative measures: assess stutter thresholds and compare the thresholds, assess AI, minus A, PCR arts, inter-locus balance etc.

Baseline – reassessing baseline is required after changes to the optical components of the 3500xL are made (i.e. laser, CCD camera) as it is measure of the background fluoresce produced by the genetic analyser optical components. I am not aware of any requirement to redo baseline for a new thermal cycler – or thermal cyclers. If you have a reference can you please provide and I will disseminate to the Management Team for consideration given this would be a large project to redo baseline for one or all of the new Proflex.

Stutter, assess locus efficiency – as per above we will include additional quantitative measures in the data analysis and acceptance criteria.

Thanks
Luke

From: Kylie Rika <
Sent: Tuesday, 23 March 2021 2:40 PM
To: Luke Ryan <
Subject: RE: Proposal #199 - Verification of Proflex for PP21

Hi Luke

Feedback as follows:

I think we need to do more than what is currently listed in the proposal. From the ENSFI guidelines I note that for a new thermal cycler model, it is suggested that a number of samples previously profiled are repeated using the kit in question. They further recommend that the selected samples will obviously allow examination of parameters such as reproducible results, including from mixtures and low DNA concentration samples. For a new thermal cycler that is of the same model as others already in use, a certificate from the manufacturer detailing a technical performance check done after installation in the lab and an internal sensitivity and homogeneity check would be sufficient.

I note from thermofisher that the ProFlex and 9700 are different models. Therefore, we need the following minimum parameters to be validated :

- Sensitivity (limit of detection) : a series of dilutions tested in three replicates.

- Repeatability : the three replicates of the same sample, distributed over the entire heating block can be used to evaluate the repeatability.

- Reproducibility : 3 repetitions of the amplification reactions used in the sensitivity test.

- Homogeneity of heating block : temperature control
of the heating block or a comparison
of the replicates allows the evaluation of the homogeneity of the heating block.

I also think we need to get advice from the STRmix support group to see if we need to do MM again etc..

I don't think we can rely just on intuitive qualitative comparisons, we need some form of statistical analysis. I suspect we may need to re-do b/line, stutter, assess locus efficiency (APH for each sample across each locus) etc

Thanks
Kylie

From: Luke Ryan <
Sent: Monday, 22 March 2021 12:23 PM
To: Allan McNevin < Allison Lloyd < Cathie Allen < Justin Howes < Kirsten Scott < Kylie Rika < Paula Brisotto < Sharon Johnstone <
Cc: Generosa Lundie < Megan Mathieson <
Subject: Proposal #199 - Verification of Proflex for PP21

Afternoon All
Please see the attached Experimental Design for the verification of the Proflex thermal cyclers for PP21. Can you please provide feedback by COB Monday 29/03/2021.

Thanks
Luke

Luke Ryan
Senior Scientist – Analytical Team

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