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

ADDENDUM STATEMENT OF DAVID HAROLD NEVILLE

I, **David Harold Neville,** of 200 Roma Street, Brisbane, Queensland state as follows:

The following statement is provided in response to a notice I received from the Commission of Inquiry into Forensic DNA Testing in Queensland requiring me to give information in a written statement regarding my knowledge of matters set out in the Schedule attached to that notice. Attached and marked '**Exhibit 187'** is a copy of that notice.

Advice about reporting from Queensland Health

1. I have no information, other than what appears in my original statement dated 26 August 2022 ('Original Statement'), in relation to advice from the DNA laboratory on the use and the meaning of "DNA insufficient for further processing" as reported in the FR and witness statements. That information included details about the Options Paper and subsequent emails between Cathie Allen and I which are all attached as exhibits to that statement.

2. I have had no specific advice from the DNA laboratory explaining the use and the meaning of "No DNA Detected".

3. I have no file notes in relation to or minutes of the meeting held on 15 January 2019. The detail provided in my Original Statement has exhausted my memory of the event.

4. I am aware that since that meeting staff from the DNA Management Section, including Sgt Libby Harris and Sgt Carolyn Hoffman, have worked with members of QHFSS, including Justin Howes, to reduce the number of result lines reported and to simplify their content. Much of this occurred between June 2021 and July 2022. Together they managed to reduce the number of types of results from 253 to 76 in a proposed new reporting scheme. A copy of the proposed reporting scheme is attached and marked **'Exhibit 188'.**

[redacted]
....
David Harold Neville

[redacted]
....
Witness

5. The proposed reporting scheme is yet to be introduced. Justin advised QPS in an email dated 20 July 2022 that QHFSS did not have time to progress the new reporting scheme. A copy of the email is attached and marked **'Exhibit 189'.**

6. Copies of relevant correspondence regarding the introduction of the proposed reporting scheme are attached and marked **'Exhibits 190 to 194'.**

Advice about reporting to Office of the Director of Public Prosecutions.

7. I am not aware of any communications provided by the QPS to the Office of the Director of Public Prosecutions explaining the meaning of the phrases "DNA insufficient for further processing" and "No DNA Detected". The provision of such information would need to be provided by QHFSS as they report those results and hold the expertise in that area.

QPRIME

8. Part 8 of the Options Paper dated January 2018 indicates that QHFSS would commence reporting results in the microconcentration range as "DNA insufficient for further processing". This was agreed to by QPS on 2 February 2018, as detailed in paragraphs [96] and [97] of my Original Statement.

9. I have been provided with two emails by Ms Olivia McIntyre. These emails indicate the series of events that led to the expanded wording of the result "DNA Insufficient for further processing". In an email dated 12 February 2018, Justin Howes of QHFSS formulated the expanded wording and sent it to Troy O'Malley, QPS, for inclusion in the FR-QPRIME interface (i.e. The FR-QPRIME interface is a term that I use to describe the functionality within the FR that transfers information to QPRIME, it includes preformatted wording that is populated with details of the relevant sample identifier and details of of any persons identified). The wording developed by Justin was:

   (a) "DNA INSUFFICIENT FOR FURTHER PROCESSING. This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling. Please contact

Forensic DNA Analysis if this sample is requested to be assessed for further processing."

Ms Olivia McIntyre then discussed a change to the wording so that requests for further processing were managed by the QPS DNA Management Section rather than QHFSS. The wording was changed to:

(b) "DNA INSUFFICIENT FOR FURTHER PROCESSING. This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling. Please contact the DNA Management Section if this sample is requested to be assessed for further processing via QPRIME task to Unit Code 3209".

The relevant email correspondence is attached and marked **'Exhibits 195 and 196'**.

10. In January 2019, Gerard Simpfendorfer negotiated a change with QHFSS to the expanded wording for "DNA insufficient for further processing" results. This was in response to concerns that I raised on 14 November 2018 about the reporting process, as detailed in paragraphs [162] to [170] of my Original Statement. The purpose of the new wording was to ensure investigators were aware of the testing options available to them. The expanded wording was as follows:

(a) "DNA INSUFFICIENT FOR FURTHER PROCESSING. This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling. Please contact the DNA Management Section if this sample is requested to be assessed for further processing. Further processing could include concentration of the low levels of DNA obtained, pooling with other samples (where appropriate), resampling of the parent item (where appropriate), or a combination of processes".

Copies of emails provided to me by Senior Sergeant Gerard Simpfendorfer that include conversations with QHFSS during the development of the amended wording are attached and marked **'Exhibits 197 and 198'**.

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

David Harold Neville Witness

11. According to FR records, the first result of 'No DNA Detected' was received by the QPS in about June 2011. I have been provided an email dated 3 January 2013 authored by Scott McLaren. Scott previously worked at the QPS DNA Management Section. I discussed the content of the email with Scott on 7 September 2022. As a result, I am aware that the original wording developed by QHFSS was:

    (a) NO DNA DETECTED. This item/sample was submitted for DNA analysis; however no DNA was detected above the limit of detection at the quantitation stage. No further processing was conducted on this item. QPS can submit a request to QHFSS for a continuation of this processing if required.

    On, or just prior to, 3 January 2013 the result wording was changed to:

    (b) NO DNA DETECTED. This item/sample was submitted for DNA analysis; however no DNA was detected above the limit of detection at the quantitation stage. No further processing was conducted on this item.

    Scott told me the reason for the change was that a person at QHFSS had advised there was no chance of getting a result from such samples. The email pertaining to this issue is attached and marked **'Exhibit 199'**.

Decision on 6 June 2022

12. As outlined in paragraph [210] of my Original Statement, on 30 May 2022 I advised Lara Keller and Cathie Allen by email that "the QPS is no longer comfortable with the automatic discontinuation of testing of samples below the .008ng/uL threshold". I did not receive a response.

13. On 6 June 2022 I watched a live television broadcast where the Premier of Queensland and Minister for the Olympics, and the Minister for Health and Ambulance Services announced the Commission of Inquiry and that the threshold for testing was to be dropped. As far as I am aware, no one in the QPS was consulted in relation to this announcement.

[redacted] [redacted]

David Harold Neville — Witness

14. There is an error in paragraph [232] of my Original Statement. The email from Lara Keller advising that they were no longer reporting the result *Insufficient DNA* was sent on 21 June 2022, not 6 June 2022; however, the advice provided to QPS suggested that this change occurred / took effect as of 6 June 2022. Lara advised that all samples with a concentration above 0.001ng/uL would be profiled. This information was contained in an email to Bruce McNab that was forwarded to me. Attached and marked **'Exhibit 200'** is a copy of that email.

15. Other than advising Queensland Health via email that QPS was no longer comfortable with stopping testing of samples in the range as outlined in paragraph [12] I had no involvement in the 6 June 2022 decision to remove the threshold to report samples as "DNA insufficient for further processing". I later became concerned that this decision resulted in samples in the range being processed without concentration as outlined in paragraph [20]. I do not know why that option was chosen. The only information I have is that which was later provided by Helen Gregg as outlined in paragraph [22].

16. As outlined in paragraph [167] of my Original Statement, I had been advised by Cathie Allen that automatic concentration of samples in the range will result in all extract being consumed. In an email Cathie sent on 15 November 2018 she was unequivocal stating, "A*utomatic progression of samples through the Microcon process means that all available DNA extract will be consumed, so no further testing can be conducted on these samples after this step. This means that if a sample could yield a profile by specific Y chromosome testing for example, there would be no extract available for that testing to be conducted. It also means that samples that are eligible to be pooled together, as they are from the same item or area, are not able to be as there is no DNA extract left to undertake pooling.*" Based on this advice I did not pursue the reintroduction of automatic microconcentration.

17. On 24 June 2022, Lara sent Bruce an email that included a report titled, "*Assessment of Low Quantification Value DNA Samples*". Bruce forwarded the email to me for comment. The attached report presented some options for testing low quant samples including:

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

David Harold Neville Witness

(a) Continuing the current workflow;

(b) Reducing the threshold for DNA Insufficient to a lower level with samples in the new range being concentrated and processed on request;

(c) Concentrating P1 and P2 samples in the existing or new range whilst P3 are processed without concentration;

(d) Concentrating P1 samples in the existing or new range whilst P2 and P3 are processed without concentration.

I replied to Bruce advising him that I was not in favour of any of the options. I advised him that my preference was to:

(e) Maintain a 'stop testing threshold' for volume crime matters, however potentially decrease it; and

(f) Introduce a threshold for major crime that is not a hard bar. At that threshold the scientist would make analytical decisions (including assessment of photos, presumptive screening results and QuantTrio values) on how best to process the sample to maximise the opportunity of profiling success.

I do not know if my reply to Bruce was forwarded to QHFSS and I was not advised of a response from QHFSS. The email chain and report appear as '**Exhibits 73 and 75'** to my Original Statement.

18. On 15 July 2022, I met with Acting Superintendent Darren Pobar and Acting Assistant Commissioner Marcus Hill to discuss my concern that the new workflow might unduly impact on turnaround times. At that time, I was of the belief that all samples in the low concentration range, including volume crime samples, were being microconcentrated. It was decided that Darren would send an email to QHFSS requesting that they advise what strategies they had in place to minimise backlogs. Darren sent the email later that day to Acting Executive Director Helen Gregg, QHFSS. He copied me into the email.

[redacted] [redacted]

David Harold Neville Witness

19. On or before 20 July 2022, Olivia McIntyre advised me that Alison Lloyd from QHFSS had told her that all samples in the low concentration range were being processed without microconcentration.

20. I was concerned about processing low concentration samples without microconcentration because the Options Paper stated that samples in this range were subject to stochastic effects making obtaining a reliable profile problematic. This appeared to be contrary to the laboratory's validation study cited in the Options Paper. I was concerned that, by doing this, they were wasting extract and diminishing any opportunity to obtain a result.

21. I raised this as a concern to Darren on 20 July 2022 and he sent an email to Helen Gregg asking what the new process was and if samples might benefit from concentration.

22. I am aware that Helen Gregg replied to Darren on 20 July 2022 stating, "The DG requested options for processing that did not include the 'DNA insufficient' process. Options were provided and the Premier announced Cabinet had decided the DNA insufficient process was no longer to be used and all samples were being processed. From this we take it that Premier and Cabinet did not appear to choose the option that included concentration of samples with a particular range, given potential workplace health and safety issues." Darren forwarded me Helen's response on 17 August 2022.

23. On the morning of 17 August 2022, I sent an email to Helen asking if there was a risk that profiles may be missed due to the lack of microconcentration and requested information on the policy that might trigger microconcentration to occur.

24. At about 2pm on 17 August 2022 I received a message via email from one of my staff to call Matt Rigby from Queensland Health (QH). I returned the call and he told me that he and Mr David Rosengren wanted to talk to me and that he would call me back. They called me back on my mobile telephone. I assumed the telephone call would relate to the issue of QHFSS witness statements reporting the result of 'Insufficient DNA' as I had been nominated as the key point of contact within QPS for that matter.

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

David Harold Neville Witness

25. I was not fully aware of who either David or Matt were when they called. I now know that David was the Acting Director-General, QH. David asked me to approve or support a directive to the laboratory to automatically microconcentrate samples in the 0.001-0.0088 ng/uL range. I advised that the Managing Scientist had warned that the microconcentration of all samples in the range would consume the extract leaving no opportunity for further testing. I told him I suspected now this was untrue given concentration produced 35uL and they only needed 15uL for testing, however, I advised I was not in a position to really know. They requested I provide advice on the process QPS wanted. I told them I would consult and get back to them.

26. I met with Acting Assistant Commissioner Marcus Hill and we discussed the request. We agreed that QH were the experts and that it was up to them to provide us with advice on the best process to follow.

27. I called Matt Rigby back and advised I was hesitant to accept risk for a QH decision given I had no expertise to advise on best practice. I told him I was still consulting and would get back to him.

28. At about 7pm I received an email from Matt that included a draft memorandum to the laboratory. The email is attached and marked **'Exhibit 201'.**

29. I responded to Matt by email on 19 August 2022 thanking them for the chance to comment on the draft procedure. I advised that the risk of the draft was that it may result in a sample being exhausted, making alternative testing impossible. I advised this was a risk that could not be assessed by the QPS. I said that this was an internal decision that QH had to make in the context of the QPS holding a desire to maximise the potential to obtain a profile from every sample, whether by services delivered by QH or another provider (if QH was not able to deliver that service). The email is attached and marked **'Exhibit 202'.**

30. At 3:42pm on 19 August 2022, Helen Gregg sent me an email (responding to my email dated 17 August 2022) advising that all P1 and P2 samples in the concentration range of 0.001-.0088ng/uL would be concentrated down to 35uL and undergo one

[redacted] [redacted]

amplification process. The full email trail including the previous discussions between Darren and Helen is attached and marked **'Exhibit 203'**.

31. At 4.30pm on 19 August 2022, Matt responded by email and provided me with a copy of the signed memorandum addressed to Helen Gregg. The memorandum indicated that the sample should be concentrated to 35uL and undergo one amplification process. It instructed that QPS must be consulted if additional testing might exhaust the sample. The email is attached and marked **'Exhibit 204'.**

32. On 7 September 2022, I had a telephone conversation with [redacted] She reached out to me through Olivia McIntyre wanting to raise concerns with QPS about the recent decision to concentrate all low concentration samples to 35uL. With her permission I recorded the conversation. Olivia was also in the room on speaker phone. [redacted] raised some concerns about the directive issued by the Acting Director-General of QH and that the microconcentration of all samples to 35uL was resulting in the potential loss of probative evidence. Additionally, she raised issues around the data included in the Options Paper, the impact it had on testing and the attitude of QHFSS management when such concerns were raised internally. A copy of the transcript of that recording is attached and marked **'Exhibit 205'**.

33. On 8 September 2022, I sent an email to Matt Rigby outlining QPS' concerns about the testing process adopted at QHFSS as a result of the directive sent by the Acting Director-General of QH on 19 August 2022. The concerns raised in my email were based on the advice received from [redacted] including the blanket microconcentration of samples in the range to 35uL. A copy of the email is attached and marked **'Exhibit 206'**.

34. Other than what is detailed in this statement, I had no other involvement in any of the decisions made on or about 6 June 2022 or 19 August 2022. I do not know who made the decisions, when they were made, the reasons for the decisions, or the material information the decisions were based on.

[redacted]

David Harold Neville

[redacted]

Witness

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

……[redacted]……………………………… ……[redacted]……………………

David Harold Neville   Witness

COMMISSIONER FOR DECLARATIONS
Reg.No.: 17182
DEPT. OF JUSTICE & ATTORNEY-GENERAL

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

David Harold Neville   Witness

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

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STATEMENT OF DAVID HAROLD NEVILLE
INDEX TO EXHIBITS

Exhibit no.	**Description**
187.	Notice number 2022/00136 – Requirement to give information in a written statement – dated 06/09/2022
188.	Spreadsheet of proposed reporting scheme – undated
189.	Email chain between Carolyn Hoffman (QPS) and Justin Howes (QHFSS) – dated 20/07/2022
190.	Email from Olivia McIntyre (QPS) to Paula Brisotto (QHFSS) and Justin Howes (QHFSS) – dated 01/07/2021
191.	Email from Olivia McIntyre (QPS) to Justin Howes (QHFSS), Allison Lloyd (QHFSS) and Adrian Pippia – dated 21/07/2021
192.	Email from Justin Howes (QHFSS) to Stephan Foxover (QPS), Libby Harris (QPS) and Olivia McIntyre (QPS) – dated 22/07/2021
193.	Email from Olivia McIntyre (QPS) to Allison Lloyd (QHFSS) – dated 09/09/2021
194.	Email chain between Olivia McIntyre (QPS), Justin Howes (QHFSS) and Allison Lloyd (QHFSS) – dated 08/09/2021
195.	Email chain between Olivia McIntyre (QPS), Ewen Taylor (QPS) and Libby Harris (QPS) – dated 09/02/2018
196.	Email from Olivia McIntyre (QPS) to Justin Howes (QHFSS) – dated 02/03/2018
197.	Email chain between Gerard Simpfendorfer (QPS) and Cathie Allen (QHFSS) – dated 19/11/2018
198.	Email chain between Gerard Simpfendorfer (QPS) and Cathie Allen (QHFSS) – dated 20/11/2018
199.	Email from Scott McLaren (QPS), Danielle Ayscough (QPS), Patricia Holden (QPS), Gerard Simpfendorfer (QPS), Emma Whittle (QPS), Marney Nauschutz (QPS) and Olivia McIntyre (QPS) – dated 03/01/2013
200.	Email from Lara Keller (QHFSS) to Bruce McNab (QPS) – dated 21/06/2022
201.	Email from Matt Rigby (QH) to David Neville (QPS) – dated 17/08/2022
202.	Email from David Neville (QPS) to Matt Rigby (QH) – dated 19/08/2022
203.	Email from Helen Gregg (QHFSS) to David Neville (QPS) – dated 19/08/2022
204.	Email from Matt Rigby (QH) to David Neville (QPS) – dated 19/08/2022

Exhibit no.	Description
205.	[redacted]
206.	Email from David Neville (QPS) to Matt Rigby (QH) – dated 08/09/2022

EXHIBIT 187

Notice number: 2022/00136

COMMISSION OF INQUIRY INTO FORENSIC DNA TESTING IN QUEENSLAND

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

REQUIREMENT TO GIVE INFORMATION IN A WRITTEN STATEMENT

To: David Neville

Of: Queensland Police Service

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

YOU MUST COMPLY WITH THIS REQUIREMENT BY:

Giving a written statement signed and witnessed as a declaration in accordance with the *Oaths Act 1867* to the Commission of Inquiry on or before **12.00pm on 12 September 2022** by delivering it to Level 21, 111 George Street, Brisbane.

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

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

DATED this 6th day of September 2022

[redacted]

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

Notice number: 2022/00136
Schedule of topics for statement
Inspector David Neville
Queensland Police Service (QPS)

Advice about reporting from Queensland Health

1. Explain and provide copies of all communications (whether verbal or written) from management of the DNA laboratory to the QPS since 2018 explaining the use and meaning of "*DNA insufficient for further processing*", or words to similar effect, as reported in:
    a. the forensic register; and
    b. witness statements.
2. Explain and provide copies of all communications (whether verbal or written) from management of the DNA laboratory to the QPS since 2018 explaining the use and meaning of "*No DNA Detected*", or words to similar effect, as reported in:
    a. the forensic register; and
    b. witness statements.
3. At [146] – [150] of your statement dated 26 August 2022 you refer to a meeting with Cathie Allen and other QHFSS employees on 15 January 2019. Further:
    a. provide a detailed account of what was said at the meeting;
    b. provide any file notes or other records of the meeting on 15 January 2019; and
    c. explain what changes were made as a result of QPS and QHFSS working together "*to consolidate the number of result lines used*" ([147]).

Advice about reporting to Office of the Director of Public Prosecutions

4. Explain and provide copies of all communications (whether verbal or written) in which the QPS provided formal advice to the Office of the Director of Public Prosecutions, and related material explaining the use and meaning of the following words, or words to similar effect, as reported in QHFSS witness statements:
    a. "*DNA insufficient for further processing*"; and

   b. "*No DNA Detected*".

QPRIME

5. Explain how the wording and explanation used in QPRIME to describe a sample reported in the Forensic Register as "*DNA insufficient for further processing*" was developed between 2018 and August 2022, including:
   a. when it was developed;
   b. who was involved in developing the wording;
   c. what materials were considered in developing the wording;
   d. any changes to that wording and what those changes were based on.
6. Explain how the wording and explanation used in QPRIME to describe a sample reported in the Forensic Register as "*No DNA Detected*" was developed between 2015 and August 2022, including:
   a. when it was developed;
   b. who was involved in developing the wording;
   c. what materials were considered in developing the wording;
   d. any changes to that wording and what those changes were based on.
7. Provide any internal correspondence, memorandum, briefing notes or similar document relating to the development of QPRIME entries displaying "*DNA insufficient for further processing*" or "*No DNA detected"* sample results since 2018.

Decision on 6 June 2022

8. Explain your involvement in two decisions made on or about 6 June 2022, namely:
   a. That the threshold for reporting samples as "DNA insufficient for further processing" be removed, and samples in the range 0.001–0.0088 ng/µL (**range**) be processed; and
   b. that some or all new samples in the range 0.001–0.0088 ng/µL will go directly for amplification rather than for concentration,

   including identifying:
   a. Your understanding of who made each decision, when it was made and on what information.
   b. What other options were considered as part of the decision-making process.

c. Your understanding at that time of sample concentration and the significance of omitting this step for the reliability of testing and/or the likelihood of obtaining profiles that are adequate for comparison to a reference sample for samples in that range, and the basis of your understanding.

d. Your understanding at that time of any other impacts of sample concentration, and the basis of your understanding.

e. The discussion or consideration of the difference between those two options, why they were offered and why one was preferred over the other.

f. What discussions or correspondence took place to consider each decision, who was involved and your role in those discussions or correspondence.

g. For any discussion or correspondence in which you were involved, identify the persons involved in those discussions or correspondence, what material was considered, what was said and by whom. Attach all notes made of discussions or correspondence.

h. Your understanding of the reasons for each decision, and for not choosing any other option presented, and the basis of your understanding.

i. Whether, to your knowledge, prior to the announcement of each decision, the options were communicated or discussed with scientists or management working within the DNA Analysis Unit, and if so, how, when and by whom.

j. Whether, to your knowledge, prior to the announcement of each decision, the options were communicated to, explained to or discussed with persons outside of the DNA Unit or Queensland Health, including the Queensland Police Service, the office of the Director-General for Health or any member of the Executive Government or their advisors, or any person whose interests might be affected by the carrying out of the relevant processes in the DNA Unit, and if so, who was involved and what was communicated, explained or discussed.

k. Whether, following either decision, your understanding of the options or decisions made have changed. Identify the basis for any change in your understanding.

Decision on 19 August 2022

9. Explain any discussion about or reconsideration of the decision of 6 June 2022 that occurred between 6 June 2022 and 19 August 2022 between you or other members of the QPS and management of the forensic DNA laboratory, FSS or Queensland Health and identify:

   a. Who was involved;

  b. What occurred in any correspondence or discussions, including by attaching correspondence and any notes, minutes or recordings of meetings or discussions;
  c. The reason for any discussion or reconsideration.

10. Explain your involvement in a decision made on or about 19 August 2022 formalised in a memorandum from A/Director-General of Queensland Health, Dr David Rosengren titled 'Reversion to concentration of all Priority 2 samples in range'. Explain your involvement in detail, with reference to material and information you had access to in relation to the decision, meetings, discussions or correspondence in relation to the decision, and others' contribution to the decision. Include in your answer your understanding of:
    a. Who made that decision;
    b. When the decision was made;
    c. The reasons for the decision;
    d. The reason for reconsidering the decision made on 6 June 2022, and how, when and by what means that reason came to your attention;
    e. The material or information on which the decision was based;
    f. The meetings, discussions or correspondence in relation to the decision.
11. In relation to the memorandum of 19 August 2022, explain the consultation undertaken by you or (to your knowledge) by members of the Department of Health, before or after the decision was made with any other members of the Queensland Police Service.
12. Describe any further discussions between members of the Department of Health and members of the Queensland Police Service following the decision on 19 August 2022 in relation to:
    a. The change in process from 19 August 2022;
    b. Turnaround times;
    c. The process of concentrating a sample, including any risks and benefits associated with concentration.

EXHIBIT 188

Mnemonic	**EXH Line**	**Expanded Comment**	Additional QPS information to be added	QPS notes 18/08/2021	Analytical / Reporting teams	FSS comments	QPS RMU Reporting Notes
SS	Single source DNA profile	The DNA profile obtained from this item/sample indicated the presence of one contributor.		To be used as an overaching line for single source results.		New line with no barcodes needed in associated barcode field	1. Received with SS1 with Linked Unknown & 1SSNCD - Auto Interface (unless LKR previously received in case) 2. Received with SS1 with Linked Unknown - Auto-Interface (Unless LKR previously received in case) 3. Received with SS1 with a Linked person barcode - Auto Update by RMU 4. Received with LR1-LR8; AC - Auto update by RMU
SS1	Single source DNA profile - Intel	The DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.		To be used for all single source unknown and intelligence link results that are validated. To be programmed in the same way as 1SS currently is to split the result wording depending if it is an unknown or intel barcode linked. QHFSS to have the ability to add either an unknown / intel barcode in linked field.	Reporting	No comment	1. Must be received with SS, if not to come into RMU worklist for review 2. Received with linked Unknown & 1SSNCD - Auto Interface (Unless LKR previously received in case) 3. Received with linked Unknown - Auto Interface (Unless LKR previously received in case) 4. Received with Linked Intel person barcode & 1SSNCD -Processed by RMU (Wait for LKR) 5. Received with Linked Intel person barcode - Processed by RMU (Cold link prev reported)
1SSNCD	NCIDD upload single source DNA profile	A single source DNA profile was obtained from the item/sample. This DNA profile has been selected for loading to NCIDD, and it will be searched against any DNA profiles held on NCIDD (as per the NCIDD matching rules). Further advice will be provided in the event a match is received.					1. Must be received with SS & SS1 or LR1-LK8 or AC. 2. Must not have anything in linked field. 3. Received with SS and SS1 with linked unknown - auto interface 4. Received with SS1 with Linked person barcode - Processed by RMU (Write off line) 5. Received with LR1-LR8; AC - Processed by RMU (Write off line)
NUP	Mix - NCIDD Upload	This item/sample yielded a DNA profile that matches the associated barcode, or has been designated as an Unknown profile. This DNA contribution has been uploaded to NCIDD for searching. If an Unknown profile was uploaded to NCIDD, further advice will be provided in the event a match is received.			Reporting	No comment	1. Must be received with MIX 2. Received with linked unknown - Auto Interface (Unless LKR previously received in case) 3. Received with Linked Intel person barcode - Processed by RMU (Wait for LKR) 4. Received with linked evidence person barcode - Processed by RMU (write off line)
MIX	Mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from at least two contributors.			Reporting	No comment	1. Received with NUP with Linked Unknown- Auto Interface 2. Received with NUP with Linked Unknown & LKR previously received in case - Auto-update by RMU 3. Received with NUP with a Linked person barcode - Auto Update by RMU 4. Received with LR1-LR8; AC - Auto update by RMU
LR1	Support for contribution: LR >100 billion	This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.			Reporting	No comment	1. Must be received with either SS or MIX 2. Received with Linked evidence barcode - Process by RMU (create RMR)
LR2	Support for contribution: LR 1 billion to 100 billion	This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.			Reporting	No comment	1. Must be received with either SS or MIX 2. Received with Linked evidence barcode - Process by RMU (create RMR)

LR3	Support for contribution: LR 1 million to 1 billion	This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.			Reporting	No comment	1. Must be received with either SS or MIX 2. Received with Linked evidence barcode - Process by RMU (create RMR)
LR4	Support for contribution: LR 100 000 to 1 million	This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.			Reporting	No comment	1. Must be received with either SS or MIX 2. Received with Linked evidence barcode - Process by RMU (create RMR)
LR5	Support for contribution: 10 000 to 100 000	This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.			Reporting	Agree with change	1. Must be received with either SS or MIX 2. Received with Linked evidence barcode - Process by RMU (create RMR)
LR6	Support for contribution: 1000 to 10 000	This DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.			Reporting	Agree with change	1. Must be received with either SS or MIX 2. Received with Linked evidence barcode - Process by RMU (create RMR)
LR7	Support for contribution: 100 to 1000	This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.			Reporting	Agree with change	1. Must be received with either SS or MIX 2. Received with Linked evidence barcode - Process by RMU (create RMR)
LR8	Support for contribution: 2 to 100	This DNA profile is between 2 and 100 times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.			Reporting	Agree with change	1. Must be received with either SS or MIX 2. Received with Linked evidence barcode - Process by RMU (create RMR)
LR9	Inconclusive	The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other reference samples may provide a different statistical interpretation.			Reporting	No comment	1. Must be received with MIX 2. Received with Linked evidence barcode - Process by RMU (create RMR)
LR10	Supports non contribution	The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.			Reporting	No comment	1. Must be received with MIX 2. Received with Linked evidence barcode - Process by RMU (create RMR)
AC	Assumed Contributor	Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this DNA profile. Given the assumption for this person, no statistical interpretation has been performed.			Reporting	No comment	1. Must be received with either SS or MIX 2. Received with Linked evidence barcode - Process by RMU (create RMR)
ACINT	Assumed contributor - Intel	For Intelligence purposes, it has been assumed that the designated unknown has contributed to this DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically evaluated against the DNA profile without a contribution being assumed and the result reported as a likelihood ratio.			Reporting	No comment	1. Must be received with either SS or MIX 2. Received with Linked Unknown - Process by RMU - either Auto update or Cold link prev reported)
REMINT	Contribution for NCIDD - Intel purposes	The DNA profile from the designated unknown sent with this exhibit report could be a contributor to the DNA profile along with the assumed known contributor. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.			Reporting	No comment	1. Must be received with either MIX 2. Received with Linked Unknown - Process by RMU - auto update 2. Received with Linked intel barcode - Process by RMU (create RMR)
CCUNK	Remaining contribution consistent with unknown	Based on this assumption, a remaining DNA profile has been separated. This is consistent with the unknown designation (previously identified within this case and loaded to NCIDD) sent with this exhibit report.			Reporting	No comment	1. Must be received with either MIX 2. Received with Linked Unknown - Process by RMU - auto update or Cold link prev reported - received on P1 cases
EVEX	Single evidence sample excluded	The statistical interpretation shows that the associated barcode sent with this exhibit report has been compared, and can be excluded as having contributed to this mixed DNA profile.			Reporting	No comment	1. Must be received with either MIX 2. Received with Linked evidence barcode - Process by RMU (create RMR)

INT1	Interim result - Intel NCIDD. Rework Required.	A DNA contribution has been uploaded to NCIDD for intelligence purposes only. Final results are pending.			Reporting	No comment	1. Must be received with either MIX 2. Received with Linked Unknown - Process by RMU - auto update
IRRFI	Intel report required for further information	The results for this item/sample require further explanation which will follow in an intelligence report.			Reporting	No comment	Processed by RMU - Intel report received via email from QHFSS.
CWBC	Consistent with being child of	The DNA profile obtained from this exhibit was consistent with being the biological child of the barcode sent with this exhibit report			Reporting	No comment	Processed by RMU - create RMR
NCWBC	Not consistent with being child of	The DNA profile obtained from this exhibit is not consistent with being the biological child of the barcode sent with this exhibit report.			Reporting	No comment	Processed by RMU - create RMR
SC1	Suspect check - support for contribution: LR 2 to 100	The DNA profile is between 2 and 100 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.			Reporting	No comment	1. Must be received with either SS or MIX 2. Received with Linked intelligence barcode - Process by RMU (create RMR)
SC2	Suspect check - support for contribution: LR 100 to 1000	This DNA profile is between 100 and 1000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.			Reporting	No comment	1. Must be received with either SS or MIX 2. Received with Linked intelligence barcode - Process by RMU (create RMR)
SC3	Suspect check - support for contribution: LR 1000 to 10 000	This DNA profile is between 1000 and 10 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.			Reporting	No comment	1. Must be received with either SS or MIX 2. Received with Linked intelligence barcode - Process by RMU (create RMR)
SC4	Suspect check- support for contribution: LR 10 000 to 100 000	This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.			Reporting	No comment	1. Must be received with either SS or MIX 2. Received with Linked intelligence barcode - Process by RMU (create RMR)
SC5	Suspect check - support for contribution: LR 100 000 - 1 million	This DNA profile is between 100 000 and 1 million times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.			Reporting	No comment	1. Must be received with either SS or MIX 2. Received with Linked intelligence barcode - Process by RMU (create RMR)
SC6	Suspect check- support for contribution: LR 1 million - 1 billion	This DNA profile is between 1 million and 1 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.			Reporting	No comment	1. Must be received with either SS or MIX 2. Received with Linked intelligence barcode - Process by RMU (create RMR)
SC7	Suspect check- support for contribution:LR 1 billion- 100 billion	This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.			Reporting	No comment	1. Must be received with either SS or MIX 2. Received with Linked intelligence barcode - Process by RMU (create RMR)
SC8	Suspect check - support for contribution: LR > 100 billion	This DNA profile is greater than 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.			Reporting	No comment	1. Must be received with either SS or MIX 2. Received with Linked intelligence barcode - Process by RMU (create RMR)
SC9	Suspect check inconclusive	The interpretation in relation to the nominated suspect is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other nominated suspects may provide a different interpretation. A reference evidence sample should be provided if this information is required in a statement for Court.			Reporting	No comment	1. Must be received with MIX 2. Received with Linked intelligence barcode - Process by RMU (create RMR)
SC10	Suspect check - supports non contribution	The statistical interpretation provides support for the proposition that the nominated suspect has not contributed to this DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.			Reporting	No comment	1. Must be received with MIX 2. Received with Linked intelligence barcode - Process by RMU (create RMR)

SC11	Suspect check - Excluded	The nominated suspect can be excluded as a potential contributor to the DNA profile obtained from this item/sample.			Reporting	No comment	1. Must be received with MIX 2. Received with Linked intelligence barcode - Process by RMU (create RMR)
CPU	Complex profile unsuitable for interp or comparison	This item/sample gave a complex DNA profile. This DNA profile is not suitable for meaningful interpretation due to either its complexity relating to the unknown and potentially large number of contributors and/or the limited amount of information within the DNA profile.			Reporting	No comment	Auto interface
IRSUR	Interim Result. Sample undergoing rework	This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.			Reporting	No comment	Auto interface
NDPPTP	No DNA profile – possible sub-threshold peaks	A DNA profile was not obtained from this item/sample, however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds.		Removed last sentence from expanded wording	Reporting	Agree - removal of last line is acceptable.	Auto interface
NOPRO	No DNA profile	A DNA profile was not obtained from this item/sample.			Reporting	No comment	Auto interface
NWQPSR	QPS advised no further work required - results available	QPS have provided advice that no further work is required for this item/sample. Please note that this item/sample has undergone DNA processing and results are available. These results may be Quantification results alone, or DNA profile results that have not been interpreted at this stage. QPS can submit a request to QHFSS for further work which may include the interpretation of the DNA results if required. results alone, or DNA profile results that have not been interpreted at this stage. QPS can submit a request to QHFSS for further work which may include the interpretation of the DNA results if required.			Reporting	No comment	Auto interface
PRNCID	DNA profile removed from NCIDD	The DNA profile obtained from this item/sample has been removed from NCIDD following advice from QPS, a change in the NCIDD category, or a profile with more information has been obtained.			Reporting	No comment	Processed by RMU - auto update
PSTI	Possible sub-threshold information	The presence of possible additional DNA was observed within the DNA profile obtained from this item. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. This sub-threshold information did not interfere with the interpretation of the reportable DNA components in the DNA profile obtained from this item.			Reporting	No comment	1. Must be received with SS or MIX. 2. Received with SS1 or NUP with linked unknown - Auto Interface (unless LKR previously received in case) 3. Received with SS1 with a Linked person barcode - Auto Update by RMU 4. Received with LR1-LR8; AC - Auto update by RMU
SPFRU	Sample processed and final results under	This item/sample was processed under the barcode sent with this exhibit report. The final results will be reported under that barcode.			Reporting	No comment	Processed by RMU - write off
SPP	Sample pooled and processed under	This item/sample was pooled and submitted for DNA testing under the barcode sent with this exhibit report. The final results will be reported under the barcode.			Reporting	No comment	Processed by RMU - write off
SUFP	This sample has undergone further processing	This item/sample has undergone further processing and an improved DNA profile has been obtained.			Reporting	No comment	Processed by RMU - write off
NSIP	No statistical interpretation performed	In the absence of a reference sample/s for comparison, a statistical interpretation has not been performed.	To nominate a person of interest for comparison to the mixed DNA Profile obtained from this exhibit, please send a task to the DNA Liaison and Major Crime Unit (3211)		Reporting	No comment	1. Must be received with MIX 2. Auto updated by RMU
TRQ	Testing restarted on advice from QPS	QPS have provided advice that testing is now required for this item/sample. Testing has been restarted.			Reporting	No comment	This is a movement line visible within the FSS Analysis table within the exhibit record
SRP	Submitted-results pending	This item/sample was submitted for DNA testing. Results are pending.		Change from exhibit movement to Auto filed examination result line.	Evidence Recovery	Evidence Recovery	This is a movement line visible within the FSS Analysis table within the exhibit record
PHNFA	Possible hair located – not examined further	Possible hair/s were located on this item/sample. These have not been examined further and have been retained with the exhibit.			Evidence Recovery	Evidence Recovery	Auto interface
PHNSA	Possible hair located. Not suitable for analysis	Possible hair/s were located on this item/sample. These have not been submitted for DNA testing and have been retained with the exhibit.			Evidence Recovery	Evidence Recovery	Auto interface
PHSRP	Possible hair located. Submitted for analysis	Possible hair/s were located on this item/sample. These have been submitted for DNA testing. Results are pending.			Evidence Recovery	Evidence Recovery	Auto interface

MPS	Micro positive for sperm	Spermatozoa were detected on this item/sample by microscopy.			Evidence Recovery	Evidence Recovery	Auto interface
AINT	All items now tested	All items for this exhibit have now been examined			Evidence Recovery	Evidence Recovery	Query with QHFSS
DIFP	DNA insufficient for further processing	This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling.	Please send a task to the DNA Liaison and Major Crime Unit (3211) if this sample is required to be assessed for further processing.		Analytical	Analytical	Auto interface
IPNE	Items Prioritised. Not examined at this time	This item/sample has been prioritised based on case information provided by QPS. Examinations may be conducted in the future.			Evidence Recovery	Evidence Recovery	Auto interface
IPNST	Items prioritised, not submitted at this time	This item/sample has been prioritised and as such samples taken from this exhibit have not been submitted at this time.			Evidence Recovery	Evidence Recovery	Auto interface
MNS	Micro neg for sperm	Spermatozoa were not detected on this item/sample by microscopy.			Evidence Recovery	Evidence Recovery	Auto interface
NDNAD	No DNA detected	This item/sample was submitted for DNA analysis; however no DNA was detected above the limit of detection at the quantitation stage. No further processing was conducted on this item.			Analytical	Analytical	Auto interface
NFEC	No further examinations conducted	This item/sample was tested for the possible presence of biological material. All testing has been completed for this item.			Evidence Recovery	Evidence Recovery	Auto interface
NWQPS	No further work required as per advice from QPS	QPS have provided advice that no further work is required for this item/sample. Testing has been ceased and the sample stored.			Evidence Recovery	Evidence Recovery	Auto interface
PSAP	Presump. PSA test positive	This item/sample tested positive to a presumptive test for Prostate Specific Antigen (PSA) which is a component of seminal fluid			Evidence Recovery	Evidence Recovery	Auto interface
PBTN	Presumptive blood test neg.	This item/sample tested negative to a presumptive test for blood (TMB).			Evidence Recovery	Evidence Recovery	Auto interface
PREBT	Presumptive blood test positive	This item/sample tested positive to a presumptive test for blood (TMB).			Evidence Recovery	Evidence Recovery	Auto interface
PSTN	Presump saliva test negative	This item/sample tested negative to a presumptive test for saliva (Phadebas).			Evidence Recovery	Evidence Recovery	Auto interface
PSTP	Presump saliva test positive	This item/sample tested positive to a presumptive test for saliva (Phadebas).			Evidence Recovery	Evidence Recovery	Auto interface
SEMND	Semen not detected	Spermatozoa were not observed and/or seminal fluid was not detected on the item/sample tested. QHFSS recommends QPS to commence further examination on items relating to this case if applicable.			Evidence Recovery	Evidence Recovery	Auto interface
SOHAA	Sample on hold, awaiting advice	This item/sample has been placed on hold and is awaiting additional information from QPS before processing can recommence. This information may relate to, but is not limited to; examination priority, screening requirements.			Evidence Recovery	Evidence Recovery	Auto interface
INT	Item has been examined / sub-sampled	Item has been examined / sub-sampled. DNA testing has not progressed under this barcode; however sub-samples from this item have been submitted for DNA testing under new barcodes.	Please send a task to the DNA Liaison and Major Crime Unit (3211) if this sample is required to be assessed for further processing.	This needs to be changed to a result - it is currently only a movement, so does not go to QPRIME.	Evidence Recovery	Evidence Recovery	Auto interface
ENAQS	ENVM additional quality search co	Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against QHFSS DNA Analysis staff DNA database, the QPS staff DNA database and (if required) searching against the quality database to aid QPS in their investigation of any potential contamination events. In this instance, a match was obtained from this additional quality assurance search. Further information is contained within the intelligence report that will accompany this exhibit report. This search capability is restricted within DNA Analysis to the Managing Scientist and the Quality Scientists.		Lab clean - not reported	Environmental		Result to be reviewed by RMU
ENCMPU	ENVM- Complex mixture unsuitab	This environmental sample provided a DNA profile that indicated the presence of DNA from multiple contributors. This mixture is not suitable for meaningful interpretation due to either its complexity relating to the unknown and potentially large number of contributors and/or the limited amount of information within the DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.		Lab clean - not reported	Environmental		Result to be reviewed by RMU

New	ENVM - SS DNA profile	This environmental sample provided a DNA profile that indicated the presence of DNA from one contributor. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against QHFSS DNA Analysis staff DNA database, the QPS staff DNA database and (if required) searching against the quality database, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality Scientists. In this instance, no matches were obtained.		Lab clean - not reported - new	Environmental		Result to be reviewed by RMU
New	ENVM - Mixed DNA profile	This environmental sample provided a DNA profile that indicated the presence of DNA from at least two contributors. An attempt was made to resolve the contributors of this mixed DNA profile for the purposes of quality checking only, and as such no STRmix methods were undertaken. This quality checking identified a potential contributor to this mixed DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against QHFSS DNA Analysis staff DNA database, the QPS staff DNA database and (if required) searching against the quality database, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality Scientists. In this instance, no matches were obtained.		Lab clean - not reported - new	Environmental		Result to be reviewed by RMU
ENNDP	ENVM - No DNA profile	No DNA profile was obtained from this environmental sample. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.	n/a	Lab clean - not reported	Environmental		Auto file
QCF	Quality control failure – results not	During the processing of this item/sample, a failure in one of the quality control processes was identified. Investigations into this occurrence were undertaken; however any results for this sample are not reportable.	no change suggested	QHFSS quality control failure	Quality failure result		Result to be reviewed by RMU
QCFRQ	Quality control failure, refer to QP	During the processing of this item/sample, QHFSS quality control processes identified the integrity of this sample is compromised. Results for this sample are not reportable.	no change suggested	QPS quality issue	Quality failure result		Result to be reviewed by RMU
QFIH	Quality flag identified, on hold awa	During the processing of this item/sample, QHFSS quality control processes indentified the integrity of this sample may be compromised. Advice is required from QPS to determine whether any results for this sample are reportable.	no change suggested	QHFSS quality control failure	Quality failure result		Result to be reviewed by RMU

Result type	Mnemonic	Cold link line	Review by DRMU	Recommndations
Powerplex21 / Verifiler Plus	FULLCL	Full DNA profile	DNA COLD LINK - This item/sample gave a full DNA profile which matches the DNA profile obtained from Barcode Number ********* a DNA sample obtained from SURNAME, GIVEN NAMES DOB **/**/**** CNI No. ********* DNA Profile Number LKR0000***.	New cold link line
Powerplex21 / Verifiler Plus	PARTCL	Partial DNA profile	DNA COLD LINK - This item/sample gave a partial DNA profile which matches the DNA profile obtained from Barcode Number ********* a DNA sample obtained from SURNAME, GIVEN NAMES DOB **/**/**** CNI No. ********* DNA Profile Number LKR0000***.	New cold link line
Powerplex21	MIXL	Mixed DNA profile	DNA COLD LINK - This item/sample gave a DNA profile that indicated the presence of DNA from more than one contributor. Represented within the mixed DNA profile are some or all of the components of the DNA profile obtained from Barcode Number ********* a DNA sample obtained from SURNAME, GIVEN NAMES DOB **/**/**** CNI No. ********* DNA Profile Number LKR00*****.	New cold link line
Powerplex21	INTST	Interstate DNA profile		Retain
Profiler Plus	9L*	9 loci DNA profile *		Retain for legacy purposes
Profiler Plus	FUPROF	9 loci DNA profile		Retain for legacy purposes
Profiler Plus	DPPTP	9 loci DNA Profile – possible sub-threshold peaks		Retain for legacy purposes
Profiler Plus	PDNA	Partial DNA Profile		Retain for legacy purposes
Profiler Plus	PDPTP	Partial DNA Profile – possible sub-threshold peaks		Retain for legacy purposes
Profiler Plus	MINMAC	Mixed DNA profile, 9 Loci Major Component		Retain for legacy purposes
Profiler Plus	MPPMA	Mixed Profile, partial Major component		Retain for legacy purposes
Profiler Plus	MINMIC	Mixed DNA profile, 9 Loci Minor Component		Retain for legacy purposes
Profiler Plus	MPPMI	Mixed Profile, partial minor component		Retain for legacy purposes
Profiler Plus	MIXREM	Mixed profile - component remaining after conditioning		Retain for legacy purposes
Profiler Plus	MIXCON	Mixed profile - profile conditioned on		Retain for legacy purposes
Profiler Plus	INCOU	INTEL – 9 loci mixed – remaining after cond on unknown		Retain for legacy purposes
Profiler Plus	INMAJ	INTEL – 9 loci mixed DNA profile – major cannot exclude		Retain for legacy purposes
Profiler Plus	NMIN	INTEL – 9 loci mixed profile – minor cannot exclude		Retain for legacy purposes
Powerplex21	MIXREM	Mixed DNA profile – remaining contribution		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	MIXCON	Mixed DNA profile – conditioned contribution		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	INT2M1	INTEL – 2 person mix LR < 100		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	2MIXT	2 person mixed DNA profile		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	3MIXT	3 person mixed DNA profile		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	INT2MX	INTEL – (2 person mix)		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	INT3MX	INTEL – (3 person mix)		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	INTRE	INTEL – remaining contribution		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	INTREP	See INTEL report		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	FULL21	Full DNA Profile (PP21)		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	PART21	Partial DNA profile (PP21)		Decommission - not necessarily deleted - required for legacy purposes

Possible hair located on the outside of an in-tube submission

Mnemonic	**EXH line**	**Expanded Comment**	FSS agree decommission	FR coding	QPS comments
1SS	Single source DNA profile	The DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.	Thinking: could 1SS just have the expanded comment changed as per SS1?	Thinking: could 1SS just have the expanded comment changed as per SS1?	Discussed with Justin, agreed to move to SS1
1SS20L	Single source 20 loci DNA profile LR > 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It obtained all of the DNA information potentially available. This DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	Agreed	FR code to operate for LR1	
1S9L10	SS DNA profile 9 loci and above LR > 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	Agreed	FR code to operate for LR1	
1SS9L9	SS DNA profile 9 loci and above LR 1 billion- 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	Agreed	FR code to operate for LR2	
1SS9L8	SS DNA profile 9 loci and above LR 1 million - 1 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	Agreed	FR code to operate for LR3	
1SS9L7	SS DNA profile less than 9 loci LR > 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	Agreed	FR code to operate for LR1	

1SS9L6	SS DNA profile < 9 loci LR 1 billion - 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	Agreed	FR code to operate for LR2
1SS9L5	SS DNA profile < 9 loci LR 1 million - 1 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	Agreed	FR code to operate for LR3
1SS9L4	Single source DNA profile < 9 loci LR 100 000 - 1 million	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	Agreed	FR code to operate for LR4
1SSAKN	Single Source DNA profile - assumed known contributor	This item/sample provided a DNA profile that indicated the presence of one contributor. The associated barcode matches this DNA profile. Based on information provided to the laboratory, it has been assumed that the associated barcode is the donor of this DNA. Given this assumption, no statistical interpretation has been performed.	Agreed	FR code to operate for AC
2MX	Two person mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors.	Agreed	FR code to operate for MIX
3MX	Three person mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors.	Agreed	FR code to operate for MIX
MIX3	Mix - support for contrib > 100 billion	This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than has not contributed.	Agreed	FR code to operate for LR1
MIX4	Mix - inconclusive	The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other reference samples may provide a different statistical interpretation.	Agreed	FR code to operate for LR8
MIX5	Mix - supports non contribution	The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.	Agreed	FR code to operate for LR9
new	Mix - Assumed contributor	Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this DNA profile. Given the assumption for this person, no statistical interpretation has been performed.	Agreed	FR code to operate for AC

MIX16	NCIDD upload - assumed contribution	The assumed contributor described by the associated barcode has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile.	Agreed	FR code to operate for NUP
MIX7	Mix - assumed contributor - Intel	For Intelligence purposes, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically evaluated against the mixture without a contribution being assumed and the result reported as a likelihood ratio.	Agreed	FR code to operate for ACINT
MIX8	Mix - NCIDD upload	Statistical analysis resulted in a DNA profile that was able to be loaded to NCIDD. The associated barcode/unknown designation sent with this exhibit report is a possible contributor to this mixed DNA profile. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	FR codeto operate for NUP
MIX9	Mix - intel interp -contribution for NCIDD	The DNA profile from the designated unknown sent with this exhibit report could be a contributor to the DNA profile along with the assumed known contributor. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	FR code to operate for REMINT
MIX12	Mix - contribution consistent with unknown	Based on this assumption, a remaining DNA profile has been separated. This is consistent with the unknown designation (previously identified within this case and loaded to NCIDD) sent with this exhibit report. It is important to note that this information is provided for intelligence purposes only and a statistical evaluation has not been performed at this time. Any reference samples subsequently received for the identification of an unknown component will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the likelihood ratio will vary. In this instance the likelihood ratio could favour non-contribution.	Agreed	FR code to operate for CCUNK
MIX13	Mix - DNA contrib < NCIDD matching stringency	Based on this assumption, a remaining DNA profile has been separated. This DNA profile is of unknown origin and therefore does not match any DNA profiles obtained from reference samples associated to this case. This DNA contribution is below the QHFSS stringency for reporting a match on NCIDD and has therefore not been loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this DNA contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary. In this instance the likelihood ratio could favour non-contribution.	Agreed	no code

MIX14	Mix - DNA contrib unsuitable for NCIDD searching	Based on this assumption, a remaining DNA profile has been separated. This DNA profile is unsuitable for searching on NCIDD, and is therefore unable to be loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this DNA contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary. In this instance the likelihood ratio could favour non-contribution.	Agreed	no code
EVDEXC	Single evidence sample excluded	This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or three contributors. The statistical interpretation shows that the associated barcode sent with this exhibit report has been compared, and can be excluded as having contributed to this mixed DNA profile.	Agreed	FR code to operate for EVEX
INTER5	Interim result- mixed profile - Intel NCIDD. Rework Reqd	This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a mixed DNA profile that has been interpreted for intelligence purposes only. This mixed DNA profile indicated the presence of DNA from at least two contributors. An attempt has been made to separate major and minor DNA profiles within this mixed DNA profile in order to load to NCIDD for intelligence purposes only. The major DNA profile has been loaded to NCIDD and further interpretations are required. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD (within Australia) will be searched against this DNA profile. This mixed DNA profile is only reportable by statement in order to clarify interpretation assumptions. Final results are pending.	Agreed	No code: manual line
INTSSR	Interim Result- incomplete single source. Rework reqd	The interim result obtained from this sample/item was an incomplete single source DNA profile.This is not a final result and the sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.	Agreed	No code: manual line
CWBM	Consistent with being biological mother	The DNA profile obtained from this exhibit is consistent with being a biological child of the barcode sent with this exhibit report.	Agreed	No code: manual line
EXBF	Excluded as biological father	The DNA profile obtained from the barcode sent with this exhibit report is excluded as being a biological father of the DNA profile obtained from the exhibit.	Agreed	No code: manual line
NCWBM	Not consistent with being biological mother	The DNA profile obtained from the barcode is not consistent with being a biological mother of the DNA profile obtained from the exhibit.	Agreed	No code: manual line
NEXBF	Not excluded as biological father	The DNA profile obtained from the barcode sent with this exhibit report is not excluded as being a biological father of the DNA profile obtained from the exhibit.	Agreed	No code: manual line
SCLOW	Suspect check - low support for contribution	The DNA profile provides low support for the proposition that the nominated suspect is a possible donor of DNA to this mixed DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line

SCSC1	Suspect check - support for contribution 100 to 1000	This DNA profile is between 100 and 1000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line
SCSC2	Suspect check - support for contribution 1000 to 10 000	This DNA profile is between 1000 and 10 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line
SCSC3	Suspect check- support for contribution 10 000 to 100 000	This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line
SCSC4	Suspect check - support for contrib 100 000 - 1 million	This DNA profile is between 100 000 and 1 million times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line
SCSC5	Suspect check- support for contrib 1 million - 1 billion	This DNA profile is between 1 million and 1 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line
SCSC6	Suspect check- support for contrib 1 billion- 100 billion	This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line
SCSC7	Suspect check - support for contribution > 100 billion	This DNA profile is greater than 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line
SCINMX	Suspect check inconclusive - mixed DNA profile	The statistical interpretation in relation to the nominated suspect is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other nominated suspects may provide a different statistical interpretation. A reference evidence sample should be provided if this information is required in a statement for Court.	Agreed	No code: manual line
SCSNC	Suspect check - supports non contribution	The statistical interpretation provides support for the proposition that the nominated suspect has not contributed to this mixed DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line
SCANM	Suspect check Action - No Match	The nominated suspect can be excluded as a potential contributor to the DNA profile obtained from this item/sample.	Agreed	No code: manual line

CMPU	Complex mixed profile unsuitable for interp or comparison	This item/sample gave a complex Mixed DNA profile with multiple contributors. This mixture is not suitable for meaningful interpretation due to either its complexity relating to the unknown and potentially large number of contributors and/or the limited amount of information within the DNA profile.	Agreed	FR code to operate for CPU	
DIFP	DNA insufficient for further processing	This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling. Please contact the DNA Management Section if this sample is requested to be assessed for further processing. Further processing could include concentration of the low levels of DNA obtained, pooling with other samples (where appropriate), resampling of the parent item (where appropriate), or a combination of processes.	Thinking: could DIFP just have the expanded comment changed as per DIFP1, or makes no difference given already in the FR?	Thinking: could DIFP just have the expanded comment changed as per DIFP1, or makes no difference given already in the FR?	Discussed with Justin, agreed to move to SS1
INTER4	Interim result- mixed profile obtained. Rework Reqd	The interim DNA profile obtained from this sample/item indicated the presence of DNA from two or more contributors. This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.	Agreed	No code: manual line	
INTER6	Interim result- no profile obtained- undergoing rework	This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is no DNA profile. Final results are pending.	Agreed	No code: manual line	
NOPROF	No DNA profile	A DNA profile was not obtained from this item/sample, due to, but not limited to: no DNA present, poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.		FR code to operate for NOPRO	
PAPPRP	Presump. PSA test positive, submitted - results pending	This item/sample tested positive to a presumptive test for Prostate Specific Antigen (PSA) which is a component of seminal fluid. This item was submitted for DNA testing. Results are pending.	NOT TO DECOMMISSION until new lines available.		
PBNSC	Presumptive blood test neg. Submitted for cells	This item/sample tested negative to a presumptive test for blood (TMB). This item was submitted for general cell DNA testing.	Agreed		
PPUCP	Partial DNA profile unsuitable for comparison purposes	This item/sample gave a partial DNA profile which was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information within the DNA profile. This may be due to, but not limited to: poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.	Agreed	FR code for CPU	
PSNSC	Presump saliva negative. Submitted for cells	This item/sample tested negative to a presumptive test for saliva (Phadebas). This item/sample was submitted for general cell DNA testing.	Agreed		
SUFWC	Sample undergone further work - conditioned	This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or more contributors. Based on information provided to the laboratory, this mixed DNA profile has now been conditioned.	Agreed	No code: manual line	
SUFNS	Sample undergone reprocessing - new software	This item/sample has undergone further processing and/or assessment with new software available to the laboratory. An updated DNA profile interpretation has been provided.	Agreed	No code: manual line	
HLSRP	Hair located. Submitted results pending	Hair/s were located on this item/sample. These hairs have been submitted for DNA testing. Results are pending.	NOT TO DECOMMISSION until new lines available.		

SPPDNA	Micro positive for sperm. Submitted-results pending	Spermatozoa were detected on this item/sample by microscopy. This item/sample was submitted for DNA testing. Results are pending.	NOT TO DECOMMISSION until new lines available.	
EMDP	Excluded from mixed DNA profile	This item/sample provided a mixed DNA profile that indicated the presence of DNA from two or three contributors. All of the reference DNA profiles associated with this case have been compared with this DNA profile separately.The statistical interpretation shows that some or all of the donors of the reference DNA profiles associated with this case are excluded as having contributed to this mixed DNA profile.	Agreed	
MINAL	Multiple items - not all tested	This exhibit consisted of multiple items packaged together under one exhibit barcode, of which not all were selected for examination. If more or all of the remaining items are required to be examined, this can be completed upon request.	Agreed	
MLSONC	Mixture - low support for contrib or supports non contrib	This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or three contributors. One or more of the contributors to this DNA profile has limited information associated with it. All of the reference DNA profiles associated with this case have been compared with this DNA profile separately.The DNA profile provides limited information as to whether or not some or all of donors of the reference DNA profiles associated with this case are possible donors of DNA to this mixed DNA profile. Please contact the laboratory if more information is required.	Agreed	
NFWA	No further work able to be conducted on this sample	This item/sample has been assessed and it has been determined that no further processing can be conducted on this sample, due to, but not limited to: no DNA extract left for further testing, current DNA profile improvement processes have already been exhausted.	Agreed	
NRDP	No reportable DNA profile	A DNA profile above QHFSS standard reporting thresholds was not obtained from this sample/item. This may be due to, but not limited to: no DNA present, poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.	Agreed	
SRPP	Similar result to previous DNA profile	This item/sample provided a mixed DNA profile that indicated the presence of DNA from two or three contributors. This DNA profile has been assessed and is considered to provide similar information to the DNA profile obtained from the sample barcode sent with this exhibit report and therefore has not been statistically evaluated at this time. Please contact the laboratory if you require a more detailed interpretation of this DNA profile.	Agreed	
UNSS	Sample unsuitable for analysis	This item/sample is unsuitable for DNA testing due to, but not limited to: excess dirt, or the presence of mould.	Agreed	
1SSLOW	Single Source- low support for contribution	This item/sample provided a partial DNA profile which indicated the presence of one contributor. Only limited information has been obtained and this information matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. Statistically, this DNA profile provides low support that the associated barcode sent with this exhibit report is the donor of this DNA. Further information can be provided if required.	Agreed	

1SSIND	NCIDD Intel upload - single source partial profile	This item/sample gave an incomplete single source DNA profile which contained insufficient information for NCIDD matching as it was below the QHFSS stringency for reporting a match on NCIDD. The profile has been selected for loading to NCIDD for intelligence purposes. This incomplete DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be statistically evaluated and reported as a likelihood ratio. Depending on the amount of information in this DNA profile, the strength of the support for inclusion will vary.	Agreed	
1SSINI	NCIDD Intel upload - interim single source profile	This item/sample gave an interim result of an apparent single source DNA profile. This DNA profile has been selected for loading to NCIDD for intelligence purposes, as this sample is currently undergoing further processing. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that the final result may vary. Any reference samples subsequently received will be statistically evaluated against the final DNA profile and reported as a likelihood ratio.	Agreed	
1SSUND	Single source DNA profile- unsuitable for NCIDD searching	The incomplete DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. The DNA profile contained insufficient information for searching on NCIDD, and is therefore unable to be loaded to NCIDD. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.	Agreed	
2MX1	2 person mix - support for contribution 100 to 1000	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
2MX2	2 person mix - support for contribution 1000 to 10 000	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	

2MX3	2 person mix, support for contrib 10 000 - 100 000	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
2MX4	2 person mix- support for contrib 100 000 to 1 million	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
2MX5	2 person mix - support for contrib 1 million - 1 billion	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
2MX6	2 person mix- support for contrib 1 billion - 100 billion	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
2MX7	2 person mix profile - support for contrib > 100 billion	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
2MXCI	2 person mixed profile - conditioned on - Intel	This item/sample provided a DNA profile that indicated the presence of two contributors. For Intelligence purposes, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically evaluated against the mixture without a contribution being assumed and the result reported as a likelihood ratio.	Agreed	
2MXCON	2 person mixed profile - conditioned on	This item/sample provided a DNA profile that indicated the presence of two contributors. Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this mixed DNA profile. Given this assumption, no statistical interpretation has been performed.	Agreed	

2MXINC	2 person mixed DNA profile - inconclusive	This item/sample provided a DNA profile that indicated the presence of two contributors. The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other reference samples may provide a different statistical interpretation.	Agreed	
2MXIND	NCIDD upload - Intel mixed DNA profile	The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a partially deconvoluted DNA profile able to be loaded to NCIDD for intelligence purposes. The associated barcode/unknown designation sent with this exhibit report is consistent with this partially deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this partially deconvoluted DNA profile has been assigned a sub-sample barcode number. The partially deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	
2MXLOW	2 person mix - low support for contribution	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. The DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Please contact DNA Analysis if further information is required.	Agreed	
2MXNC	2 person mix - supports non contribution	This item/sample provided a DNA profile that indicated the presence of two contributors. The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.	Agreed	
2MXNCD	NCIDD upload - mixed DNA profile	The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a fully deconvoluted DNA profile. The associated barcode/unknown designation sent with this exhibit report is consistent with this fully deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this fully deconvoluted DNA profile has been assigned a sub-sample barcode number. The fully deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	

2MXNIR	Mixture contribution loaded to NCIDD - see Intel report	The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. A DNA contribution was able to be deconvoluted for loading to NCIDD, and further information about this will follow in an intelligence report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile the, strength of the support for contribution will vary.	Agreed	
2MXR1	2 person mix remaining - support for contrib 100 to 1000	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.	Agreed	
2MXR2	2 person mix remaining- support for contrib 1000 to 10000	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.	Agreed	
2MXR3	2 person mix rem - support for contrib 10 000 to 100 000	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.	Agreed	
2MXR4	2 person mix rem- support for contrib 100000 to 1 million	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.	Agreed	

2MXR5	2 person rem- support for contrib 1 million to 1 billion	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.	Agreed	
2MXR6	2 person rem - support for contrib 1 billion -100 billion	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.	Agreed	
2MXR7	2 person mix rem - support for contribution > 100 billion	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual.	Agreed	
2MXRL	2 person mix remaining - low support for contrib	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, then the DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.	Agreed	
2MXRCU	2 pers mix remaining consistent with unknown	The mixed DNA profile result for this sample indicated the presence of DNA from two contributors and has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and 'remaining' have been applied. A remaining contribution has been separated after conditioning the mixed DNA profile. This remaining contribution is consistent with the unknown designation (previously identified within this case and loaded to NCIDD) sent with this exhibit report. This unknown is therefore a possible donor of DNA to the 'remaining' contribution. It is important to note that this information is provided for intelligence purposes only and a statistical evaluation has not been performed at this time. Any reference samples subsequently received for the identification of an unknown component will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the likelihood ratio will vary. In this instance the likelihood ratio could favour non-contribution.	Agreed	

2MXRLM	Mix Rem DNA contrib < NCIDD matching stringency	The mixed DNA profile result for this sample indicates two contributors and has been deconvoluted in an attempt to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and ‘remaining’ have been applied. The remaining contribution separated after conditioning the mixed DNA profile is of unknown origin and therefore does not match any DNA profiles obtained from reference samples associated to this case. This remaining contribution is below the QHFSS stringency for reporting a match on NCIDD and has therefore not been loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this remaining contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	
2MXRNC	2 person mix remaining - supports non contribution	This item/sample provided a DNA profile that indicated the presence of two contributors. If it is assumed that the barcode sent with the above exhibit report (2 contributor mixed profile, conditioned on) has contributed, the statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.	Agreed	
2MXRIN	2 person mixed profile - remaining Intel - NCIDD	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor for intelligence purposes only, some or all of the components of the DNA profile from the designated unknown sent with this exhibit report are represented within the remaining DNA profile. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	
2MXRND	NCIDD upload remaining contribution	The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and ‘remaining’ have been applied. A remaining contribution has been separated after conditioning the mixed DNA profile. The associated barcode/unknown designation sent with this exhibit report is a possible donor of DNA to the 'remaining contribution’. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received for the identification of an unknown component will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	

3MX1	3 person mix - support for contribution 100 to 1000	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.	Agreed	
3MX2	3 person mix - support for contribution 1000 to 10 000	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.	Agreed	
3MX3	3 person mix - support for contrib 10 000 - 100 000	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.	Agreed	
3MX4	3 person mix - support for contrib 100 000 to 1 million	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.	Agreed	
3MX5	3 person mix - support for contrib 1 million - 1 billion	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.	Agreed	
3MX6	3 person mix- support for contrib 1 billion - 100 billion	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.	Agreed	

3MX7	3 person mix profile - support for contrib > 100 billion	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.	Agreed	
3MXCI	3 person mixed profile - conditioned on - Intel	This item/sample provided a DNA profile that indicated the presence of three contributors. For Intelligence purposes, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically evaluated against the mixture without a contribution being assumed and the result reported as a likelihood ratio.	Agreed	
3MXCON	3 person mixed profile - conditioned on	This item/sample provided a DNA profile that indicated the presence of three contributors. Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this mixed DNA profile. Given this assumption, no statistical interpretation has been performed.	Agreed	
3MXINC	3 person mixed DNA profile - inconclusive	This item/sample provided a DNA profile that indicated the presence of three contributors. The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other reference samples may provide a different statistical interpretation.	Agreed	
3MXIND	3 pers mixed profile, mix remaining intel NCIDD	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, a remaining contribution has been separated. This remaining contribution is a mixed DNA profile which has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a partially deconvoluted DNA profile able to be loaded to NCIDD for intelligence purposes. The associated barcode/unknown designation sent with this exhibit report is consistent with this partially deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this partially deconvoluted DNA profile has been assigned a sub-sample barcode number. The partially deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	
3MXLOW	3 person mix - low support for contribution	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. The DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.	Agreed	

3MXNC	3 person mix - supports non contribution	This item/sample provided a DNA profile that indicated the presence of three contributors. The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.	Agreed	
3MXND	3 person mixed DNA profile not deconvoluted	This item/sample gave a mixed DNA profile which indicated the presence of DNA from three contributors. This mixed DNA profile has been assessed and it is considered that, if the DNA profile were to be deconvoluted, it may provide sufficient information for upload to NCIDD. Deconvolution of this DNA profile has not been performed at this time. Please contact the laboratory if further interpetation is required.	Agreed	
3MXR1	3 person mix remaining - support for contrib 100 to 1000	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
3MXR2	3 person mix remaining- support for contrib 1000 to 10000	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
3MXR3	3 person mix rem - support for contrib 10 000 to 100 000	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
3MXR4	3 person mix rem- support for contrib 100000 to 1 million	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	

2MXCND	NCIDD upload - conditioned contribution	The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and 'remaining' have been applied. The conditioned contribution described by the associated barcode has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile.	Agreed	
3MXR5	3 person rem - support for contrib 1 million to 1 billion	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
3MXR6	3 person rem - support for contrib 1 billion-100 billion	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
3MXR7	3 person mix rem - support for contribution > 100 billion	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
3MXRIN	3 per mix, intel cond, remaining intel NCIDD	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor for intelligence purposes only, some or all of the components of the DNA profile from the designated unknown sent with this exhibit report are represented within the remaining DNA profile. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	

3MXRL	3 person mix remaining - low support for contrib	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, then the DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.	Agreed	
3MXRNC	3 person mix remaining - supports non contribution	This item/sample provided a DNA profile that indicated the presence of three contributors. If it is assumed that the barcode sent with the above exhibit report (3 contributor mixed profile, conditioned on) has contributed, the statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.	Agreed	
3MXRND	3 person mixed profile, mixture remaining NCIDD	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, a remaining contribution has been separated. This remaining contribution is a mixed DNA profile which has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a fully deconvoluted DNA profile. The associated barcode/unknown designation sent with this exhibit report is consistent with this fully deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this fully deconvoluted DNA profile has been assigned a sub-sample barcode number. The fully deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	
3MXRUN	3 Person Mix Rem DNA contrib unsuitable for NCIDD	The mixed DNA profile result for this sample indicates three contributors and has been deconvoluted in an attempt to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and ‘remaining’ have been applied. The remaining contribution separated after conditioning the mixed DNA profile was unsuitable for searching on NCIDD, and is therefore unable to be loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this remaining contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	
MXREMI	Remaining contribution - inconclusive	This item/sample provided a DNA profile that indicated the presence of two or three contributors. When conditioning on the assumed known contributor, the statistical interpretation in relation to the associated barcode is inconclusive.	Agreed	
2MXUNM	Mix Remaining DNA contribution indicates male origin	The remaining contribution separated after conditioning the mixed DNA profile indicates male origin	Agreed	

2MXUNS	Mix Rem DNA contrib unsuitable for NCIDD searching	The mixed DNA profile result for this sample indicates two contributors and has been deconvoluted in an attempt to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and 'remaining' have been applied. The remaining contribution separated after conditioning the mixed DNA profile is of unknown origin. This remaining contribution is unsuitable for searching on NCIDD, and is therefore unable to be loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this remaining contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	
SCLNSC	Suspect check - low support or non contrib	One or more of the contributors to this DNA profile has limited information associated with it. All of the profiles from nominated reference barcodes have been compared with this DNA profile separately.The DNA profile provides limited information as to whether or not some or all of the donors are possible donors of DNA to this mixed DNA profile. Please contact the laboratory if more information is required.	Agreed	
1SS9L3	Single source DNA profile < 9 loci LR 10 000 - 100 000	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	Agreed	
1SS9L2	Single source DNA profile < 9 loci LR 1000 - 10 000	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	Agreed	
1SS9L1	Single source DNA profile < 9 loci LR 100 - 1000	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	Agreed	

1SSLND	Single source DNA profile < NCIDD matching stringency	The incomplete DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. The DNA profile was below the QHSS stringency for reporting a match on NCIDD, and has therefore not been loaded to NCIDD. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.	Agreed	
NHLNE	No hair located. No further examination conducted	The item/sample was examined for the presence of hair and none was located. This could be due to no hair present or item is substance other than hair. No further testing for hair was conducted on this item.	NOT TO DECOMMISSION until new lines available.	
OHPFW	On hold, pending further work	These results are currently subject to quarantine pending the completion of further quality checks. The outcome of these quality checks will be reported once complete.	Agreed	
PPSANS	Presump. PSA test positive, no sperm found	This item/sample tested positive to a presumptive test for Prostate Specific Antigen (PSA) which is a component of seminal fluid. No spermatozoa were detected by microscopy. This item was submitted for DNA testing. Results are pending.	Agreed	
PSPSRP	Presump saliva positive. Submitted-results pendin	This item/sample tested positive to a presumptive test for saliva (Phadebas) and was submitted for DNA testing. Results are pending.	Agreed	
SAC	Submitted as cells	This item/sample was submitted for general cell DNA testing.	Agreed	
SACPSP	Submitted as cells, Presump saliva test pending	This item/sample was submitted for general cell DNA testing. The item/sample will be tested with the presumptive test for saliva (Phadebas). Results are pending.	Agreed	
HLNSA	Hair located. Not suitable for analysis	Hair/s were located on this item/sample. They were observed using microscopy and deemed unsuitable for DNA testing due to no observed cellular material, or possible animal origin.	Agreed	
HAIRNFA	Hair located – not examined at this time.	During the examination of this exhibit one or more hairs were located. Based on case information available or testing requested, this has not been submitted at this time, however has been retained for potential future analysis if requested.		
1BPPSR	Presumptive blood test pos. Submitted-results pending	This item/sample tested positive to a presumptive test for blood (TMB) and was submitted for DNA testing. Results are pending.	Agreed	
PPSRP	Presump. AP test positive, submitted - results pending	This item/sample tested positive to a presumptive test for seminal fluid (AP). This item was submitted for DNA testing. Results are pending.		
ENCMDP	ENVM - Complex mixed DNA profile	This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles), and as such, no further interpretation can be conducted as this time. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.	**Decommission**	Lab clean - not reported

ENFDP	ENVM - Full DNA profile	This environmental sample gave a full DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained	**Decommission**	Lab clean - not reported
ENPDP	ENVM -Partial DNA profile	This environmental sample gave a partial DNA. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained	**Decommission**	Lab clean - not reported
ENPDPU	ENVM - Partial profile unsuitable for comparison p	This environmental sample gave a partial DNA profile which was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information obtained. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.	**Decommission**	Lab clean - not reported

Mnemonic	EXH line	Expanded Comment	Change for next version/ alternative wording	Notes	10/08/2021 JAH
CMPCE	Complex mixed DNA profile – cannot exclude	This item/sample gave a full or partial mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles) and therefore could not be loaded to NCIDD. The DNA profile obtained from the barcode sent with this exhibit report cannot be excluded as being a possible contributor of DNA to this mixed DNA profile.	no change suggested	Profiler plus result	Retain as required for old cases
CMPULN	Complex mixed DNA profile. Unable to load to NCIDD	This item/sample gave a full or partial mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles) and therefore could not be loaded to NCIDD. This complex mixed DNA profile cannot be interpreted further as no reference sample has been received for direct comparison; or alternatively, comparison with additional reference samples may be possible if forthcoming.	no change suggested	Profiler plus result	
DPNPTP	9 loci DNA profile- NCIDD- possible sub-threshold peaks	This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. These sub-threshold peaks did not interfere with the interpretation of the reportable DNA components in the 9 loci DNA profile obtained, which has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
DPPTP	9 loci DNA profile - possible sub-threshold peaks	This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the 9 loci DNA profile obtained.	n/a	Profiler plus result	
FUPNPN	9 loci DNA profile. Uploaded to NCIDD	This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile has been selected for loading to NCIDD and will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
FUPROF	9 loci DNA profile	This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result	
MDPIL	Minor/Remaining DNA profile - Intel profile loaded NCIDD	This item/sample gave a mixed DNA profile, of which the minor or remaining DNA profile contained insufficient information for NCIDD matching as it was below the QHFSS stringency for reporting a match on NCIDD. The profile has been selected for loading to NCIDD for intelligence purposes only and any resulting matches will be reported in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution.	n/a	Profiler plus result	

MIPDNA	Mixed DNA profile conditioned on – NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that the DNA profile obtained from the barcode sent with this exhibit report has contributed to this mixed DNA profile. This result should always be used in conjunction with "Mixed DNA profile. Remaining profile after conditioning". This DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
MIPMAC	Mixed DNA profile. Major component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The full major DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result	
MIPMIC	Mixed DNA profile. Minor Component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The full minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result	
MIPMUN	Mixed DNA profile. Major component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile has been selected for loading to NCIDD. The full major DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
MIPPRO	Mixed profile. Remaining profile after conditioning – NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the "Mixed DNA profile conditioned on" exhibit report. The DNA profile remaining after the conditioning matches the DNA profile obtained from the barcode sent with this report. This DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
MIRIN	Mixture Interp reqd - Intel profile loaded to NCIDD	This item/sample gave a mixed DNA profile that has been interpreted for intelligence purposes only. This interpretation may not be able to be used for evidentiary purposes. This means that we may have lowered our routine interpretational and NCIDD matching guidelines in order to assist with the generation of intelligence information. This intelligence DNA profile has been selected for loading to NCIDD and further explanation of the interpretations made will follow in an intelligence report. It should be noted that the interpretation provided within this intelligence report may not meet the stringent court reporting guidelines and therefore wording within an evidential statement may be different. The Intelligence DNA profile loaded to NCIDD will be searched against any DNA profiles currently held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this intelligence DNA profile. It will be outlined in the Intelligence report that this mixed DNA profile may be reported differently in an evidentiary statement.	n/a	Profiler plus result	

MPCMU	Mixed profile- complex minor unsuit for interp or compar.	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile indicated the presence of DNA from more than one contributor. This minor DNA profile is too complex for meaningful interpretation or comparison purposes due to the unknown number of potential contributors and/or the limited amount of information within the minor DNA profile.	n/a	Profiler plus result	
MPCO	Mixed DNA profile conditioned on	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that the DNA profile obtained from the barcode sent with this exhibit report has contributed to this mixed DNA profile. This result should always be used in conjunction with "Mixed DNA profile. Remaining profile after conditioning"	n/a	Profiler plus result	
MPMAIN	Mixed profile, major component insuff for NCIDD matching	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	
MPMC3	Mixed profile, minor comp. 3 of 18 DNA components	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 3 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	
MPMC4	Mixed profile, minor comp. 4 of 18 DNA components	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 4 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	

MPMC5	Mixed profile, minor comp. 5 of 18 DNA components	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 5 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	
MPMIIN	Mixed profile, minor component insuff for NCIDD matching	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	
MPMINC	Mixed profile, minor component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile has been loaded to NCIDD. The full minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
MPMPIM	Mixed profile,minor profile insuff– indicated male origin	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile did not contain sufficient information for comparison purposes other that to say it indicated it was of male origin.	n/a	Profiler plus result	
MPMUC	Mixed profile Minor component unsuitable for comparison	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information obtained.	n/a	Profiler plus result	
MPNMM	Mixed profile, No major/minor – cannot exclude	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could not be separated into major and minor DNA profiles and could not be loaded to NCIDD. The DNA profile obtained from the barcode sent with this exhibit report cannot be excluded as being a possible contributor of DNA to this mixed DNA profile.	n/a	Profiler plus result	
MPNMUN	Mixed profile, No major/minor. Unable to load to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could not be separated into major and minor DNA profiles and could not be loaded to NCIDD. In the absence of reference samples, no further interpretation can be conducted; or comparison with additional reference samples may be possible if forthcoming.	n/a	Profiler plus result	

MPPMA	Mixed profile, partial major component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile. Where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result	
MPPMAN	Mixed DNA profile, partial major component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile which has been selected for loading to NCIDD. Where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
MPPMI	Mixed profile, partial minor component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile. Where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result	
MPPMIN	Mixed DNA profile, partial minor component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which has been selected for loading to NCIDD. Where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
MPRO	Mixed profile, complex mixed minor component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from more than two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile indicated the presence of DNA from more than one contributor. This minor DNA profile cannot be interpreted further as no reference sample has been received for direct comparison; or alternatively, comparison with additional reference samples may be possible if forthcoming.	n/a	Profiler plus result	
MPRP	Mixed DNA profile. Remaining profile after conditioning	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the “Mixed DNA profile conditioned on” exhibit report. The DNA profile remaining after the conditioning matches the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result	

MPRPAC	Mixed profile. Remain profile after cond – insuff NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the “Mixed DNA profile conditioned on” exhibit report. The DNA profile remaining after the conditioning was a partial DNA profile which which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This remaining DNA profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this remaining partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	
MPRPC	Mixed profile. Remain profile after cond–unsuitable NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the “Mixed DNA profile conditioned on” exhibit report. The DNA profile remaining after the conditioning was a partial DNA profile which contained insufficient information for searching on NCIDD, and therefore is unable to be loaded to NCIDD. This remaining DNA profile may contain enough information to compare to other DNA profiles for either inclusion or exclusionary purposes. Where information was obtained, the DNA components of this remaining partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	
PAPNPN	Partial DNA profile. Uploaded to NCIDD	This item/sample gave a partial DNA profile. Where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This partial DNA profile has been selected for loading to NCIDD and will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
PD3C	Partial DNA profile, 3 of 18 DNA components	This item/sample gave a partial DNA profile which contained 3 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	
PD4C	Partial DNA profile, 4 of 18 DNA components	This item/sample gave a partial DNA profile which contained 4 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	

PD5C	Partial DNA profile, 5 of 18 DNA components	This item/sample gave a partial DNA profile which contained 5 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	
PDNA	Partial DNA profile	This item/sample gave a partial DNA profile. Where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result	
PDNAIN	Partial DNA profile. Insufficient for NCIDD matching	This item/sample gave a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	
PDNPTP	Partial DNA profile- NCIDD- possible sub-threshold peaks	This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained, which has been selected for loading to NCIDD. This partial DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
PDPTP	Partial DNA profile - possible sub-threshold peaks	This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained.	n/a	Profiler plus result	
PIRIN	Partial profile Interp reqd – Intel profile loaded NCIDD	This item/sample gave a partial DNA profile which contained an indication of DNA at a level less than the laboratorys standard reporting threshold. This profile was submitted for further analysis below QHFSS standard reporting thresholds for intelligence purposes. The subsequent profile has been selected for loading to NCIDD for intelligence purposes only and further explanation of the interpretations made will follow in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution.	n/a	Profiler plus result	

PPINPT	Partial profile, insuff NCIDD- pos. sub-threshold peaks	This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained. This partial DNA profile was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	
PPIPL	Partial profile - Intel profile loaded to NCIDD	This item/sample gave a partial DNA profile which contained insufficient information for NCIDD matching as it was below the QHFSS stringency for reporting a match on NCIDD. This profile may also have indications of DNA at a level less than the laboratorys standard reporting threshold, therefore the profile may have been submitted for further analysis below standard reporting thresholds for intelligence purposes. The profile has been selected for loading to NCIDD for intelligence purposes only and any matches will be reported in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution.	n/a	Profiler plus result	
SCANM	Suspect check actioned - no match	The nominated suspect can be excluded as a potential contributor to the DNA profile obtained from this item/sample.	n/a	Profiler plus result	
SCII	Suspect check - insufficient information to compare	There was insufficient information in the DNA profile obtained from this item/sample to determine if the nominated suspect could be a potential contributor.	n/a	Profiler plus result	
SCM	Suspect check - match	The DNA profile obtained from the nominated reference barcode sent with this exhibit report matches, where information was obtained, the DNA components of this full or partial DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information and subsequent statistical calculations are required in a statement for court.	n/a	Profiler plus result	
SCMAJM	Suspect check - major profile match	The DNA profile obtained from the nominated reference barcode sent with this exhibit report matches, where information was obtained, the full or partial major DNA profile separated from this mixed DNA profile.This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information and subsequent statistical calculations are required in a statement for court.	n/a	Profiler plus result	
SCMINM	Suspect check - minor profile match	The DNA profile obtained from the nominated reference barcode sent with this exhibit report matches, where information was obtained, the full or partial minor DNA profile separated from this mixed DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information and subsequent statistical calculations are required in a statement for court.	n/a	Profiler plus result	
SCCE	Suspect check - cannot exclude	The DNA profile obtained from the nominated reference barcode sent with this exhibit report cannot be excluded as a possible contributor of DNA to this mixed DNA profile. A reference evidence sample should be provided if this information is required in a statement for court. A statistical analysis may not be possible for this interpretation.	n/a	Profiler plus result	

IMAJUN	Mixed profile-no major/minor. INTEL Major loaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors and could not be clearly separated into major and minor DNA profiles. An attempt was made to separate the contributors to this mixed DNA profile in order to load intelligence information to the National Criminal Investigation DNA Database (NCIDD) for intelligence purposes only. The Intel Major DNA profile loaded to NCIDD for matching purposes will be searched against any DNA profiles currently held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this intelligence DNA profile. It is important to note that this process has been performed for intelligence purposes only, and any reference samples subsequently received which match these DNA components will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile.	n/a	Profiler plus result	
IMINUN	Mixed profile-no major/minor. INTEL Minor loaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors and could not be clearly separated into major and minor DNA profiles. An attempt was made to separate the contributors to this mixed DNA profile in order to load intelligence information to the National Criminal Investigation DNA Database (NCIDD) for intelligence purposes only. The Intel minor DNA profile loaded to NCIDD for matching purposes will be searched against any DNA profiles currently held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this intelligence DNA profile. It is important to note that this process has been performed for intelligence purposes only, and any reference samples subsequently received which match these DNA components will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile.	n/a	Profiler plus result	
IMCOU	INTEL- mix DNA profile conditioned on unknown DNA profile	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors and could not be separated into major and minor DNA profiles. For intelligence purposes only, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile and may include a statistical analysis. This result should always be used in conjunction with “INTEL- mix profile remaining after cond on unknown-NCIDD”	n/a	Profiler plus result	
IMROU	INTEL - mix profile remaining after cond on unknown- NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors and could not be separated into major and minor DNA profiles. When conditioning on the assumed known contributor for intelligence purposes only, a remaining DNA profile was obtained. This Intel remaining DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only. If the assumption for conditioning no longer holds, then any reference sample will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile and may include a statistical analysis. This result should always be used in conjunction with “INTEL- mix DNA profile conditioned on unknown DNA profile”.	n/a	Profiler plus result	

ENMDP	ENVM - Major DNA profile	This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles, of which the major was a full or partial DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained.	n/a	Lab clean - not reported	
ENMDPU	ENVM – Minor DNA profile unsuitable for comparison	This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles, of which the minor DNA profile contained insufficient information for comparison purposes due to the limited amount of information obtained. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.		Lab clean - not reported	
ENMIDP	ENVM – Minor DNA profile	This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles, of which the minor DNA profile was a full or partial DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained	n/a	Lab clean - not reported	

Mnemonic	EXH line	Expanded Comment	Change for next version/ alternative wording	Notes	10/08/2021 JAH
HOIS	Hair located on the outside of an in-tube submission	A hair was located either outside the tube or partially hanging in and out of the tube. It is unclear if this hair was part of the collected item or incorrectly transferred during collection. This hair/hair portion has been stored and will only be analysed if a request is provided.	no change suggested	Information sent via Examination request notification by QHFSS to SOC / SCI officer	Retain for discussion with QPS in the future
ISCB	Incorrect submission of cigarette butt	This cigarette butt was received in a tube. Items provided in a tube are intended to be submitted directly for DNA processing with minimal manual intervention. This sample required further examination as it was received as a whole cigarette butt. Please submit whole cigarette butts in a Crime Scene Sample envelope or as a sub-sample of the filter paper.	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer	Retain for discussion with QPS in the future
LDIS	Labelling discrepancy	There is a labelling discrepancy (Occurrence number or sample description) between the exhibit packaging and the AUSLAB/Forensic Register interface records. This sample can not be processed until the labelling discrepancy is resolved. The discrepancy will be highlighted to the QPS Sample Management Unit for clarification in the first instance, and if unable to be resolved, will be referred to the appropriate QPS officer for resolution. Please ensure all labelling details are correct before submission to the DNA Analysis Laboratory	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer	Retain for discussion with QPS in the future
MIES	Sample required manual intervention - excess substrate	This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as excess substrate was contained within the tube. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process.	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer	Retain for discussion with QPS in the future
MIISB	Multiple items incorrectly submitted under single barcode	Multiple items, or multiple AP positive areas have been submitted under a single barcode identifier. Each item requires its own unique barcode, as the barcode is used for reporting purposes to both the forensic register and the National Criminal Investigation DNA Database. Each item will be allocated a new barcode for processing and reporting purposes.	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer	Retain for discussion with QPS in the future
MISSTL	Sample required manual intervention - swab stick too lon	This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as the swab stick was too long and required shortening to enable downstream processing. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process. The ideal stick length should be no more than 24mm total length (swab stick plus swab head).	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer	Retain for discussion with QPS in the future

MITRI	Sample reqd manual intervention- tlift rolled incorrectly	This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as the tapelift was rolled incorrectly, impeding downstream processing. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process.	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer	Retain for discussion with QPS in the future
NBOS	No barcode on sample	The item/sample provided in a tube was not labelled with a barcode. A barcode is required for the processing of the item and for continuity purposes. A barcode the same as that attached to the packaging has been affixed to the item.	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer	Retain for discussion with QPS in the future
ESCD	Entire sample consumed	The entire item/sample was consumed during examination	n/a	Exhibit movement - result report not received by RMU	Retain for discussion with QPS in the future
OHII	On hold - insufficient information provided for testing	There was insufficient information provided with this submission to determine what type of analysis is required for this item/sample eg, saliva, semen. This sample is to be placed on hold until further information on the testing requirements for this sample is provided.	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer- not used since 2015	Retain for discussion with QPS in the future
SRMI	Sample required manual intervention prior to extraction	This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the extraction process.		Information sent via Examination request notification by QHFSS to SOC / SCI officer - not used since 2011	Retain for discussion with QPS in the future

Possible hair located on the outside of an in-tube submission

EXHIBIT 189

[redacted]

From: Hoffman.CarolynP[OSC]
Sent: Wednesday, 7 September 2022 08:55
To: Neville.DavidH[OSC]
Subject: Fwd: New result lines

Sir,

Response from Justin as requested.

Kind regards

Carolyn HOFFMAN
Sergeant 18298
DNA Management Section
Police Headquarters
Lvl 4, 200 Roma St
Brisbane QLD 4000
Ph: [redacted]
PHQ ext: [redacted]
Email: [redacted]
DNA banner_v3_FA

From: Justin Howes <[redacted]
Sent: Wednesday, July 20, 2022 11:20 am
To: Hoffman.CarolynP[OSC] <[redacted]
Cc: Paula Brisotto <[redacted]
Subject: RE: New result lines

CAUTION: This email originated from outside of Queensland Police Service. Do not click links or open attachments unless you recognise the sender and know the content is safe.

Hi Carolyn
We have an extraordinary amount of work on here at the moment, and unfortunately there is no time to spare to anything else at the moment. I can't see a time when that might change in the near future, but certainly for now we cannot afford time to this.

Regards
Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team
Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health
p [redacted] **m** [redacted]
a 39 Kessels Road, Coopers Plains, QLD 4108
e [redacted] **w** **www.health.qld.gov.au/fss**
Please note that I may be working from a different location during the COVID-19 Pandemic. The best contact method is via email.

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

From: Hoffman.CarolynP[OSC] <[redacted]
Sent: Wednesday, 20 July 2022 6:58 AM
To: Justin Howes <[redacted]
Subject: New result lines

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

Hi Justin,

I was wondering if we could maybe have a final meeting prior to release to discuss:

1. Commencement date
2. Single source lines
3. ITEM HAS BEEN EXAMINED/SUB-SAMPLED

Olivia and I are happy to come out for a face to face if you can get a room, unless you would prefer a Teams meeting.

Could you please let me know when you would be available?

Many thanks

'H'

Carolyn HOFFMAN
Sergeant 18298
Senior DNA Management Officer
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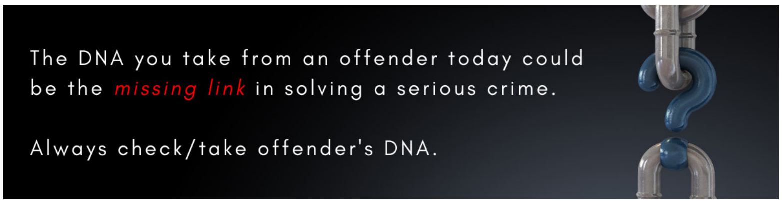

EXHIBIT 190

[redacted]

From: Harris.LibbyA[ESC]
Sent: Wednesday, 7 September 2022 09:30
To: Neville.DavidH[OSC]
Subject: FW: Review of proposed changes to EXH lines
Attachments: Copy of EXH_Proposed changes_draft copy JAH working on_March 2021 (003).xls

OFFICIAL

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From: McIntyre.OliviaM[OSC] <[redacted]
Sent: Thursday, 1 July 2021 11:45
To: Paula Brisotto <[redacted] Justin Howes <[redacted]
Cc: Harris.LibbyA[OSC] <[redacted] Foxover.StephanP[OSC]
<[redacted]
Subject: Review of proposed changes to EXH lines

Hi Paula and Justin,

Libby and I have reviewed the attached spreadsheet this morning, tab PP21 final results.

It is now colour coded as follows:

Green – recommended
Pink – Further discussion required
Blue – Paula for review
Purple – Decommission

We have been advised by BDNA that they are commencing discussions with the DNA Management Section re the upgrade and changes required for the new Forensic Register within the next few weeks.

We were wanting to have the new result changes included in this process. We would appreciate if you could review the spreadsheet at your earliest convenience, with the view to having a meeting between QPS and QHFSS mid-July to go over these changes

Kind regards

Olivia McIntyre
DNA Management Officer
DNA Management Section, Forensic Services Group
Operations Support Command
Ph: [redacted] Mobile [redacted]
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200 Roma Street, Brisbane
[redacted]

INTEGRITY PROFESSIONALISM COMMUNITY RESPECT & FAIRNESS

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

							16/03/2021 Comments				RMU review 01/07/2021			
Mnemonic	**EXH line**	**Expanded Comment**	**Review by DRMU**	**Notes**	**Recommendations**	**Expanded result wording changes**	**Mnemonic**	**EXH Line**	**Expanded Comment**	**16/03/2021 Notes**	**Mnemonic**	**EXH Line**	**Expanded Comment**	**01/07/2021 Notes RMU**
1SS	Single source DNA profile	The DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.	The DNA profile obtained from this item/sample indicated the presence of one contributor. This profile has been designated as UNKNOWN MALE / FEMALE.	PP21 - reported -	Recommend this is only used when single source unknown results are being validated. Nil value in continuing to validate the 'intel' link results as these are not reported by RMU. RMU waits for confirming cold link result	Changes recommended	SS1	Single source DNA profile	The DNA profile obtained from this item/sample indicated the presence of one contributor. This profile has been designated as UNKNOWN MALE / FEMALE.	Needs further QPS discussion	SS1	Single source DNA profile	The DNA profile obtained from this item/sample indicated the presence of one contributor. This profile has been designated as UNKNOWN MALE / FEMALE.	Further discussion required re moving away from receiving intelligence links, instead receiving all results as unknowns where applicable.
1SS20L	Single source 20 loci DNA profile LR > 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It obtained all of the DNA information potentially available. This DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	This item/sample provided a complete DNA profile that indicated the presence of one contributor. This DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	PP21 - reported	I think it is important that we include information that it matched the person sample. For discussion.	Nil change recommended by RMU	LR1	Support for contribution: LR >100 billion	This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.		LR1	Support for contribution: LR >100 billion	This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.	Support change
1S9L10	SS DNA profile 9 loci and above LR > 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	This item/sample provided a DNA profile that indicated the presence of one contributor. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	PP21 - reported	I think it is important that we include information that it matched the person sample. For discussion.	Changes recommended	DECOMMISSION				1S9L10	SS DNA profile 9 loci and above LR > 100 billion		Decommission - agree with QHFSS
1SS9L9	SS DNA profile 9 loci and above LR 1 billion- 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	This item/sample provided a partial DNA profile that indicated the presence of one contributor. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this report. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	PP21 - reported	I think it is important that we include information that it matched the person sample. For discussion.	Changes recommended	LR2	Support for contribution: LR 1 billion to 100 billion	This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.		LR2	Support for contribution: LR 1 billion to 100 billion	This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.	Support change
1SS9L8	SS DNA profile 9 loci and above LR 1 million - 1 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	This item/sample provided a partial DNA profile that indicated the presence of one contributor. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this report. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	PP21 - reported	I think it is important that we include information that it matched the person sample. For discussion.	Changes recommended	LR3	Support for contribution: LR 1 million to 1 billion	This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.		LR3	Support for contribution: LR 1 million to 1 billion	This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.	Support change
1SS9L7	SS DNA profile less than 9 loci LR > 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	This item/sample provided a partial DNA profile that indicated the presence of one contributor. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	PP21 - reported	I think it is important that we include information that it matched the person sample. For discussion.	Changes recommended	DECOMMISSION				1SS9L7	SS DNA profile less than 9 loci LR > 100 billion		Decommission - agree with QHFSS
1SS9L6	SS DNA profile < 9 loci LR 1 billion - 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	This item/sample provided a partial DNA profile that indicated the presence of one contributor. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this report. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	PP21 - reported	I think it is important that we include information that it matched the person sample. For discussion.	Changes recommended	DECOMMISSION				1SS9L6	SS DNA profile < 9 loci LR 1 billion - 100 billion		Decommission - agree with QHFSS
1SS9L5	SS DNA profile < 9 loci LR 1 million - 1 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	This item/sample provided a partial DNA profile that indicated the presence of one contributor. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this report. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	PP21 - reported	I think it is important that we include information that it matched the person sample. For discussion.	Changes recommended	DECOMMISSION				1SS9L5	SS DNA profile < 9 loci LR 1 million - 1 billion		Decommission - agree with QHFSS
1SS9L4	Single source DNA profile < 9 loci LR 100 000 - 1 million	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	This item/sample provided a partial DNA profile that indicated the presence of one contributor. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this report. This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	PP21 - reported	I think it is important that we include information that it matched the person sample. For discussion.	Changes recommended	LR4	Support for contribution: LR 100 000 to 1 million	This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.		LR4	Support for contribution: LR 100 000 to 1 million	This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.	Support change
1SSAKN	Single Source DNA profile - assumed known contributor	This item/sample provided a DNA profile that indicated the presence of one contributor. The associated barcode matches this DNA profile. Based on information provided to the laboratory, it has been assumed that the associated barcode is the donor of this DNA. Given this assumption, no statistical interpretation has been performed.	This item/sample provided a DNA profile that indicated the presence of one contributor. The associated barcode matches this DNA profile. Based on information provided to the laboratory, it has been assumed that the associated barcode is the donor of this DNA. Given this assumption, no statistical interpretation has been performed.	PP21 - reported		Nil change recommended by RMU	DECOMMISSION: see AC				1SSAKN	Single Source DNA profile - assumed known contributor		Decommission - agree with QHFSS - see AC
1SSNCD	NCIDD upload single source DNA profile	A single source DNA profile was obtained from the item/sample. This DNA profile has been selected for loading to NCIDD, and it will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile.	This item/sample yielded a DNA profile that has been uploaded to NCIDD for searching. Further advice will be provided in the event a match is received.	PP21 - auto update if received with unknown / written off if receive with evidence result		Changes recommended	NUP	NCIDD Upload	This item/sample yielded a DNA profile that has been uploaded to NCIDD for searching. Further advice will be provided in the event a match is received.		NUP	NCIDD Upload	This item/sample yielded a DNA profile that has been uploaded to NCIDD for searching. Further advice will be provided in the event a match is received.	Further discussion with QHFSS. How is this going to work with mixture unknown results
MIX	Mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from at least two contributors.	This item/sample provided a DNA profile that indicated the presence of DNA from at least two contributors.	PP21 - reported	Recommend that this line is no longer required if we are able to get the Four person mixed DNA profile line		MIX	Mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from at least two contributors.		MIX	Mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from at least two contributors.	Support use of this for all mixtures
2MX	Two person mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors.	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors.	PP21 - reported	No change suggested	Nil change recommended by RMU	DECOMMISSION: see MIX				2MX	Two person mixed DNA profile		Decommission - agree with QHFSS
3MX	Three person mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors.	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors.	PP21 - reported	No change suggested	Nil change recommended by RMU	DECOMMISSION: see MIX				3MX	Three person mixed DNA profile		Decommission - agree with QHFSS
new	Mix - Support for contribution 2 to 100	New Result line	This DNA profile is between 2 and 100 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than has not contributed.	FOR DISCUSSION: Original LR brackets as follows: Low support (2-100) 100-1000 1000-10,000 10,000-100,000 100,000-1 million 1 million - 1 billion 1 billion - 100 billion >100 billion	New Result	New Result	LR7	Support for contribution: 2 to 100	This DNA profile is between 2 and 100 times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.		LR7	Support for contribution: 2 to 100	This DNA profile is between 2 and 100 times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.	Support change
new	Mix - Support for contribution 100 to 1000	New Result line	This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than has not contributed.		New Result	New Result	LR6	Support for contribution: 100 to 1000	This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.		LR6	Support for contribution: 100 to 1000	This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.	Support change
new	Mix - Support for contribution 1000 to 100,000	New Result line	This DNA profile is between 1000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than has not contributed.		New Result	New Result	LR5	Support for contribution: 1000 to 100 000	This DNA profile is between 1000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.		LR5	Support for contribution: 1000 to 100 000	This DNA profile is between 1000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.	Support change
MIX3	Mix - support for contrib > 100 billion	This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than has not contributed.	This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than has not contributed.	PP21 - reported		Nil change recommended by RMU	see LR1				MIX3	Mix - support for contrib > 100 billion		Decommission - agree with QHFSS - see LR1
MIX4	Mix - inconclusive	The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other reference samples may provide a different statistical interpretation.	The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other reference samples may provide a different statistical interpretation.	PP21 - reported		Nil change recommended by RMU	LR8	LR inconclusive	The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other reference samples may provide a different statistical interpretation.		LR8	LR inconclusive	The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other reference samples may provide a different statistical interpretation.	Further discussion with QHFSS re EXH title - suggestion..(Inconclusive)
MIX5	Mix - supports non contribution	The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.	The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.	PP21 - reported		Nil change recommended by RMU	LR9	Supports non contribution	The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.		LR9	Supports non contribution	The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.	Support change
new	Mix - Assumed contributor	Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this DNA profile. Given the assumption for this person, no statistical interpretation has been performed.	Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this DNA profile. Given the assumption for this person, no statistical interpretation has been performed.	PP21 - reported		Nil change recommended by RMU	AC	Assumed Contributor	Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this DNA profile. Given the assumption for this person, no statistical interpretation has been performed.		AC	Assumed Contributor	Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this DNA profile. Given the assumption for this person, no statistical interpretation has been performed.	Support change
MIX16	NCIDD upload - assumed contribution	The assumed contributor described by the associated barcode has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile.	The assumed contributor described by the associated barcode has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile.	PP21 - this result line is written off and not reported to QPRIME		Nil change recommended by RMU	DECOMMISSION: see NUP				MIX16	NCIDD upload - assumed contribution		Supported - however further discussion - we will need to ensure QHFSS are still using the linked barcode of the assumed known contributor on mixtures so we known who the NCIDD upload relates to

MIX7	Mix - assumed contributor - Intel	For Intelligence purposes, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically evaluated against the mixture without a contribution being assumed and the result reported as a likelihood ratio.	For Intelligence purposes, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically evaluated against the mixture without a contribution being assumed and the result reported as a likelihood ratio.	PP21 - reported	Further discussion, appears this result has not been received	Nil change recommended by RMU	ACINT	Assumed contributor - Intel	For Intelligence purposes, it has been assumed that the designated unknown has contributed to this DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically evaluated against the DNA profile without a contribution being assumed and the result reported as a likelihood ratio.	Changed some words to make very generic (removed 'mix')	ACINT	Assumed contributor - Intel	For Intelligence purposes, it has been assumed that the designated unknown has contributed to this DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically evaluated against the DNA profile without a contribution being assumed and the result reported as a likelihood ratio.	Support change
MIX8	Mix - NCIDD upload	Statistical analysis resulted in a DNA profile that was able to be loaded to NCIDD. The associated barcode/unknown designation sent with this exhibit report is a possible contributor to this mixed DNA profile. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Statistical analysis resulted in a DNA profile that was able to be loaded to NCIDD. The associated barcode/unknown designation sent with this exhibit report is a possible contributor to this mixed DNA profile. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	PP21 - reported		Nil change recommended by RMU	DECOMMISSION see NUP				MIX8	Mix - NCIDD upload		Further discussion with QHFSS required - how will the new NUP line work with mix unknown uploads, as currently unknown is next to NCIDD load line on mixtures, and on single source it is next to single source line not the NCIDD line
MIX9	Mix - intel interp -contribution for NCIDD	The DNA profile from the designated unknown sent with this exhibit report could be a contributor to the DNA profile along with the assumed known contributor. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	The DNA profile from the designated unknown sent with this exhibit report could be a contributor to the DNA profile along with the assumed known contributor. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	PP21 - reported		Nil change recommended by RMU	REMINT	Contribution for NCIDD - Intel purposes	The DNA profile from the designated unknown sent with this exhibit report could be a contributor to the DNA profile along with the assumed known contributor. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.		REMINT	Contribution for NCIDD - Intel purposes	The DNA profile from the designated unknown sent with this exhibit report could be a contributor to the DNA profile along with the assumed known contributor. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Support change
MIX12	Mix - contribution consistent with unknown	Based on this assumption, a remaining DNA profile has been separated. This is consistent with the unknown designation (previously identified within this case and loaded to NCIDD) sent with this exhibit report. It is important to note that this information is provided for intelligence purposes only and a statistical evaluation has not been performed at this time. Any reference samples subsequently received for the identification of an unknown component will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the likelihood ratio will vary. In this instance the likelihood ratio could favour non-contribution.	Based on this assumption, a remaining DNA profile has been separated. This is consistent with the unknown designation (previously identified within this case and loaded to NCIDD) sent with this exhibit report. It is important to note that this information is provided for intelligence purposes only and a statistical evaluation has not been performed at this time. Any reference samples subsequently received for the identification of an unknown component will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the likelihood ratio will vary. In this instance the likelihood ratio could favour non-contribution.	PP21 - reported	Is this currently only used for P1 cases? This result has only been received once (18/12/2020) do we need this line?	Nil change recommended by RMU	CCUNK	Remaining contribution consistent with unknown	Based on this assumption, a remaining DNA profile has been separated. This is consistent with the unknown designation (previously identified within this case and loaded to NCIDD) sent with this exhibit report. It is important to note that this information is provided for intelligence purposes only and a statistical evaluation has not been performed at this time. Any reference samples subsequently received for the identification of an unknown component will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the likelihood ratio will vary. In this instance the likelihood ratio could favour non-contribution.	Is all the wording required? It could end before 'It is important…'	CCUNK	Remaining contribution consistent with unknown	Based on this assumption, a remaining DNA profile has been separated. This is consistent with the unknown designation (previously identified within this case and loaded to NCIDD) sent with this exhibit report.	Support change - removed wording from 'it is important…'
MIX13	Mix - DNA contrib < NCIDD matching stringency	Based on this assumption, a remaining DNA profile has been separated. This DNA profile is of unknown origin and therefore does not match any DNA profiles obtained from reference samples associated to this case. This DNA contribution is below the QHFSS stringency for reporting a match on NCIDD and has therefore not been loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this DNA contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary. In this instance the likelihood ratio could favour non-contribution.	Based on this assumption, a remaining DNA profile has been separated. This DNA profile is of unknown origin and therefore does not match any DNA profiles obtained from reference samples associated to this case. This DNA contribution is below the QHFSS stringency for reporting a match on NCIDD and has therefore not been loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this DNA contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary. In this instance the likelihood ratio could favour non-contribution.	PP21 - reported		Nil change recommended by RMU	QPS will consider whether there is ongoing need for this				MIX13	Mix - DNA contrib < NCIDD matching stringency		Decommission
MIX14	Mix - DNA contrib unsuitable for NCIDD searching	Based on this assumption, a remaining DNA profile has been separated. This DNA profile is unsuitable for searching on NCIDD, and is therefore unable to be loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this DNA contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary. In this instance the likelihood ratio could favour non-contribution.	Based on this assumption, a remaining DNA profile has been separated. This DNA profile is unsuitable for searching on NCIDD, and is therefore unable to be loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this DNA contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary. In this instance the likelihood ratio could favour non-contribution.	PP21 - reported		Nil change recommended by RMU	QPS will consider whether there is ongoing need for this				MIX14	Mix - DNA contrib unsuitable for NCIDD searching		Decommission
EVDEXC	Single evidence sample excluded	This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or three contributors. The statistical interpretation shows that the associated barcode sent with this exhibit report has been compared, and can be excluded as having contributed to this mixed DNA profile.	This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or more contributors. The associated barcode sent with this exhibit report has been compared, and can be excluded as having contributed to this mixed DNA profile.	PP21 - reported		Changes recommended	EVEX	Single evidence sample excluded	The statistical interpretation shows that the associated barcode sent with this exhibit report has been compared, and can be excluded as having contributed to this mixed DNA profile.	replace with this line which has already been created	EVEX	Single evidence sample excluded	The statistical interpretation shows that the associated barcode sent with this exhibit report has been compared, and can be excluded as having contributed to this mixed DNA profile.	Support change
INTER5	Interim result- mixed profile - Intel NCIDD. Rework Reqd	This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a mixed DNA profile that has been interpreted for intelligence purposes only. This mixed DNA profile indicated the presence of DNA from at least two contributors. An attempt has been made to separate major and minor DNA profiles within this mixed DNA profile in order to load to NCIDD for intelligence purposes only. The major DNA profile has been loaded to NCIDD and further interpretations are required. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD (within Australia) will be searched against this DNA profile. This mixed DNA profile is only reportable by statement in order to clarify interpretation assumptions. Final results are pending.	This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a mixed DNA profile that has been interpreted for intelligence purposes only. This mixed DNA profile indicated the presence of DNA from at least two contributors. An attempt has been made to separate major and minor DNA profiles within this mixed DNA profile in order to load to NCIDD for intelligence purposes only. The major DNA profile has been loaded to NCIDD and further interpretations are required. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD (within Australia) will be searched against this DNA profile. This mixed DNA profile is only reportable by statement in order to clarify interpretation assumptions. Final results are pending.	PP21 - reported (used for P1 cases)		Nil change recommended by RMU	INT1	Interim result - Intel NCIDD. Rework Required.	A DNA contribution has been uploaded to NCIDD for intelligence purposes only. Final results are pending.	new expanded comment.	INT1	Interim result - Intel NCIDD. Rework Required.	A DNA contribution has been uploaded to NCIDD for intelligence purposes only. Final results are pending.	Support change
INTSSR	Interim Result- incomplete single source. Rework reqd	The interim result obtained from this sample/item was an incomplete single source DNA profile.This is not a final result and the sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.	The interim result obtained from this sample/item was an incomplete single source DNA profile.This is not a final result and the sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.	PP21 - reported (used for P1 cases)		Nil change recommended by RMU	DECOMMISSION: see IRSUR				INTSSR	Interim Result- incomplete single source. Rework reqd		Decommission
IRRFI	Intel report required for further information	The results for this item/sample require further explanation which will follow in an intelligence report.	The results for this item/sample require further explanation which will follow in an intelligence report.	Intelligence report used - information changes each time		Nil change recommended by RMU	IRRFI	Intel report required for further information	The results for this item/sample require further explanation which will follow in an intelligence report.	no change	IRRFI	Intel report required for further information	The results for this item/sample require further explanation which will follow in an intelligence report.	QPS agree
CWBC	Consistent with being child of	The DNA profile obtained from this exhibit was consistent with being the biological child of the barcode sent with this exhibit report	The DNA profile obtained from this exhibit is consistent with being the biological child of the barcode sent with this exhibit report	PP21 - reported		Changes recommended	CWBC	Consistent with being child of	The DNA profile obtained from this exhibit is consistent with being the biological child of the barcode sent with this exhibit report	no change	CWBC	Consistent with being child of	The DNA profile obtained from this exhibit is consistent with being the biological child of the barcode sent with this exhibit report	QPS agree
CWBM	Consistent with being biological mother	The DNA profile obtained from this exhibit is consistent with being a biological child of the barcode sent with this exhibit report.	The DNA profile obtained from this exhibit is consistent with being a biological mother of the barcode sent with this exhibit report.	PP21 - reported		Changes recommended	DECOMMISSION				CWBM	Consistent with being biological mother		Decommission
EXBF	Excluded as biological father	The DNA profile obtained from the barcode sent with this exhibit report is excluded as being a biological father of the DNA profile obtained from the exhibit.	The DNA profile obtained from the barcode sent with this exhibit report is excluded as being a biological father of the DNA profile obtained from the exhibit.	PP21 - reported		Changes recommended	DECOMMISSION				EXBF	Excluded as biological father		Decommission
NCWBC	Not consistent with being child of	The DNA profile obtained from this exhibit was not consistent with being the biological child of the barcode sent with this exhibit report.	The DNA profile obtained from this exhibit is not consistent with being the biological child of the barcode sent with this exhibit report.	PP21 - reported		Changes recommended	NCWBC	Not consistent with being child of	The DNA profile obtained from this exhibit is not consistent with being the biological child of the barcode sent with this exhibit report.	no change	NCWBC	Not consistent with being child of	The DNA profile obtained from this exhibit is not consistent with being the biological child of the barcode sent with this exhibit report.	QPS agree
NCWBM	Not consistent with being biological mother	The DNA profile obtained from the barcode is not consistent with being a biological mother of the DNA profile obtained from the exhibit.	The DNA profile obtained from the barcode is not consistent with being the biological mother of the DNA profile obtained from the exhibit.	PP21 - reported		Changes recommended	DECOMMISSION				NCWBM	Not consistent with being biological mother		Decommission
NEXBF	Not excluded as biological father	The DNA profile obtained from the barcode sent with this exhibit report is not excluded as being a biological father of the DNA profile obtained from the exhibit.	The DNA profile obtained from the barcode sent with this exhibit report is not excluded as being the biological father of the DNA profile obtained from the exhibit.	PP21 - reported		Changes recommended	DECOMMISSION				NEXBF	Not excluded as biological father		Decommission
SCLOW	Suspect check - low support for contribution Suspect check - support for contribution 2 to 100	The DNA profile provides low support for the proposition that the nominated suspect is a possible donor of DNA to this mixed DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	The DNA profile is between 2 and 99 times more 100 more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	PP21 - reported	Recommend change to EXH line as well as expanded wording.	Changes recommended	SC1	Suspect check - support for contribution: LR 2 to 100	The DNA profile is between 2 and 100 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.		SC1	Suspect check - support for contribution: LR 2 to 100	The DNA profile is between 2 and 100 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Support change

SCSC1	Suspect check - support for contribution 100 to 1000	This DNA profile is between 100 and 1000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	This DNA profile is between 100 and 1000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	PP21 - reported		Nil change recommended by RMU	SC2	Suspect check - support for contribution: LR 100 to 1000	This DNA profile is between 100 and 1000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.		SC2	Suspect check - support for contribution: LR 100 to 1000	This DNA profile is between 100 and 1000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	QPS agree
SCSC2	Suspect check - support for contribution 1000 to 10 000	This DNA profile is between 1000 and 10 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	This DNA profile is between 1000 and 10 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	PP21 - reported		Nil change recommended by RMU	SC3	Suspect check - support for contribution: LR 1000 to 10 000	This DNA profile is between 1000 and 10 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.		SC3	Suspect check - support for contribution: LR 1000 to 10 000	This DNA profile is between 1000 and 10 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	QPS agree
SCSC3	Suspect check- support for contribution 10 000 to 100 000	This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	PP21 - reported		Nil change recommended by RMU	SC4	Suspect check- support for contribution: LR 10 000 to 100 000	This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.		SC4	Suspect check- support for contribution: LR 10 000 to 100 000	This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	QPS agree
SCSC4	Suspect check - support for contrib 100 000 - 1 million	This DNA profile is between 100 000 and 1 million times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	This DNA profile is between 100 000 and 1 million times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	PP21 - reported		Nil change recommended by RMU	SC5	Suspect check - support for contribution: LR 100 000 - 1 million	This DNA profile is between 100 000 and 1 million times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.		SC5	Suspect check - support for contribution: LR 100 000 - 1 million	This DNA profile is between 100 000 and 1 million times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	QPS agree
SCSC5	Suspect check- support for contrib 1 million - 1 billion	This DNA profile is between 1 million and 1 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	This DNA profile is between 1 million and 1 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	PP21 - reported		Nil change recommended by RMU	SC6	Suspect check- support for contribution: LR 1 million - 1 billion	This DNA profile is between 1 million and 1 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.		SC6	Suspect check- support for contribution: LR 1 million - 1 billion	This DNA profile is between 1 million and 1 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	QPS agree
SCSC6	Suspect check- support for contrib 1 billion- 100 billion	This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	PP21 - reported		Nil change recommended by RMU	SC7	Suspect check- support for contribution:LR 1 billion- 100 billion	This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.		SC7	Suspect check- support for contribution:LR 1 billion- 100 billion	This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	QPS agree
SCSC7	Suspect check - support for contribution > 100 billion	This DNA profile is greater than 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	This DNA profile is greater than 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	PP21 - reported		Nil change recommended by RMU	SC8	Suspect check - support for contribution: LR > 100 billion	This DNA profile is greater than 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.		SC8	Suspect check - support for contribution: LR > 100 billion	This DNA profile is greater than 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	QPS agree
SCINMX	Suspect check inconclusive - mixed DNA profile	The statistical interpretation in relation to the nominated suspect is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other nominated suspects may provide a different statistical interpretation. A reference evidence sample should be provided if this information is required in a statement for Court.	The interpretation in relation to the nominated suspect is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other nominated suspects may provide a different interpretation. A reference evidence sample should be provided if this information is required in a statement for Court.	PP21 - reported		Nil change recommended by RMU	SC9	Suspect check inconclusive	The interpretation in relation to the nominated suspect is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other nominated suspects may provide a different interpretation. A reference evidence sample should be provided if this information is required in a statement for Court.		SC9	Suspect check inconclusive	The interpretation in relation to the nominated suspect is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other nominated suspects may provide a different interpretation. A reference evidence sample should be provided if this information is required in a statement for Court.	Support change
SCSNC	Suspect check - supports non contribution	The statistical interpretation provides support for the proposition that the nominated suspect has not contributed to this mixed DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	The statistical interpretation provides support for the proposition that the nominated suspect has not contributed to this mixed DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	PP21 - reported		Nil change recommended by RMU	SC10	Suspect check - supports non contribution	The statistical interpretation provides support for the proposition that the nominated suspect has not contributed to this DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	slight change to suggested wording. Removed 'mixed'.	SC10	Suspect check - supports non contribution	The statistical interpretation provides support for the proposition that the nominated suspect has not contributed to this DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Support change
SCANM	Suspect check Action - No Match	The nominated suspect can be excluded as a potential contributor to the DNA profile obtained from this item/sample.	The nominated suspect can be excluded as a potential contributor to the DNA profile obtained from this item/sample.			Nil change recommended by RMU	SC11	Suspect check - Excluded	The nominated suspect can be excluded as a potential contributor to the DNA profile obtained from this item/sample.	slight change to description	SC11	Suspect check - Excluded	The nominated suspect can be excluded as a potential contributor to the DNA profile obtained from this item/sample.	Support change
1BPPSR	Presumptive blood test pos. Submitted-results pending	This item/sample tested positive to a presumptive test for blood (TMB) and was submitted for DNA testing. Results are pending.	This item/sample tested positive to a presumptive test for blood (TMB) and was submitted for DNA testing. Results are pending.	prelim - auto update		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
AINT	All items now tested	All items for this exhibit have now been examined	All items for this exhibit have now been examined	Automatically filed on FR		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
CMPU	Complex mixed profile unsuitable for interp or comparison	This item/sample gave a complex Mixed DNA profile with multiple contributors. This mixture is not suitable for meaningful interpretation due to either its complexity relating to the unknown and potentially large number of contributors and/or the limited amount of information within the DNA profile.	This item/sample gave a complex Mixed DNA profile with multiple contributors. This mixture is not suitable for meaningful interpretation due to either its complexity relating to the unknown and potentially large number of contributors and/or the limited amount of information within the DNA profile.	PP21 - reported		Nil change recommended by RMU	CPU	Complex profile unsuitable for interp or comparison	This item/sample gave a complex DNA profile. This DNA profile is not suitable for meaningful interpretation due to either its complexity relating to the unknown and potentially large number of contributors and/or the limited amount of information within the DNA profile.	replace with this line which has already been created	CPU	Complex profile unsuitable for interp or comparison	This item/sample gave a complex DNA profile. This DNA profile is not suitable for meaningful interpretation due to either its complexity relating to the unknown and potentially large number of contributors and/or the limited amount of information within the DNA profile.	Support change
DIFP	DNA insufficient for further processing	This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling. Please contact the DNA Management Section if this sample is requested to be assessed for further processing. Further processing could include concentration of the low levels of DNA obtained, pooling with other samples (where appropriate), resampling of the parent item (where appropriate), or a combination of processes.	This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling. Please send a task to the DNA Results Management Unit (3209) if this sample is required to be assessed for further processing.	PP21 - reported		Change recommended including task information.	DIFP1	DNA insufficient for further processing	This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling. Please send a task to the DNA Results Management Unit (3209) if this sample is required to be assessed for further processing.	change in exp comment	DIFP1	DNA insufficient for further processing	This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling. Please send a task to the DNA Liaison and Major Crime Unit (3211) if this sample is required to be assessed for further processing.	Refer to Paula Brisotto - slight changes recommended
HLNSA	Hair located. Not suitable for analysis	Hair/s were located on this item/sample. They were observed using microscopy and deemed unsuitable for DNA testing due to no observed cellular material, or possible animal origin.	Hair/s were located on this item/sample. They were observed using microscopy and deemed unsuitable for DNA testing due to no observed cellular material, or possible animal origin.	PP21 - reported		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
HLSRP	Hair located. Submitted results pending	Hair/s were located on this item/sample. These hairs have been submitted for DNA testing. Results are pending.	Hair/s were located on this item/sample. These hairs have been submitted for DNA testing. Results are pending.	prelim - auto update		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
INTER4	Interim result- mixed profile obtained. Rework Reqd	The interim DNA profile obtained from this sample/item indicated the presence of DNA from two or more contributors. This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.	The interim DNA profile obtained from this sample/item indicated the presence of DNA from two or more contributors. This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.	PP21 - reported (used for P1 cases)		Nil change recommended by RMU	DECOMMISSION: see IRSUR				INTER4	Interim result- mixed profile obtained. Rework Reqd		Decommission - see IRSUR
INTER6	Interim result- no profile obtained-undergoing rework	This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is no DNA profile. Final results are pending.	This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is no DNA profile. Final results are pending.	PP21 - reported (used for P1 cases)		Nil change recommended by RMU	DECOMMISSION: see IRSUR				INTER6	Interim result- no profile obtained-undergoing rework		Decommission - see IRSUR
IPNE	Items Prioritised. Not examined at this time	This item/sample has been prioritised based on case information provided by QPS. Examinations may be conducted in the future.	n/a	Automatically filed on FR		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
IPNST	Items prioritised, not submitted at this time	This item/sample has been prioritised and as such samples taken from this exhibit have not been submitted at this time.	n/a	Automatically filed on FR		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
IRSUR	Interim Result. Sample undergoing rework	This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. This rework could be due to: instrument failure, requiring the sample to be re-processed; interpretation difficulties, requiring the sample to be re-run to resolve any issues. Final results are pending.	This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.			Changes recommnded	IRSUR	Interim Result. Sample undergoing rework	This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.	no change	IRSUR	Interim Result. Sample undergoing rework	This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.	QPS agree

MNS	Micro neg for sperm	Spermatozoa were not detected on this item/sample by microscopy.	Spermatozoa were not detected on this item/sample by microscopy.	prelim - auto update		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
NDNAD	No DNA detected	This item/sample was submitted for DNA analysis; however no DNA was detected above the limit of detection at the quantitation stage. No further processing was conducted on this item.	This item/sample was submitted for DNA analysis; however no DNA was detected above the limit of detection at the quantitation stage. No further processing was conducted on this item.	PP21 - reported		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
NDPPTP	No DNA profile – possible sub-threshold peaks	A DNA profile was not obtained from this item/sample, however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. This could be due to, but not limited to: poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.	A DNA profile was not obtained from this item/sample, however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. This could be due to, but not limited to: poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.	PP21 - reported		Nil change recommended by RMU	NDPPTP	No DNA profile – possible sub-threshold peaks	A DNA profile was not obtained from this item/sample, however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. This could be due to, but not limited to: poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.	no change	NDPPTP	No DNA profile – possible sub-threshold peaks	A DNA profile was not obtained from this item/sample, however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. This could be due to, but not limited to: poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.	QPS agree
NFEC	No further examinations conducted	This item/sample was tested for the possible presence of biological material and none were detected. No further testing was conducted on this item.	This item/sample was tested for the possible presence of biological material. All testing has been completed for this item.	PP21 - reported		Changes already recommended on this	NFEC	No further examinations conducted	This item/sample was tested for the possible presence of biological material. All testing has been completed for this item.	QPS request slight change to wording	NFEC	No further examinations conducted	This item/sample was tested for the possible presence of biological material. All testing has been completed for this item.	Further discussion to be had to have this line in conjunction with Item has been examined/sub-sampled
NOPROF	No DNA profile	A DNA profile was not obtained from this item/sample, due to, but not limited to: no DNA present, poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.	A DNA profile was not obtained from this item/sample,	PP21 - reported		Change recommended	NOPRO	No DNA profile	A DNA profile was not obtained from this item/sample,	new expanded comment.	NOPRO	No DNA profile	A DNA profile was not obtained from this item/sample.	Support change
NWQPS	No further work required as per advice from QPS	QPS have provided advice that no further work is required for this item/sample. Testing has been ceased and the sample stored.	QPS have provided advice that no further work is required for this item/sample. Testing has been ceased and the sample stored.	Result automatically filed on FR		Nil change recommended by RMU	NWQPS	No further work required as per advice from QPS	QPS have provided advice that no further work is required for this item/sample. Testing has been ceased and the sample stored.	no change	NWQPS	No further work required as per advice from QPS	QPS have provided advice that no further work is required for this item/sample. Testing has been ceased and the sample stored.	QPS agree
NWQPSR	QPS advised no further work required - results available	QPS have provided advice that no further work is required for this item/sample. Please note that this item/sample has undergone DNA testing and results are available, however these have not been interpreted at this stage. QPS can submit a request to QHFSS for an interpretation of the DNA results if required.	QPS have provided advice that no further work is required for this item/sample. Please note that this item/sample has undergone DNA processing and results are available. These results may be Quantification results alone, or DNA profile results that have not been interpreted at this stage. QPS can submit a request to QHFSS for further work which may include the interpretation of the DNA results if required. results alone, or DNA profile results that have not been interpreted at this stage. QPS can submit a request to QHFSS for further work which may include the interpretation of the DNA results if required.	PP21 - reported		Wording has recently changed for Q&H exhibits	NWQPSR	QPS advised no further work required - results available	QPS have provided advice that no further work is required for this item/sample. Please note that this item/sample has undergone DNA processing and results are available. These results may be Quantification results alone, or DNA profile results that have not been interpreted at this stage. QPS can submit a request to QHFSS for further work which may include the interpretation of the DNA results if required. results alone, or DNA profile results that have not been interpreted at this stage. QPS can submit a request to QHFSS for further work which may include the interpretation of the DNA results if required.	no change	NWQPSR	QPS advised no further work required - results available	QPS have provided advice that no further work is required for this item/sample. Please note that this item/sample has undergone DNA processing and results are available. These results may be Quantification results alone, or DNA profile results that have not been interpreted at this stage. QPS can submit a request to QHFSS for further work which may include the interpretation of the DNA results if required. results alone, or DNA profile results that have not been interpreted at this stage. QPS can submit a request to QHFSS for further work which may include the interpretation of the DNA results if required.	QPS agree
PAPPRP	Presump. PSA test positive, submitted - results pending	This item/sample tested positive to a presumptive test for Prostate Specific Antigen (PSA) which is a component of seminal fluid. This item was submitted for DNA testing. Results are pending.	This item/sample tested positive to a presumptive test for Prostate Specific Antigen (PSA) which is a component of seminal fluid. This item was submitted for DNA testing. Results are pending.	prelim - auto update		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
PBNSC	Presumptive blood test neg. Submitted for cells	This item/sample tested negative to a presumptive test for blood (TMB). This item was submitted for general cell DNA testing.	This item/sample tested negative to a presumptive test for blood (TMB). This item was submitted for general cell DNA testing.	prelim - auto update		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
PBTN	Presumptive blood test neg.	This item/sample tested negative to a presumptive test for blood (TMB).	This item/sample tested negative to a presumptive test for blood (TMB).	prelim - auto update		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
PPSRP	Presump. AP test positive, submitted - results pending	This item/sample tested positive to a presumptive test for seminal fluid (AP). This item was submitted for DNA testing. Results are pending.	This item/sample tested positive to a presumptive test for seminal fluid (AP). This item was submitted for DNA testing. Results are pending.	prelim - auto update		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
PPUCP	Partial DNA profile unsuitable for comparison purposes	This item/sample gave a partial DNA profile which was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information within the DNA profile. This may be due to, but not limited to: poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.	This item/sample gave a partial DNA profile which was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information within the DNA profile.	PP21 - reported		Changes recommnded	DECOMMISSION: see CPU				PPUCP	Partial DNA profile unsuitable for comparison purposes		DECOMMISSION: see CPU
PREBT	Presumptive blood test positive	This item/sample tested positive to a presumptive test for blood (TMB).	This item/sample tested positive to a presumptive test for blood (TMB).	prelim - auto update		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
PRNCID	DNA profile removed from NCIDD	The DNA profile obtained from this item/sample has been removed from NCIDD following advice from QPS, a change in the NCIDD category, or a profile with more information has been obtained.	The DNA profile obtained from this item/sample has been removed from NCIDD following advice from QPS, a change in the NCIDD category, or a profile with more information has been obtained.	PP21 - reported		Nil change recommended by RMU	PRNCID	DNA profile removed from NCIDD	The DNA profile obtained from this item/sample has been removed from NCIDD following advice from QPS, a change in the NCIDD category, or a profile with more information has been obtained.		PRNCID	DNA profile removed from NCIDD	The DNA profile obtained from this item/sample has been removed from NCIDD following advice from QPS, a change in the NCIDD category, or a profile with more information has been obtained.	QPS agree
PSNSC	Presump saliva negative. Submitted for cells	This item/sample tested negative to a presumptive test for saliva (Phadebas). This item/sample was submitted for general cell DNA testing.	This item/sample tested negative to a presumptive test for saliva (Phadebas). This item/sample was submitted for general cell DNA testing.	PP21 - reported		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
PSTI	Possible sub-threshold information	The presence of possible additional DNA was observed within the DNA profile obtained from this item. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. This sub-threshold information did not interfere with the interpretation of the reportable DNA components in the DNA profile obtained from this item.	The presence of possible additional DNA was observed within the DNA profile obtained from this item. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. This sub-threshold information did not interfere with the interpretation of the reportable DNA components in the DNA profile obtained from this item.	PP21 - reported		Nil change recommended by RMU	PSTI	Possible sub-threshold information	The presence of possible additional DNA was observed within the DNA profile obtained from this item. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. This sub-threshold information did not interfere with the interpretation of the reportable DNA components in the DNA profile obtained from this item.		PSTI	Possible sub-threshold information	The presence of possible additional DNA was observed within the DNA profile obtained from this item. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. This sub-threshold information did not interfere with the interpretation of the reportable DNA components in the DNA profile obtained from this item.	QPS agree
PSTN	Presump saliva test negative	This item/sample tested negative to a presumptive test for saliva (Phadebas).	This item/sample tested negative to a presumptive test for saliva (Phadebas).	PP21 - reported		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
PSTP	Presump saliva test positive	This item/sample tested positive to a presumptive test for saliva (Phadebas).	This item/sample tested positive to a presumptive test for saliva (Phadebas).	PP21 - reported		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
SEMND	Semen not detected	Spermatozoa were not observed and/or seminal fluid was not detected on the item/sample tested. QHFSS recommends QPS to commence further examination on items relating to this case if applicable.	Spermatozoa were not observed and/or seminal fluid was not detected on the item/sample tested. QHFSS recommends QPS to commence further examination on items relating to this case if applicable.	PP21 - reported		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
SOHAA	Sample on hold, awaiting advice	This item/sample has been placed on hold and is awaiting additional information from QPS before processing can recommence. This information may relate to, but is not limited to; examination priority, screening requirements.	n/a	Exhibit movement only - not reported to QPRIME		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
SPFRU	Sample processed and final results under	This item/sample was processed under the barcode sent with this exhibit report. The final results will be reported under that barcode.		PP21 - not reported to QPRIME		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
SPP	Sample pooled and processed under	This item/sample was pooled and submitted for DNA testing under the barcode sent with this exhibit report. The final results will be reported under the barcode.	n/a	PP21 - not reported to QPRIME		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
SPPDNA	Micro positive for sperm. Submitted-results pending	Spermatozoa were detected on this item/sample by microscopy. This item/sample was submitted for DNA testing. Results are pending.	Spermatozoa were detected on this item/sample by microscopy. This item/sample was submitted for DNA testing. Results are pending.	PP21 - reported		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
SRP	Submitted-results pending	This item/sample was submitted for DNA testing. Results are pending.	n/a	Received as a exhibit movement only		Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
SUFP	This sample has undergone further processing	This item/sample has undergone further processing and an improved DNA profile has been obtained.	n/a	PP21 - not reported to QPRIME		Nil change recommended by RMU	SUFP	This sample has undergone further processing	This item/sample has undergone further processing and an improved DNA profile has been obtained.	no change	SUFP	This sample has undergone further processing	This item/sample has undergone further processing and an improved DNA profile has been obtained.	QPS agree
NSIP	No statistical interpretation performed	In the absence of a reference sample/s for comparison, a statistical interpretation has not been performed.	In the absence of a reference sample/s for comparison, a statistical interpretation has not been performed. To nominate a person of interest for comparison to the mixed DNA Profile obtained from this exhibit, please contact the DNA Management Section	PP21 - reported		Chnages recommended	NSIP	No statistical interpretation performed	In the absence of a reference sample/s for comparison, a statistical interpretation has not been performed. To nominate a person of interest for comparison to the mixed DNA Profile obtained from this exhibit, please send a task to org unit 3211.	exp comment had already changed. Continue with new comment.	NSIP	No statistical interpretation performed	In the absence of a reference sample/s for comparison, a statistical interpretation has not been performed. To nominate a person of interest for comparison to the mixed DNA Profile obtained from this exhibit, please send a task to the DNA Liaison and Major Crime Unit (3211)	Changed expanded wording
SUFWC	Sample undergone further work - conditioned	This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or three contributors. Based on information provided to the laboratory, this mixed DNA profile has now been conditioned.	This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or more contributors. Based on information provided to the laboratory, this mixed DNA profile has now been conditioned.	PP21 - not reported to QPRIME			SUFWC	Sample undergone further work - conditioned	This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or more contributors. Based on information provided to the laboratory, this mixed DNA profile has now been conditioned.	no change	SUFWC	Sample undergone further work - conditioned	This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or more contributors. Based on information provided to the laboratory, this mixed DNA profile has now been conditioned.	QPS agree
SUFNS	Sample undergone reprocessing - new software	This item/sample has undergone further processing and/or assessment with new software available to the laboratory. An updated DNA profile interpretation has been provided.					SUFNS	Sample undergone reprocessing - new software	This item/sample has undergone further processing and/or assessment with new software available to the laboratory. An updated DNA profile interpretation has been provided.	no change	SUFNS	Sample undergone reprocessing - new software	This item/sample has undergone further processing and/or assessment with new software available to the laboratory. An updated DNA profile interpretation has been provided.	QPS agree
TRQ	Testing restarted on advice from QPS	QPS have provided advice that testing is now required for this item/sample. Testing has been restarted.					TRQ	Testing restarted	QPS have provided advice that testing is now required for this item/sample. Testing has been restarted.	no change	TRQ	Testing restarted on	QPS have provided advice that testing is now required for this item/sample. Testing has been restarted.	QPS agree
Query Mnen	Hair located - not examined at this time	During the examination of this exhibit one or more hairs were located. Based on case information available or testing requested, this has not been submitted at this time, however has been retained for potential future analysis if requested.									??	Hair located - not examined at this time	During the examination of this exhibit one or more hairs were located. Based on case information available or testing requested, this has not been submitted at this time, however has been retained for potential future analysis if requested.	Refer to Paula Brisotto - unsure what Mnemonic is

Mnemonic	Cold link line	Expanded Comment	Review by Insp David Neville	Review by DRMU	Notes	Recommndations
	Exhibit # QP******* S Full DNA profile (PP21)	DNA COLD LINK - This item/sample gave a full DNA profile which matches the DNA profile obtained from Barcode Number ********* a DNA sample obtained from SURNAME, GIVEN NAMES DOB **/**/**** CNI No. ********* DNA Profile Number LKR0000***.		DNA COLD LINK - This item/sample gave a full DNA profile which matches the DNA profile obtained from Barcode Number ********* a DNA sample obtained from SURNAME, GIVEN NAMES DOB **/**/**** CNI No. ********* DNA Profile Number LKR0000***.	Full single source DNA profile	Nil changes recommended by RMU
	Exhibit # QP******* S Partial DNA profile (PP21) -	DNA COLD LINK - This item/sample gave a partial DNA profile which matches the DNA profile obtained from Barcode Number ********* a DNA sample obtained from SURNAME, GIVEN NAMES DOB **/**/**** CNI No. ********* DNA Profile Number LKR0000***.		DNA COLD LINK - This item/sample gave a partial DNA profile which matches the DNA profile obtained from Barcode Number ********* a DNA sample obtained from SURNAME, GIVEN NAMES DOB **/**/**** CNI No. ********* DNA Profile Number LKR0000***.	Partial single source DNA profile	Nil changes recommended by RMU
	1. Exhibit # QP******* S 2 person mixed DNA profile 2. Exhibit # QP***** I INTEL (2 person mix) - 3. Exhibit # QP******* S 3 person mixed DNA profile 4. Exhibit # QP******* I INTEL (3 person mix) -- **Change to:** **Exhibit # QP******* S mixed DNA profile**	DNA COLD LINK - This item/sample gave a DNA profile that indicated the presence of DNA from more than one contributor. Represented within the mixed DNA profile are some or all of the components of the DNA profile obtained from Barcode Number ********* a DNA sample obtained from SURNAME, GIVEN NAMES DOB **/**/**** CNI No. ********* DNA Profile Number LKR00*****.		DNA COLD LINK - This item/sample gave a DNA profile that indicated the presence of DNA from more than one contributor. Represented within the mixed DNA profile are some or all of the components of the DNA profile obtained from Barcode Number ********* a DNA sample obtained from SURNAME, GIVEN NAMES DOB **/**/**** CNI No. ********* DNA Profile Number LKR00*****.	1 Full profile 2. Partial profile 3. Full profile 4. Partial profile Suggested changed: If required - RMU staff can confirm from NCIDD if it is a full or partial DNA profile.	RECOMMEND CHANGE -when RMU are creating the cold link result, they will be able to refer to the Exhibit register and FSS DNA Analaysis table to determine if caveat wording needs to be added.

EXH line	Expanded Comment

Mnemonic	EXH line	Expanded Comment	Change for next version/ alternative wording	Notes
CMPCE	Complex mixed DNA profile – cannot exclude	This item/sample gave a full or partial mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles) and therefore could not be loaded to NCIDD. The DNA profile obtained from the barcode sent with this exhibit report cannot be excluded as being a possible contributor of DNA to this mixed DNA profile.	no change suggested	Profiler plus result
CMPULN	Complex mixed DNA profile. Unable to load to NCIDD	This item/sample gave a full or partial mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles) and therefore could not be loaded to NCIDD. This complex mixed DNA profile cannot be interpreted further as no reference sample has been received for direct comparison; or alternatively, comparison with additional reference samples may be possible if forthcoming.	no change suggested	Profiler plus result
DPNPTP	9 loci DNA profile- NCIDD- possible sub-threshold peaks	This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. These sub-threshold peaks did not interfere with the interpretation of the reportable DNA components in the 9 loci DNA profile obtained, which has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result
DPPTP	9 loci DNA profile - possible sub-threshold peaks	This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the 9 loci DNA profile obtained.	n/a	Profiler plus result
FUPNPN	9 loci DNA profile. Uploaded to NCIDD	This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile has been selected for loading to NCIDD and will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result
FUPROF	9 loci DNA profile	This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result

INTER7	Interim result- Mixed major comp.- NCIDD. Rework Reqd	This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a mixed DNA profile which indicates the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD (within Australia) will be searched against this DNA profile. Where information was obtained, the major DNA profile matched the DNA profile for the barcode sent with this exhibit report. Final results are pending.	N/A	Profiler plus result
IPTPR	Interim- 9 loci, pos.sub-thresh peaks-NCIDD.Rework Reqd	This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a complete 9 loci DNA profile; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be use for comparison purposes, as it was below QHFSS standard reporting thresholds These sub-threshold peaks did not interfere with the interpretation of the reportable DNA components in the 9 loci DNA profile obtained, which has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD (within Australia) will be searched against this DNA profile. Final results are pending.	n/a	Profiler plus result
IRMMC	Interim result- Mixed minor comp.- NCIDD. Rework Reqd	This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a mixed DNA profile which indicates the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD (within Australia) will be searched against this DNA profile. Where information was obtained, the minor DNA profile matched the DNA profil for the barcode sent with this exhibit report. Final results are pending.	n/a	Profiler plus result
MDNA1	Mixed DNA profile, complex minor component cannot exclude	This item/sample gave a mixed DNA profile DNA profile which indicated the presence of DNA from more than two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile indicated the presence of DNA from more than one contributor. The DNA profile obtained from the barcode sent with this exhibit report cannot be excluded as being a possible contributor of DNA to the minor component of this mixed DNA profile.	n/a	Profiler plus result

MDPIL	Minor/Remaining DNA profile - Intel profile loaded NCIDD	This item/sample gave a mixed DNA profile, of which the minor or remaining DNA profile contained insufficient information for NCIDD matching as it was below the QHFSS stringency for reporting a match on NCIDD. The profile has been selected for loading to NCIDD for intelligence purposes only and any resulting matches will be reported in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution.	n/a	Profiler plus result
MIPDNA	Mixed DNA profile conditioned on – NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that the DNA profile obtained from the barcode sent with this exhibit report has contributed to this mixed DNA profile. This result should always be used in conjunction with “Mixed DNA profile. Remaining profile after conditioning”. This DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result
MIPMAC	Mixed DNA profile. Major component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The full major DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result
MIPMIC	Mixed DNA profile. Minor Component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The full minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result
MIPMUN	Mixed DNA profile. Major component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile has been selected for loading to NCIDD. The full major DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result
MIPPRO	Mixed profile. Remaining profile after conditioning – NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the “Mixed DNA profile conditioned on” exhibit report. The DNA profile remaining after the conditioning matches the DNA profile obtained from the barcode sent with this report. This DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result

MIRIN	Mixture Interp reqd - Intel profile loaded to NCIDD	This item/sample gave a mixed DNA profile that has been interpreted for intelligence purposes only. This interpretation may not be able to be used for evidentiary purposes. This means that we may have lowered our routine interpretational and NCIDD matching guidelines in order to assist with the generation of intelligence information. This intelligence DNA profile has been selected for loading to NCIDD and further explanation of the interpretations ma will follow in an intelligence report. It should be noted that the interpretation provided within this intelligence report may not meet the stringent court reporting guidelines and therefore wording within an evidential statement may be different. The Intelligence DNA profile loaded to NCIDD will be searched against any DNA profiles currently held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this intelligence DNA profile. It will be outlined in the Intelligence report that this mixed DNA profile may be reported differently in an evidentiary statement.	n/a	Profiler plus result
MPCMU	Mixed profile- complex minor unsuit for interp or compar.	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile indicated the presence of DNA from more than one contributor. This minor DNA profile is too complex for meaningful interpretation or comparison purposes due to the unknown number of potential contributors and/or the limited amount of information within the minor DNA profile.	n/a	Profiler plus result
MPCO	Mixed DNA profile conditioned on	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that the DNA profile obtained from the barcode sent with this exhibit report has contributed to this mixed DNA profile. This result should always be used in conjunction with “Mixed DNA profile. Remaining profile after conditioning”	n/a	Profiler plus result
MPMAIN	Mixed profile, major component insuff for NCIDD matching	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result

MPMC3	Mixed profile, minor comp. 3 of 18 DNA components	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 3 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result
MPMC4	Mixed profile, minor comp. 4 of 18 DNA components	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 4 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result
MPMC5	Mixed profile, minor comp. 5 of 18 DNA components	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 5 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result
MPMIIN	Mixed profile, minor component insuff for NCIDD matching	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result

MPMINC	Mixed profile, minor component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile has been loaded to NCIDD. The full minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result
MPMPIM	Mixed profile,minor profile insuff– indicated male origin	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile did not contain sufficient information for comparison purposes other that to say it indicated it was of male origin.	n/a	Profiler plus result
MPMUC	Mixed profile Minor component unsuitable for comparison	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information obtained.	n/a	Profiler plus result
MPNMM	Mixed profile, No major/minor – cannot exclude	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could not be separated into major and minor DNA profiles and could not be loaded to NCIDD. The DNA profile obtained from the barcode sent with this exhibit report cannot be excluded as being a possible contributor of DNA to this mixed DNA profile.	n/a	Profiler plus result
MPNMUN	Mixed profile, No major/minor. Unable to load to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could not be separated into major and minor DNA profiles and could not be loaded to NCIDD. In the absenc of reference samples, no further interpretation can be conducted; or comparison with additional reference samples may be possible if forthcoming.	n/a	Profiler plus result
MPPMA	Mixed profile, partial major component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile. Where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result
MPPMAN	Mixed DNA profile, partial major component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile which has been selected for loading to NCIDD. Where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result

MPPMI	Mixed profile, partial minor component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile. Where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result
MPPMIN	Mixed DNA profile, partial minor component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which has been selected for loading to NCIDD. Where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result
MPRO	Mixed profile, complex mixed minor component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from more than two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile indicated the presence of DNA from more than one contributor. This minor DNA profile cannot be interpreted further as no reference sample has been received for direct comparison; or alternatively, comparison with additional reference samples may be possible if forthcoming.	n/a	Profiler plus result
MPRP	Mixed DNA profile. Remaining profile after conditioning	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the “Mixed DNA profile conditioned on” exhibit report. The DNA profile remaining after the conditioning matches the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result
MPRPAC	Mixed profile. Remain profile after cond – insuff NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the “Mixed DNA profile conditioned on” exhibit report. The DNA profile remaining after the conditioning was a partial DNA profile which which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This remaining DNA profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this remaining partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result

MPRPC	Mixed profile. Remain profile after cond–unsuitable NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the "Mixed DNA profile conditioned on" exhibit report. The DNA profile remaining after the conditioning was a partial DNA profile which contained insufficient information for searching on NCIDD, and therefore is unable to be loaded to NCIDD. This remaining DNA profile may contain enough information to compare to other DNA profiles for either inclusion or exclusionary purposes. Where information was obtained, the DNA components of this remaining partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result
PAPNPN	Partial DNA profile. Uploaded to NCIDD	This item/sample gave a partial DNA profile. Where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This partial DNA profile has been selected for loading to NCIDD and will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result
PD3C	Partial DNA profile, 3 of 18 DNA components	This item/sample gave a partial DNA profile which contained 3 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result
PD4C	Partial DNA profile, 4 of 18 DNA components	This item/sample gave a partial DNA profile which contained 4 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result

PD5C	Partial DNA profile, 5 of 18 DNA components	This item/sample gave a partial DNA profile which contained 5 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result
PDNA	Partial DNA profile	This item/sample gave a partial DNA profile. Where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result
PDNAIN	Partial DNA profile. Insufficient for NCIDD matching	This item/sample gave a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result
PDNPTP	Partial DNA profile- NCIDD- possible sub-threshold peaks	This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be use for comparison purposes, as it was below QHFSS standard reporting threshold The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained, which has been selected for loading to NCIDD. This partial DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result
PDPTP	Partial DNA profile - possible sub-threshold peaks	This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be use for comparison purposes, as it was below QHFSS standard reporting threshold The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained.	n/a	Profiler plus result

PIRIN	Partial profile Interp reqd – Intel profile loaded NCIDD	This item/sample gave a partial DNA profile which contained an indication of DNA at a level less than the laboratorys standard reporting threshold. This profi was submitted for further analysis below QHFSS standard reporting thresholds for intelligence purposes. The subsequent profile has been selected for loading to NCIDD for intelligence purposes only and further explanation of the interpretations made will follow in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution.	n/a	Profiler plus result
PPINPT	Partial profile, insuff NCIDD- pos. sub-threshold peaks	This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be use for comparison purposes, as it was below QHFSS standard reporting thresholds The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained. This partial DN profile was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result
PPIPL	Partial profile - Intel profile loaded to NCIDD	This item/sample gave a partial DNA profile which contained insufficient information for NCIDD matching as it was below the QHFSS stringency for reporting a match on NCIDD. This profile may also have indications of DNA at a level less than the laboratorys standard reporting threshold, therefore the profile may have been submitted for further analysis below standard reporting thresholds for intelligence purposes. The profile has been selected for loading to NCIDD for intelligence purposes only and any matches will be reported in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution.	n/a	Profiler plus result
SCANM	Suspect check actioned - no match	The nominated suspect can be excluded as a potential contributor to the DNA profile obtained from this item/sample.	n/a	Profiler plus result
SCII	Suspect check - insufficient information to compare	There was insufficient information in the DNA profile obtained from this item/sample to determine if the nominated suspect could be a potential contributor.	n/a	Profiler plus result
SCM	Suspect check - match	The DNA profile obtained from the nominated reference barcode sent with this exhibit report matches, where information was obtained, the DNA components of this full or partial DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information and subsequent statistical calculations are required in a statement for court.	n/a	Profiler plus result

SCMAJM	Suspect check - major profile match	The DNA profile obtained from the nominated reference barcode sent with this exhibit report matches, where information was obtained, the full or partial major DNA profile separated from this mixed DNA profile.This comparison was done for intelligence purposes only. A reference evidence sample should be provided this information and subsequent statistical calculations are required in a statement for court.	n/a	Profiler plus result
SCMINM	Suspect check - minor profile match	The DNA profile obtained from the nominated reference barcode sent with this exhibit report matches, where information was obtained, the full or partial minor DNA profile separated from this mixed DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information and subsequent statistical calculations are required in a statement for court.	n/a	Profiler plus result
SCCE	Suspect check - cannot exclude	The DNA profile obtained from the nominated reference barcode sent with this exhibit report cannot be excluded as a possible contributor of DNA to this mixed DNA profile. A reference evidence sample should be provided if this information is required in a statement for court. A statistical analysis may not be possible for this interpretation.	n/a	Profiler plus result
IMAJUN	Mixed profile-no major/minor. INTEL Major loaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors and could not be clearly separated into major and minor DNA profiles. An attempt was made to separate the contributors to this mixed DNA profile in order to load intelligence information to the National Criminal Investigation DNA Database (NCIDD) for intelligence purposes only. The Intel Major DNA profile loaded to NCIDD for matching purposes will be searched against any DNA profiles currently held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this intelligence DNA profile. It is important to note that this process has been performed for intelligence purposes only, and any reference samples subsequently received which match these DNA components will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile.	n/a	Profiler plus result
IMINUN	Mixed profile-no major/minor. INTEL Minor loaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors and could not be clearly separated into major and minor DNA profiles. An attempt was made to separate the contributors to this mixed DNA profile in order to load intelligence information to the National Criminal Investigation DNA Database (NCIDD) for intelligence purposes only. The Intel minor DNA profile loaded to NCIDD for matching purposes will be searched against any DNA profiles currently held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this intelligence DNA profile. It is important to note that this process has been performed for intelligence purposes only, and any reference samples subsequently received which match these DNA components will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile.	n/a	Profiler plus result

IMCOU	INTEL- mix DNA profile conditioned on unknown DNA profile	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors and could not be separated into major and minor DNA profiles. For intelligence purposes only, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile and may include a statistical analysis. This result should always be used in conjunction with “INTEL- mix profile remaining after cond on unknown- NCIDD”	n/a	Profiler plus result
IMROU	INTEL - mix profile remaining after cond on unknown- NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors and could not be separated into major and minor DNA profiles. When conditioning on the assumed known contributor for intelligence purposes only, a remaining DNA profile was obtained. This Intel remaining DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only. If the assumption for conditioning no longer holds, then any reference sample will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile and may include a statistical analysis. This result should always be used in conjunction with “INTEL- mix DNA profile conditioned on unknown DNA profile”.	n/a	Profiler plus result
ENMDP	ENVM - Major DNA profile	This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could b separated into major and minor DNA profiles, of which the major was a full or partial DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained.	n/a	Lab clean - not reported
ENMDPU	ENVM – Minor DNA profile unsuitable for comparison	This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could b separated into major and minor DNA profiles, of which the minor DNA profile contained insufficient information for comparison purposes due to the limited amount of information obtained. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.		Lab clean - not reported

ENMIDP	ENVM – Minor DNA profile	This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could b separated into major and minor DNA profiles, of which the minor DNA profile was a full or partial DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained	n/a	Lab clean - not reported
INTER1	Interim result- Part profile obtained- NCIDD. Rework Reqd	This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a partial DNA profile which has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD (within Australia) will be searched against this DNA profile. Final results are pending.	n/a	Check required - is this is the same as INTSSR / or no longer used
INTER2	Interim result- Partial profile undergoing rework	This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a partial DNA profile. Final results are pending.	n/a	Check required - is this is the same as INTSSR / or no longer used
INTER3	Interim result- Partial profile -Intel NCIDD. Rework Reqd	This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a partial DNA profile which contained insufficient information for NCIDD matching according to standard reporting protocols. After further analysis below standard reporting thresholds the profile has been selected for loading to NCIDD for intelligence purposes only. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD (within Australia) will be searched against this DNA profile. Final results are pending.	n/a	Check required - is this is the same as INTSSR / or no longer used
TRQ	Testing restarted on advice from QPS	QPS have provided advice that testing is now required for this item/sample. Testing has been restarted.		No longer in use - not received since 2011

Mnemonic	EXH line	Expanded Comment	Change for next version/ alternative wording	Notes
ENAQS	ENVM additional quality search conducted see Intel report	Part of the Quality Assurance process for all environmental samples is to compare the DN profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. If the profile obtained cannot be matched to a QHFSS DNA Analysis staff or QPS staff member; a second Quality assurance process is used. This search capability is restricted within DNA Analysis to the Managing Scientist and the Quality & Projects Senior Scientist and utilises the DNA Analysis Database (DAD). This quality search is only performed to aid QPS in their investigation of any potential contamination events. In this instance, a match was obtained from this additional quality assurance search. Further information is contained within the intelligence report that will accompany this exhibit report.	n/a	Lab clean not reported
ENCMDP	ENVM - Complex mixed DNA profile	This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles), and as such, no further interpretation can be conducted as this time. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.	n/a	Lab clean not reported
ENCMPU	ENVM- Complex mixture unsuitable for interp or comparison	This environmental sample gave a complex mixed DNA profile which contained an unkno number of contributors or a limited amount of information. This mixture is not suitable for meaningful interpretation due to either its complexity relating to the unknown and potentially large number of contributors and/or the limited amount of information within the profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.	n/a	Lab clean not reported
ENFDP	ENVM - Full DNA profile	This environmental sample gave a full DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to th DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained	n/a	Lab clean not reported
ENNDP	ENVM - No DNA profile	No DNA profile was obtained from this environmental sample. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.	n/a	Lab clean not reported
ENPDP	ENVM -Partial DNA profile	This environmental sample gave a partial DNA. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to th DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained	n/a	Lab clean not reported

ENPDPU	ENVM - Partial profile unsuitable for comparison purposes	This environmental sample gave a partial DNA profile which was insufficient for comparis purposes or meaningful interpretation due to the limited amount of information obtained. It standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.	n/a	Lab clean not reported
QCF	Quality control failure – results not reportable	During the processing of this item/sample, a failure in one of the quality control processes was identified. Investigations into this occurrence were undertaken; however any results for this sample are not reportable.	no change suggested	QHFSS quality control failure
QCFRQ	Quality control failure, refer to QPS	During the processing of this item/sample, QHFSS quality control processes identified the integrity of this sample is compromised. Results for this sample are not reportable.	no change suggested	QPS quality issue
QFIH	Quality flag identified, on hold awaiting advice from QPS	During the processing of this item/sample, QHFSS quality control processes indentified the integrity of this sample may be compromised. Advice is required from QPS to determine whether any results for this sample are reportable.	no change suggested	QHFSS quality control failure

Mnemonic	EXH line	Expanded Comment	Change for next version/ alternative wording	Notes
HOIS	Hair located on the outside of an in-tube submission	A hair was located either outside the tube or partially hanging in and out of the tube. It is unclear if this hair was part of the collected item or incorrectly transferred during collection. This hair/hair portion has been stored and will only be analysed if a request is provided.	no change suggested	Information sent via Examination request notification by QHFSS to SOC / SCI officer
ISCB	Incorrect submission of cigarette butt	This cigarette butt was received in a tube. Items provided in a tube are intended to be submitted directly for DNA processing with minimal manual intervention. This sample required further examination as it was received as a whole cigarette butt. Please submit whole cigarette butts in a Crime Scene Sample envelope or as a sub-sample of the filter paper.	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer
LDIS	Labelling discrepancy	There is a labelling discrepancy (Occurrence number or sample description) between the exhibit packaging and th AUSLAB/Forensic Register interface records. This sample can not be processed until the labelling discrepancy is resolved. The discrepancy will be highlighted to the QPS Sample Management Unit for clarification in the first instance, and if unable to be resolved, will be referred to the appropriate QPS officer for resolution. Please ensure all labelling details are correct before submission to the DNA Analysis Laboratory	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer
MIES	Sample required manual intervention - excess substrate	This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as excess substrate was contained within the tube. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process.	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer
MIISB	Multiple items incorrectly submitted under single barco	Multiple items, or multiple AP positive areas have been submitted under a single barcode identifier. Each item requires its own unique barcode, as the barcode is used for reporting purposes to both the forensic register and the National Criminal Investigation DNA Database. Each item will be allocated a new barcode for processing and reporting purposes.	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer

MISSTL	Sample required manual intervention - swab stick too l	This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as the swab stick was too long and required shortening to enable downstream processing. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process. The ideal stick length should be no more than 24mm total length (swab stick plus swab head).	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer
MITRI	Sample reqd manual intervention- tlift rolled incorrectly	This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as the tapelift was rolled incorrectly, impeding downstream processing. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process.	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer
NBOS	No barcode on sample	The item/sample provided in a tube was not labelled with a barcode. A barcode is required for the processing of the item and for continuity purposes. A barcode the same as that attached to the packaging has been affixed to the item.	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer
ESCD	Entire sample consumed	The entire item/sample was consumed during examination	n/a	Exhibit movement - result report not received by RMU
OHII	On hold - insufficient information provided for testing	There was insufficient information provided with this submission to determine what type of analysis is required for this item/sample eg, saliva, semen. This sample is to be placed on hold until further information on the testing requirements for this sample is provided.	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer- not used since 2015
SRMI	Sample required manual intervention prior to extraction	This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the extraction process.		Information sent via Examination request notification by QHFSS to SOC / SCI officer - not used since 2011

EXHIBIT 191

[redacted]

From: Harris.LibbyA[ESC]
Sent: Wednesday, 7 September 2022 09:30
To: Neville.DavidH[OSC]
Subject: FW: NCIDD upload wording

OFFICIAL

OFFICIAL

From: McIntyre.OliviaM[OSC] <[redacted]
Sent: Wednesday, 21 July 2021 14:12
To: Justin Howes <[redacted] Allison Lloyd [redacted] Adrian Pippia
<[redacted]
Cc: Harris.LibbyA[OSC] <[redacted] Foxover.StephanP[OSC]
<[redacted]
Subject: NCIDD upload wording

Hi all,

Further to today's meeting, the following wording is what goes to QPRIME to Mixed DNA upload results. It appears that it is currently generic to cover both barcode and unknown results.

> Mix - NCIDD upload
>
> Statistical analysis resulted in a DNA profile that was able to be loaded to NCIDD. The associated barcode/unknown designation sent with this exhibit report is a possible contributor to this mixed DNA profile. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.
>
> NCIDD Upload
>
> This item/sample yielded a DNA profile that has been uploaded to NCIDD for searching. Further advice will be provided in the event a match is received.

Perhaps we can incorporate information from both results to cover everything we need.

> This item/sample yielded a DNA profile that has been uploaded to NCIDD for searching. The associated barcode/unknown designation sent with this exhibit report is a possible contributor to this DNA profile. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Further advice will be provided in the event a match is received.

Kind regards

Olivia McIntyre

DNA Management Officer
DNA Management Section, Forensic Services Group
Operations Support Command
Ph: [redacted] Mobile [redacted]
[redacted]
200 Roma Street, Brisbane
[redacted]

EXHIBIT 192

[redacted]

From: Harris.LibbyA[ESC]
Sent: Wednesday, 7 September 2022 09:30
To: Neville.DavidH[OSC]
Subject: FW: Minutes from meeting
Attachments: Minutes_21072021.docx

OFFICIAL

OFFICIAL

From: Justin Howes <[redacted]
Sent: Thursday, 22 July 2021 09:36
To: Foxover.StephanP[OSC] <[redacted] Harris.LibbyA[OSC] <[redacted] McIntyre.OliviaM[OSC] <[redacted]
Cc: Allison Lloyd <[redacted] Adrian Pippia <[redacted]
Subject: Minutes from meeting

Hi,
I thought best to capture our discussions as best I could in a meeting minutes format.

Please let me know if this is a fair capture, or if amendments are necessary.

Thanks
Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

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

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

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

Forensic and Scientific Services (FSS)
Exhibit Result Line Revision: Meeting with QPS – Minutes

Date: 21 July 2021
Time: 10.30am
Venue: CR103
Meeting Commenced at: 10:30am

Name	Initials	Position	Attending
Participants			
Justin HOWES	JAH	Team Leader, Forensic DNA Analysis	Y
Allison LLOYD	AKL	Senior Forensic Scientist	Y
Adrian Pippia	AAP	Reporting Scientist	Y
S/Sgt Steve Foxover	SF	QPS	Y
Sgt Libby Harris	LH	QPS	Y
Olivia McIntyre	OM	QPS	Y

Item	**Topic**
1	**Review of spreadsheet**
	** General discussion – points below are not chronological JAH: Meeting was a ‘Part A’ related to result lines only, after DNA profile interpretation. Parts B and C (Presumptive and Quality/Environmental) are with Paula Brisotto as contact point to work through. This could be handled by phone or email. Many enhancements have been placed into AZURE thus far, so will need to be extracted for discussion. Not anticipated that this will be a lengthy discussion point. LH: bdna likely to come to QPS in the next few weeks, so trying to prepare for that by progressing these revisions prior to the bdna meeting. Discussion on use of SS1 and NUP lines – could seek an enhancement to duplicate the information in the associated barcode field so that NUP could be used for mixtures and single source profile uploads. If the expanded comment for NUP could account for UK and barcode, then this could work. ACTION: edit wording for NUP slightly to facilitate this. QPS mentioned that they do not act upon the result sent with the DNA Intel barcodes; they wait for the cold link and report after receiving this link. FSS advised that with ceasing DNA Intel sample searches, it is FSS’s preference that the appropriate programming amendments be completed prior to stopping DNA Intel sample reporting due to potential quality issues regarding donor designation for large cases; eg, where manual intervention is employed by FSS to amend an DNA Intel Sample match to an

unknown designation but the FR is unable to assign the next consecutive donor label. The FR Req/Task system could be used to bilaterally communicate for specific cases.

Without the DNAIntel process, agreed that we need to ensure that when this element is no longer active, to make sure that the elimination database and scan within the case (for matches) still operates effectively. Need to ensure there is a process to address cases that are ‘in progress’ – scenarios to be devised and tested by FSS to look into numbering conventions of UKs and to ensure the sequence is clear. ACTION: FSS to perform scenario testing and seek feedback from QPS

LR8 – agree to remove ‘LR’ from line description

SUFP – discussion that the generic line could account for new software, reworking and conditioned approach. Propose that the line be used for all of these situations and the expanded comment to truncate to ‘This item/sample has undergone further processing.’ – agreed.

TRQ – discussion that this line has value in ‘starting the clock’ when notified that the sample is to progress further. This could allow metrics around TAT for identification of bottlenecks in the process and show when something has started and finished a certain process. QPS could consider a tickbox or similar enhancement that could be used to create a task/worklist entry etc. to notify FSS to restart a sample and possibly add the line at that point. ACTION: QPS to raise an enhancement on tickbox. ACTION: JAH to remind staff to use this TRQ line as it appears not to be used too often.

Tabs on spreadsheet relate to decommissioned lines. ACTION: FSS to verify the lines listed are indeed for decommissioning

Cold link lines all appear to be addressing the purpose – no further changes requested.

Parts B and C relating to presumptive testing and environmental samples – Paula Brisotto to be the contact point for these parts via phone or email.

OTHER BUSINESS

- Cold cases – JAH: QPS to check in again in 4 weeks time to see if we can take on any ‘new’ cold cases. Cathie Allen briefed on hold on new cases and check in 4 weeks time.
- OM asked about ref samples if moving to a new kit and advised that Insp has spoken to FSS about potential for upgrade, especially for old Profiler Plus samples. AKL said a good part of this would be to search for duplicates so that not upgrading the same person.
    - Discussion was that this would seem to be a big project and would there be potential for business case for funding, and whether funding could include y-STR testing in the future too. Similar work conducted at Vicpol and advice could be sought from them.
- JAH mentioned that statement requests are very high and that even when issuing record numbers, the number appearing unallocated does not change much - not great for staff morale. It is known that IOs get a message to say that the statement request won’t start until all testing is complete. Idea in future is to build upon what we have already and only have visible what is actually ready to write ie. after all results issued.

	○ Enhancement might be made that could work to populate lists only when ready to write.
8	**Actions**
	• Edit wording for NUP slightly to facilitate this: JAH • FSS to perform scenario testing and seek feedback from QPS: AAP • QPS to raise an enhancement on tickbox to inform ‘testing restarted’ for items/samples: LH • FSS staff to be reminded to use TRQ when starting a process again: JAH • FSS to verify the lines listed are indeed for decommissioning: AKL

EXHIBIT 193

[redacted]

From: Harris.LibbyA[ESC]
Sent: Wednesday, 7 September 2022 09:31
To: Neville.DavidH[OSC]
Subject: FW: QPS-FSS result line discussion document 18082021.xlsx
Attachments: QPS-FSS result line discussion document 18082021.xlsx

OFFICIAL

OFFICIAL

From: McIntyre.OliviaM[OSC] <[redacted]
Sent: Thursday, 9 September 2021 14:00
To: Allison Lloyd <[redacted]
Cc: Harris.LibbyA[OSC] <[redacted]
Subject: QPS-FSS result line discussion document 18082021.xlsx

Hi Allison,

For discussion.

Kind regards

Olivia

Olivia McIntyre
DNA Management Officer
DNA Management Section, Forensic Services Group
Operations Support Command
Ph: [redacted] Mobile [redacted]
[redacted]
200 Roma Street, Brisbane
[redacted]

Mnemonic	EXH Line	Expanded Comment	Additional QPS information to be added	QPS notes 18/08/2021	Analytical / Reporting teams	FSS comments
SS	Single source DNA profile	The DNA profile obtained from this item/sample indicated the presence of one contributor.		To be used as an overaching line for single source results.		New line with no barcodes needed in associated barcode field
SS1	Single source DNA profile - Intel	The DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.		To be used for all single source unknown and intelligence link results that are validated. To be jprogrammed in the same way as 1SS currently is to split the result wording depending if it is an unknown or intel barcode linked. QHFSS to have the ability to add either an unknown / intel barcode in linked field.	Reporting	No comment
1SSNCD	NCIDD upload single source DNA profile	A single source DNA profile was obtained from the item/sample. This DNA profile has been selected for loading to NCIDD, and it will be searched against any DNA profiles held on NCIDD (as per the NCIDD matching rules). Further advice will be provided in the event a match is received.				
NUP	Mix - NCIDD Upload	This item/sample yielded a DNA profile that matches the associated barcode, or has been designated as an Unknown profile. This DNA contribution has been uploaded to NCIDD for searching. If an Unknown profile was uploaded to NCIDD, further advice will be provided in the event a match is received.			Reporting	No comment
MIX	Mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from at least two contributors.			Reporting	No comment
LR1	Support for contribution: LR >100 billion	This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.			Reporting	No comment
LR2	Support for contribution: LR 1 billion to 100 billion	This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.			Reporting	No comment
LR3	Support for contribution: LR 1 million to 1 billion	This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.			Reporting	No comment
LR4	Support for contribution: LR 100 000 to 1 million	This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.			Reporting	No comment
LR5	Support for contribution: 10 000 to 100 000	This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.			Reporting	Agree with change
LR6	Support for contribution: 1000 to 10 000	This DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.			Reporting	Agree with change
LR7	Support for contribution: 100 to 1000	This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.			Reporting	Agree with change
LR8	Support for contribution: 2 to 100	This DNA profile is between 2 and 100 times more likely to have occurred if the barcode sent with this exhibit report has contributed to the DNA profile, rather than has not contributed.			Reporting	Agree with change
LR9	Inconclusive	The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other reference samples may provide a different statistical interpretation.			Reporting	No comment

LR10	Supports non contribution	The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.			Reporting	No comment
AC	Assumed Contributor	Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this DNA profile. Given the assumption for this person, no statistical interpretation has been performed.			Reporting	No comment
ACINT	Assumed contributor - Intel	For Intelligence purposes, it has been assumed that the designated unknown has contributed to this DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically evaluated against the DNA profile without a contribution being assumed and the result reported as a likelihood ratio.			Reporting	No comment
REMINT	Contribution for NCIDD - Intel purposes	The DNA profile from the designated unknown sent with this exhibit report could be a contributor to the DNA profile along with the assumed known contributor. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.			Reporting	No comment
CCUNK	Remaining contribution consistent with unknown	Based on this assumption, a remaining DNA profile has been separated. This is consistent with the unknown designation (previously identified within this case and loaded to NCIDD) sent with this exhibit report.			Reporting	No comment
EVEX	Single evidence sample excluded	The statistical interpretation shows that the associated barcode sent with this exhibit report has been compared, and can be excluded as having contributed to this mixed DNA profile.			Reporting	No comment
INT1	Interim result - Intel NCIDD. Rework Required.	A DNA contribution has been uploaded to NCIDD for intelligence purposes only. Final results are pending.			Reporting	No comment
IRRFI	Intel report required for further information	The results for this item/sample require further explanation which will follow in an intelligence report.			Reporting	No comment
CWBC	Consistent with being child of	The DNA profile obtained from this exhibit was consistent with being the biological child of the barcode sent with this exhibit report			Reporting	No comment
NCWBC	Not consistent with being child of	The DNA profile obtained from this exhibit is not consistent with being the biological child of the barcode sent with this exhibit report.			Reporting	No comment
SC1	Suspect check - support for contribution: LR 2 to 100	The DNA profile is between 2 and 100 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.			Reporting	No comment
SC2	Suspect check - support for contribution: LR 100 to 1000	This DNA profile is between 100 and 1000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.			Reporting	No comment
SC3	Suspect check - support for contribution: LR 1000 to 10 000	This DNA profile is between 1000 and 10 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.			Reporting	No comment

SC4	Suspect check- support for contribution: LR 10 000 to 100 000	This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court			Reporting	No comment
SC5	Suspect check - support for contribution: LR 100 000 - 1 million	This DNA profile is between 100 000 and 1 million times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court			Reporting	No comment
SC6	Suspect check- support for contribution: LR 1 million - 1 billion	This DNA profile is between 1 million and 1 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court			Reporting	No comment
SC7	Suspect check- support for contribution:LR 1 billion- 100 billion	This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court			Reporting	No comment
SC8	Suspect check - support for contribution: LR > 100 billion	This DNA profile is greater than 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court			Reporting	No comment
SC9	Suspect check inconclusive	The interpretation in relation to the nominated suspect is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other nominated suspects may provide a different interpretation. A reference evidence sample should be provided if this information is required in a statement for Court			Reporting	No comment
SC10	Suspect check - supports non contribution	The statistical interpretation provides support for the proposition that the nominated suspect has not contributed to this DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court			Reporting	No comment
SC11	Suspect check - Excluded	The nominated suspect can be excluded as a potential contributor to the DNA profile obtained from this item/sample.			Reporting	No comment
CPU	Complex profile unsuitable for interp or comparison	This item/sample gave a complex DNA profile. This DNA profile is not suitable for meaningful interpretation due to either its complexity relating to the unknown and potentially large number of contributors and/or the limited amount of information within the DNA profile.			Reporting	No comment
IRSUR	Interim Result. Sample undergoing rework	This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending			Reporting	No comment
NDPPTP	No DNA profile – possible sub-threshold peaks	A DNA profile was not obtained from this item/sample, however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds		Removed last sentence from expanded wording	Reporting	Agree - removal of last line is acceptable.
NOPRO	No DNA profile	A DNA profile was not obtained from this item/sample.			Reporting	No comment

NWQPSR	QPS advised no further work required - results available	QPS have provided advice that no further work is required for this item/sample. Please note that this item/sample has undergone DNA processing and results are available. These results may be Quantification results alone, or DNA profile results that have not been interpreted at this stage. QPS can submit a request to QHFSS for further work which may include the interpretation of the DNA results if required. results alone, or DNA profile results that have not been interpreted at this stage. QPS can submit a request to QHFSS for further work which may include the interpretation of the DNA results if required.			Reporting	No comment
PRNCID	DNA profile removed from NCIDD	The DNA profile obtained from this item/sample has been removed from NCIDD following advice from QPS, a change in the NCIDD category, or a profile with more information has been obtained			Reporting	No comment
PSTI	Possible sub-threshold information	The presence of possible additional DNA was observed within the DNA profile obtained from this item. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. This sub-threshold information did not interfere with the interpretation of the reportable DNA components in the DNA profile obtained from this item			Reporting	No comment
SPFRU	Sample processed and final results under	This item/sample was processed under the barcode sent with this exhibit report. The final results will be reported under that barcode.			Reporting	No comment
SPP	Sample pooled and processed under	This item/sample was pooled and submitted for DNA testing under the barcode sent with this exhibit report. The final results will be reported under the barcode.			Reporting	No comment
SUFP	This sample has undergone further processing	This item/sample has undergone further processing and an improved DNA profile has been obtained.			Reporting	No comment
NSIP	No statistical interpretation performed	In the absence of a reference sample/s for comparison, a statistical interpretation has not been performed.	To nominate a person of interest for comparison to the mixed DNA Profile obtained from this exhibit, please send a task to the DNA Liaison and Major Crime Unit (3211)		Reporting	No comment
TRQ	Testing restarted on advice from QPS	QPS have provided advice that testing is now required for this item/sample. Testing has been restarted.			Reporting	No comment
SRP	Submitted-results pending	This item/sample was submitted for DNA testing. Results are pending.		Change from exhibit movement to Auto filed examination result line.	Evidence Recovery	Evidence Recovery
PHNFA	Possible hair located – not examined further	Possible hair/s were located on this item/sample. These have not been examined further and have been retained with the exhibit.			Evidence Recovery	Evidence Recovery
PHNSA	Possible hair located. Not suitable for analysis	Possible hair/s were located on this item/sample. These have not been submitted for DNA testing and have been retained with the exhibit.			Evidence Recovery	Evidence Recovery
PHSRP	Possible hair located. Submitted for analysis	Possible hair/s were located on this item/sample. These have been submitted for DNA testing. Results are pending.			Evidence Recovery	Evidence Recovery
MPS	Micro positive for sperm	Spermatozoa were detected on this item/sample by microscopy.			Evidence Recovery	Evidence Recovery
AINT	All items now tested	All items for this exhibit have now been examined			Evidence Recovery	Evidence Recovery
DIFP	DNA insufficient for further processing	This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling.	Please send a task to the DNA Liaison and Major Crime Unit (3211) if this sample is required to be assessed for further processing.		Analytical	Analytical
IPNE	Items Prioritised. Not examined at this time	This item/sample has been prioritised based on case information provided by QPS. Examinations may be conducted in the future.			Evidence Recovery	Evidence Recovery
IPNST	Items prioritised, not submitted at this time	This item/sample has been prioritised and as such samples taken from this exhibit have not been submitted at this time.			Evidence Recovery	Evidence Recovery
MNS	Micro neg for sperm	Spermatozoa were not detected on this item/sample by microscopy.			Evidence Recovery	Evidence Recovery

NDNAD	No DNA detected	This item/sample was submitted for DNA analysis; however no DNA was detected above the limit of detection at the quantitation stage. No further processing was conducted on this item.			Analytical	Analytical
NFEC	No further examinations conducted	This item/sample was tested for the possible presence of biological material. All testing has been completed for this item.			Evidence Recovery	Evidence Recovery
NWQPS	No further work required as per advice from QPS	QPS have provided advice that no further work is required for this item/sample. Testing has been ceased and the sample stored.			Evidence Recovery	Evidence Recovery
PSAP	Presump. PSA test positive	This item/sample tested positive to a presumptive test for Prostate Specific Antigen (PSA) which is a component of seminal fluid			Evidence Recovery	Evidence Recovery
PBTN	Presumptive blood test neg.	This item/sample tested negative to a presumptive test for blood (TMB).			Evidence Recovery	Evidence Recovery
PREBT	Presumptive blood test positive	This item/sample tested positive to a presumptive test for blood (TMB).			Evidence Recovery	Evidence Recovery
PSTN	Presump saliva test negative	This item/sample tested negative to a presumptive test for saliva (Phadebas).			Evidence Recovery	Evidence Recovery
PSTP	Presump saliva test positive	This item/sample tested positive to a presumptive test for saliva (Phadebas).			Evidence Recovery	Evidence Recovery
SEMND	Semen not detected	Spermatozoa were not observed and/or seminal fluid was not detected on the item/sample tested. QHFSS recommends QPS to commence further examination on items relating to this case if applicable.			Evidence Recovery	Evidence Recovery
SOHAA	Sample on hold, awaiting advice	This item/sample has been placed on hold and is awaiting additional information from QPS before processing can recommence. This information may relate to, but is not limited to; examination priority, screening requirements			Evidence Recovery	Evidence Recovery
INT	Item has been examined / sub-sampled	Item has been examined / sub-sampled. DNA testing has not progressed under this barcode; however sub-samples from this item have been submitted for DNA testing under new barcodes.	Please send a task to the DNA Liaison and Major Crime Unit (3211) if this sample is required to be assessed for further processing.	This needs to be changed to a result - it is currently only a movement, so does not go to QPRIME.	Evidence Recovery	Evidence Recovery
ENAQS	ENVM additional quality search c	Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against QHFSS DNA Analysis staff DNA database, the QPS staff DNA database and (if required) searching against the quality database to aid QPS in their investigation of any potential contamination events. In this instance, a match was obtained from this additional quality assurance search. Further information is contained within the intelligence report that will accompany this exhibit report. This search capability is restricted within DNA Analysis to the Managing Scientist and the Quality Scientists.		Lab clean - not reported	Environmental	
ENCMPU	ENVM- Complex mixture unsuita	This environmental sample provided a DNA profile that indicated the presence of DNA from multiple contributors. This mixture is not suitable for meaningful interpretation due to either its complexity relating to the unknown and potentially large number of contributors and/or the limited amount of information within the DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.		Lab clean - not reported	Environmental	

New	ENVM - SS DNA profile	This environmental sample provided a DNA profile that indicated the presence of DNA from one contributor. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against QHFSS DNA Analysis staff DNA database, the QPS staff DNA database and (if required) searching against the quality database, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality Scientists. In this instance, no matches were obtained.		Lab clean - not reported - new	Environmental	
New	ENVM - Mixed DNA profile	This environmental sample provided a DNA profile that indicated the presence of DNA from at least two contributors. An attempt was made to resolve the contributors of this mixed DNA profile for the purposes of quality checking only, and as such no STRmix methods were undertaken. This quality checking identified a potential contributor to this mixed DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against QHFSS DNA Analysis staff DNA database, the QPS staff DNA database and (if required) searching against the quality database, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality Scientists. In this instance, no matches were obtained.		Lab clean - not reported - new	Environmental	
ENNDP	ENVM - No DNA profile	No DNA profile was obtained from this environmental sample. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.	n/a	Lab clean - not reported	Environmental	
QCF	Quality control failure – results no	During the processing of this item/sample, a failure in one of the quality control processes was identified. Investigations into this occurrence were undertaken; however any results for this sample are not reportable.	no change suggested	QHFSS quality control failure	Quality failure result	
QCFRQ	Quality control failure, refer to QP	During the processing of this item/sample, QHFSS quality control processes identified the integrity of this sample is compromised. Results for this sample are not reportable.	no change suggested	QPS quality issue	Quality failure result	
QFIH	Quality flag identified, on hold aw	During the processing of this item/sample, QHFSS quality control processes indentified the integrity of this sample may be compromised. Advice is required from QPS to determine whether any results for this sample are reportable.	no change suggested	QHFSS quality control failure	Quality failure result	

Result type	Mnemonic	Cold link line	Review by DRMU	Recommndations
Powerplex21 / Verifiler Plus	FULLCL	Full DNA profile	DNA COLD LINK - This item/sample gave a full DNA profile which matches the DNA profile obtained from Barcode Number ********* a DNA sample obtained from SURNAME, GIVEN NAMES DOB **/**/**** CNI No. ********* DNA Profile Number LKR0000***.	New cold link line
Powerplex21 / Verifiler Plus	PARTCL	Partial DNA profile	DNA COLD LINK - This item/sample gave a partial DNA profile which matches the DNA profile obtained from Barcode Number ********* a DNA sample obtained from SURNAME, GIVEN NAMES DOB **/**/**** CNI No. ********* DNA Profile Number LKR0000***.	New cold link line
Powerplex21	MIXL	Mixed DNA profile	DNA COLD LINK - This item/sample gave a DNA profile that indicated the presence of DNA from more than one contributor. Represented within the mixed DNA profile are some or all of the components of the DNA profile obtained from Barcode Number ********* a DNA sample obtained from SURNAME, GIVEN NAMES DOB **/**/**** CNI No. ********* DNA Profile Number LKR00*****.	New cold link line
Powerplex21	INTST	Interstate DNA profile		Retain
Profiler Plus	9L*	9 loci DNA profile *		Retain for legacy purposes
Profiler Plus	FUPROF	9 loci DNA profile		Retain for legacy purposes
Profiler Plus	DPPTP	9 loci DNA Profile – possible sub-threshold peaks		Retain for legacy purposes
Profiler Plus	PDNA	Partial DNA Profile		Retain for legacy purposes
Profiler Plus	PDPTP	Partial DNA Profile – possible sub-threshold peaks		Retain for legacy purposes
Profiler Plus	MINMAC	Mixed DNA profile, 9 Loci Major Component		Retain for legacy purposes
Profiler Plus	MPPMA	Mixed Profile, partial Major component		Retain for legacy purposes
Profiler Plus	MINMIC	Mixed DNA profile, 9 Loci Minor Component		Retain for legacy purposes
Profiler Plus	MPPMI	Mixed Profile, partial minor component		Retain for legacy purposes
Profiler Plus	MIXREM	Mixed profile - component remaining after conditioning		Retain for legacy purposes
Profiler Plus	MIXCON	Mixed profile - profile conditioned on		Retain for legacy purposes
Profiler Plus	INCOU	INTEL – 9 loci mixed – remaining after cond on unknown		Retain for legacy purposes
Profiler Plus	INMAJ	INTEL – 9 loci mixed DNA profile – major cannot exclude		Retain for legacy purposes
Profiler Plus	NMIN	INTEL – 9 loci mixed profile – minor cannot exclude		Retain for legacy purposes
Powerplex21	MIXREM	Mixed DNA profile – remaining contribution		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	MIXCON	Mixed DNA profile – conditioned contribution		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	INT2M1	INTEL – 2 person mix LR < 100		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	2MIXT	2 person mixed DNA profile		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	3MIXT	3 person mixed DNA profile		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	INT2MX	INTEL – (2 person mix)		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	INT3MX	INTEL – (3 person mix)		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	INTRE	INTEL – remaining contribution		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	INTREP	See INTEL report		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	FULL21	Full DNA Profile (PP21)		Decommission - not necessarily deleted - required for legacy purposes
Powerplex21	PART21	Partial DNA profile (PP21)		Decommission - not necessarily deleted - required for legacy purposes

Possible hair located on the outside of an in-tube submission

Mnemonic	EXH line	Expanded Comment	FSS agree decommission	FR coding	QPS comments
1SS	Single source DNA profile	The DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.	Thinking: could 1SS just have the expanded comment changed as per SS1?	Thinking: could 1SS just have the expanded comment changed as per SS1?	Discussed with Justin, agreed to move to SS1
1SS20L	Single source 20 loci DNA profile LR > 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It obtained all of the DNA information potentially available. This DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	Agreed	FR code to operate for LR1	
1S9L10	SS DNA profile 9 loci and above LR > 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	Agreed	FR code to operate for LR1	
1SS9L9	SS DNA profile 9 loci and above LR 1 billion-100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual	Agreed	FR code to operate for LR2	
1SS9L8	SS DNA profile 9 loci and above LR 1 million - 1 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of at least 9 DNA loci, however it has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual	Agreed	FR code to operate for LR3	
1SS9L7	SS DNA profile less than 9 loci LR > 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual	Agreed	FR code to operate for LR1	

1SS9L6	SS DNA profile < 9 loci LR 1 billion - 100 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	Agreed	FR code to operate for LR2
1SS9L5	SS DNA profile < 9 loci LR 1 million - 1 billion	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	Agreed	FR code to operate for LR3
1SS9L4	Single source DNA profile < 9 loci LR 100 000 - 1 million	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual.	Agreed	FR code to operate for LR4
1SSAKN	Single Source DNA profile - assumed known contributor	This item/sample provided a DNA profile that indicated the presence of one contributor. The associated barcode matches this DNA profile. Based on information provided to the laboratory, it has been assumed that the associated barcode is the donor of this DNA. Given this assumption, no statistical interpretation has been performed.	Agreed	FR code to operate for AC
2MX	Two person mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors.	Agreed	FR code to operate for MIX
3MX	Three person mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors.	Agreed	FR code to operate for MIX
MIX3	Mix - support for contrib > 100 billion	This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than has not contributed.	Agreed	FR code to operate for LR1
MIX4	Mix - inconclusive	The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other reference samples may provide a different statistical interpretation.	Agreed	FR code to operate for LR8
MIX5	Mix - supports non contribution	The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.	Agreed	FR code to operate for LR9
new	Mix - Assumed contributor	Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this DNA profile. Given the assumption for this person, no statistical interpretation has been performed.	Agreed	FR code to operate for AC
MIX16	NCIDD upload - assumed contribution	The assumed contributor described by the associated barcode has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile.	Agreed	FR code to operate for NUP

MIX7	Mix - assumed contributor - Intel	For Intelligence purposes, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically evaluated against the mixture without a contribution being assumed and the result reported as a likelihood ratio	Agreed	FR code to operate for ACINT
MIX8	Mix - NCIDD upload	Statistical analysis resulted in a DNA profile that was able to be loaded to NCIDD. The associated barcode/unknown designation sent with this exhibit report is a possible contributor to this mixed DNA profile. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary	Agreed	FR codeto operate for NUP
MIX9	Mix - intel interp -contribution for NCIDD	The DNA profile from the designated unknown sent with this exhibit report could be a contributor to the DNA profile along with the assumed known contributor. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary	Agreed	FR code to operate for REMINT
MIX12	Mix - contribution consistent with unknown	Based on this assumption, a remaining DNA profile has been separated. This is consistent with the unknown designation (previously identified within this case and loaded to NCIDD) sent with this exhibit report. It is important to note that this information is provided for intelligence purposes only and a statistical evaluation has not been performed at this time. Any reference samples subsequently received for the identification of an unknown component will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the likelihood ratio will vary. In this instance the likelihood ratio could favour non-contribution	Agreed	FR code to operate for CCUNK
MIX13	Mix - DNA contrib < NCIDD matching stringency	Based on this assumption, a remaining DNA profile has been separated. This DNA profile is of unknown origin and therefore does not match any DNA profiles obtained from reference samples associated to this case. This DNA contribution is below the QHFSS stringency for reporting a match on NCIDD and has therefore not been loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this DNA contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary. In this instance the likelihood ratio could favour non-contribution.	Agreed	no code
MIX14	Mix - DNA contrib unsuitable for NCIDD searching	Based on this assumption, a remaining DNA profile has been separated. This DNA profile is unsuitable for searching on NCIDD, and is therefore unable to be loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this DNA contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary. In this instance the likelihood ratio could favour non-contribution.	Agreed	no code

EVDEXC	Single evidence sample excluded	This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or three contributors. The statistical interpretation shows that the associated barcode sent with this exhibit report has been compared, and can be excluded as having contributed to this mixed DNA profile.	Agreed	FR code to operate for EVEX
INTER5	Interim result- mixed profile - Intel NCIDD. Rework Reqd	This is not a final result, sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is a mixed DNA profile that has been interpreted for intelligence purposes only. This mixed DNA profile indicated the presence of DNA from at least two contributors. An attempt has been made to separate major and minor DNA profiles within this mixed DNA profile in order to load to NCIDD for intelligence purposes only. The major DNA profile has been loaded to NCIDD and further interpretations are required. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD (within Australia) will be searched against this DNA profile. This mixed DNA profile is only reportable by statement in order to clarify interpretation assumptions. Final results are pending.	Agreed	No code: manual line
INTSSR	Interim Result- incomplete single source. Rework reqd	The interim result obtained from this sample/item was an incomplete single source DNA profile.This is not a final result and the sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.	Agreed	No code: manual line
CWBM	Consistent with being biological mother	The DNA profile obtained from this exhibit is consistent with being a biological child of the barcode sent with this exhibit report.	Agreed	No code: manual line
EXBF	Excluded as biological father	The DNA profile obtained from the barcode sent with this exhibit report is excluded as being a biological father of the DNA profile obtained from the exhibit.	Agreed	No code: manual line
NCWBM	Not consistent with being biological mother	The DNA profile obtained from the barcode is not consistent with being a biological mother of the DNA profile obtained from the exhibit.	Agreed	No code: manual line
NEXBF	Not excluded as biological father	The DNA profile obtained from the barcode sent with this exhibit report is not excluded as being a biological father of the DNA profile obtained from the exhibit.	Agreed	No code: manual line
SCLOW	Suspect check - low support for contribution	The DNA profile provides low support for the proposition that the nominated suspect is a possible donor of DNA to this mixed DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line
SCSC1	Suspect check - support for contribution 100 to 1000	This DNA profile is between 100 and 1000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line
SCSC2	Suspect check - support for contribution 1000 to 10 000	This DNA profile is between 1000 and 10 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line

SCSC3	Suspect check- support for contribution 10 000 to 100 000	This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line	
SCSC4	Suspect check - support for contrib 100 000 - 1 million	This DNA profile is between 100 000 and 1 million times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line	
SCSC5	Suspect check- support for contrib 1 million - 1 billion	This DNA profile is between 1 million and 1 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line	
SCSC6	Suspect check- support for contrib 1 billion- 100 billion	This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line	
SCSC7	Suspect check - support for contribution > 100 billion	This DNA profile is greater than 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather than an unknown, unrelated individual/s. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line	
SCINMX	Suspect check inconclusive - mixed DNA profile	The statistical interpretation in relation to the nominated suspect is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other nominated suspects may provide a different statistical interpretation. A reference evidence sample should be provided if this information is required in a statement for Court.	Agreed	No code: manual line	
SCSNC	Suspect check - supports non contribution	The statistical interpretation provides support for the proposition that the nominated suspect has not contributed to this mixed DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a statement for court.	Agreed	No code: manual line	
SCANM	Suspect check Action - No Match	The nominated suspect can be excluded as a potential contributor to the DNA profile obtained from this item/sample.	Agreed	No code: manual line	
CMPU	Complex mixed profile unsuitable for interp or comparison	This item/sample gave a complex Mixed DNA profile with multiple contributors. This mixture is not suitable for meaningful interpretation due to either its complexity relating to the unknown and potentially large number of contributors and/or the limited amount of information within the DNA profile.	Agreed	FR code to operate for CPU	
DIFP	DNA insufficient for further processing	This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling. Please contact the DNA Management Section if this sample is requested to be assessed for further processing. Further processing could include concentration of the low levels of DNA obtained, pooling with other samples (where appropriate), resampling of the parent item (where appropriate), or a combination of processes.	Thinking: could DIFP just have the expanded comment changed as per DIFP1, or makes no difference given already in the FR?	Thinking: could DIFP just have the expanded comment changed as per DIFP1, or makes no difference given already in the FR?	Discussed with Justin, agreed to move to SS1

INTER4	Interim result- mixed profile obtained. Rework Reqd	The interim DNA profile obtained from this sample/item indicated the presence of DNA from two or more contributors. This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. Final results are pending.	Agreed	No code: manual line
INTER6	Interim result- no profile obtained- undergoing rework	This is not a final result and sample/s are currently undergoing rework. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing to improve the DNA profile is being undertaken. The interim result is no DNA profile. Final results are pending.	Agreed	No code: manual line
NOPROF	No DNA profile	A DNA profile was not obtained from this item/sample, due to, but not limited to: no DNA present, poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.		FR code to operate for NOPRO
PAPPRP	Presump. PSA test positive, submitted - results pending	This item/sample tested positive to a presumptive test for Prostate Specific Antigen (PSA) which is a component of seminal fluid. This item was submitted for DNA testing. Results are pending.	NOT TO DECOMMISSION until new lines available.	
PBNSC	Presumptive blood test neg. Submitted for cells	This item/sample tested negative to a presumptive test for blood (TMB). This item was submitted for general cell DNA testing.	Agreed	
PPUCP	Partial DNA profile unsuitable for comparison purposes	This item/sample gave a partial DNA profile which was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information within the DNA profile. This may be due to, but not limited to: poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.	Agreed	FR code for CPU
PSNSC	Presump saliva negative. Submitted for cells	This item/sample tested negative to a presumptive test for saliva (Phadebas). This item/sample was submitted for general cell DNA testing.	Agreed	
SUFWC	Sample undergone further work - conditioned	This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or more contributors. Based on information provided to the laboratory, this mixed DNA profile has now been conditioned.	Agreed	No code: manual line
SUFNS	Sample undergone reprocessing - new software	This item/sample has undergone further processing and/or assessment with new software available to the laboratory. An updated DNA profile interpretation has been provided.	Agreed	No code: manual line
HLSRP	Hair located. Submitted results pending	Hair/s were located on this item/sample. These hairs have been submitted for DNA testing. Results are pending.	NOT TO DECOMMISSION until new lines available.	
SPPDNA	Micro positive for sperm. Submitted-results pending	Spermatozoa were detected on this item/sample by microscopy. This item/sample was submitted for DNA testing. Results are pending.	NOT TO DECOMMISSION until new lines available.	
EMDP	Excluded from mixed DNA profile	This item/sample provided a mixed DNA profile that indicated the presence of DNA from two or three contributors. All of the reference DNA profiles associated with this case have been compared with this DNA profile separately.The statistical interpretation shows that some or all of the donors of the reference DNA profiles associated with this case are excluded as having contributed to this mixed DNA profile.	Agreed	
MINAL	Multiple items - not all tested	This exhibit consisted of multiple items packaged together under one exhibit barcode, of which not all were selected for examination. If more or all of the remaining items are required to be examined, this can be completed upon request.	Agreed	

MLSONC	Mixture - low support for contrib or supports non contrib	This item/sample gave a mixed DNA profile that indicated the presence of DNA from two or three contributors. One or more of the contributors to this DNA profile has limited information associated with it. All of the reference DNA profiles associated with this case have been compared with this DNA profile separately.The DNA profile provides limited information as to whether or not some or all of donors of the reference DNA profiles associated with this case are possible donors of DNA to this mixed DNA profile. Please contact the laboratory if more information is required.	Agreed	
NFWA	No further work able to be conducted on this sample	This item/sample has been assessed and it has been determined that no further processing can be conducted on this sample, due to, but not limited to: no DNA extract left for further testing, current DNA profile improvement processes have already been exhausted.	Agreed	
NRDP	No reportable DNA profile	A DNA profile above QHFSS standard reporting thresholds was not obtained from this sample/item. This may be due to, but not limited to: no DNA present, poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.	Agreed	
SRPP	Similar result to previous DNA profile	This item/sample provided a mixed DNA profile that indicated the presence of DNA from two or three contributors. This DNA profile has been assessed and is considered to provide similar information to the DNA profile obtained from the sample barcode sent with this exhibit report and therefore has not been statistically evaluated at this time. Please contact the laboratory if you require a more detailed interpretation of this DNA profile	Agreed	
UNSS	Sample unsuitable for analysis	This item/sample is unsuitable for DNA testing due to, but not limited to: excess dirt, or the presence of mould.	Agreed	
1SSLOW	Single Source- low support for contribution	This item/sample provided a partial DNA profile which indicated the presence of one contributor. Only limited information has been obtained and this information matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. Statistically, this DNA profile provides low support that the associated barcode sent with this exhibit report is the donor of this DNA. Further information can be provided if required.	Agreed	
1SSIND	NCIDD Intel upload - single source partial profile	This item/sample gave an incomplete single source DNA profile which contained insufficient information for NCIDD matching as it was below the QHFSS stringency for reporting a match on NCIDD. The profile has been selected for loading to NCIDD for intelligence purposes. This incomplete DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be statistically evaluated and reported as a likelihood ratio. Depending on the amount of information in this DNA profile, the strength of the support for inclusion will vary.	Agreed	

1SSINI	NCIDD Intel upload - interim single source profile	This item/sample gave an interim result of an apparent single source DNA profile. This DNA profile has been selected for loading to NCIDD for intelligence purposes, as this sample is currently undergoing further processing. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that the final result may vary. Any reference samples subsequently received will be statistically evaluated against the final DNA profile and reported as a likelihood ratio	Agreed	
1SSUND	Single source DNA profile- unsuitable for NCIDD searching	The incomplete DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. The DNA profile contained insufficient information for searching on NCIDD, and is therefore unable to be loaded to NCIDD. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.	Agreed	
2MX1	2 person mix - support for contribution 100 to 1000	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
2MX2	2 person mix - support for contribution 1000 to 10 000	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
2MX3	2 person mix, support for contrib 10 000 - 100 000	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
2MX4	2 person mix- support for contrib 100 000 to 1 million	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	

2MX5	2 person mix - support for contrib 1 million - 1 billion	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
2MX6	2 person mix- support for contrib 1 billion - 100 billion	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
2MX7	2 person mix profile - support for contrib > 100 billion	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
2MXCI	2 person mixed profile - conditioned on - Intel	This item/sample provided a DNA profile that indicated the presence of two contributors. For Intelligence purposes, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically evaluated against the mixture without a contribution being assumed and the result reported as a likelihood ratio.	Agreed	
2MXCON	2 person mixed profile - conditioned on	This item/sample provided a DNA profile that indicated the presence of two contributors. Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this mixed DNA profile. Given this assumption, no statistical interpretation has been performed.	Agreed	
2MXINC	2 person mixed DNA profile - inconclusive	This item/sample provided a DNA profile that indicated the presence of two contributors. The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other reference samples may provide a different statistical interpretation.	Agreed	

2MXIND	NCIDD upload - Intel mixed DNA profile	The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a partially deconvoluted DNA profile able to be loaded to NCIDD for intelligence purposes. The associated barcode/unknown designation sent with this exhibit report is consistent with this partially deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this partially deconvoluted DNA profile has been assigned a sub-sample barcode number. The partially deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	
2MXLOW	2 person mix - low support for contribution	This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. The DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Please contact DNA Analysis if further information is required.	Agreed	
2MXNC	2 person mix - supports non contribution	This item/sample provided a DNA profile that indicated the presence of two contributors. The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.	Agreed	
2MXNCD	NCIDD upload - mixed DNA profile	The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a fully deconvoluted DNA profile. The associated barcode/unknown designation sent with this exhibit report is consistent with this fully deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this fully deconvoluted DNA profile has been assigned a sub-sample barcode number. The fully deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	

2MXNIR	Mixture contribution loaded to NCIDD - see Intel report	The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. A DNA contribution was able to be deconvoluted for loading to NCIDD, and further information about this will follow in an intelligence report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile the, strength of the support for contribution will vary.	Agreed	
2MXR1	2 person mix remaining - support for contrib 100 to 1000	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual	Agreed	
2MXR2	2 person mix remaining- support for contrib 1000 to 10000	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual	Agreed	
2MXR3	2 person mix rem - support for contrib 10 000 to 100 000	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual	Agreed	
2MXR4	2 person mix rem- support for contrib 100000 to 1 million	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual	Agreed	

2MXR5	2 person rem- support for contrib 1 million to 1 billion	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual	Agreed	
2MXR6	2 person rem - support for contrib 1 billion -100 billion	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual	Agreed	
2MXR7	2 person mix rem - support for contribution > 100 billion	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather an unknown, unrelated individual	Agreed	
2MXRL	2 person mix remaining - low support for contrib	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor, then the DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.	Agreed	
2MXRCU	2 pers mix remaining consistent with unknown	The mixed DNA profile result for this sample indicated the presence of DNA from two contributors and has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and ‘remaining’ have been applied. A remaining contribution has been separated after conditioning the mixed DNA profile. This remaining contribution is consistent with the unknown designation (previously identified within this case and loaded to NCIDD) sent with this exhibit report. This unknown is therefore a possible donor of DNA to the 'remaining' contribution. It is important to note that this information is provided for intelligence purposes only and a statistical evaluation has not been performed at this time. Any reference samples subsequently received for the identification of an unknown component will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the likelihood ratio will vary. In this instance the likelihood ratio could favour non-contribution.	Agreed	

2MXRLM	Mix Rem DNA contrib < NCIDD matching stringency	The mixed DNA profile result for this sample indicates two contributors and has been deconvoluted in an attempt to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and 'remaining' have been applied. The remaining contribution separated after conditioning the mixed DNA profile is of unknown origin and therefore does not match any DNA profiles obtained from reference samples associated to this case. This remaining contribution is below the QHFSS stringency for reporting a match on NCIDD and has therefore not been loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this remaining contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	
2MXRNC	2 person mix remaining - supports non contribution	This item/sample provided a DNA profile that indicated the presence of two contributors. If it is assumed that the barcode sent with the above exhibit report (2 contributor mixed profile, conditioned on) has contributed, the statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.	Agreed	
2MXRIN	2 person mixed profile - remaining Intel - NCIDD	This item/sample provided a DNA profile that indicated the presence of two contributors. When conditioning on the assumed known contributor for intelligence purposes only, some or all of the components of the DNA profile from the designated unknown sent with this exhibit report are represented within the remaining DNA profile. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	
2MXRND	NCIDD upload remaining contribution	The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and 'remaining' have been applied. A remaining contribution has been separated after conditioning the mixed DNA profile. The associated barcode/unknown designation sent with this exhibit report is a possible donor of DNA to the 'remaining contribution'. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received for the identification of an unknown component will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	

3MX1	3 person mix - support for contribution 100 to 1000	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.	Agreed	
3MX2	3 person mix - support for contribution 1000 to 10 000	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.	Agreed	
3MX3	3 person mix - support for contrib 10 000 - 100 000	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.	Agreed	
3MX4	3 person mix - support for contrib 100 000 to 1 million	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.	Agreed	
3MX5	3 person mix - support for contrib 1 million - 1 billion	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.	Agreed	
3MX6	3 person mix- support for contrib 1 billion - 100 billion	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.	Agreed	
3MX7	3 person mix profile - support for contrib > 100 billion	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. Some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than three unknown, unrelated individuals.	Agreed	

3MXCI	3 person mixed profile - conditioned on - Intel	This item/sample provided a DNA profile that indicated the presence of three contributors. For Intelligence purposes, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be statistically evaluated against the mixture without a contribution being assumed and the result reported as a likelihood ratio.	Agreed	
3MXCON	3 person mixed profile - conditioned on	This item/sample provided a DNA profile that indicated the presence of three contributors. Based on information provided to the laboratory, it has been assumed that the associated barcode has contributed to this mixed DNA profile. Given this assumption, no statistical interpretation has been performed.	Agreed	
3MXINC	3 person mixed DNA profile - inconclusive	This item/sample provided a DNA profile that indicated the presence of three contributors. The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report, comparison to other reference samples may provide a different statistical interpretation.	Agreed	
3MXIND	3 pers mixed profile, mix remaining intel NCIDD	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, a remaining contribution has been separated. This remaining contribution is a mixed DNA profile which has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a partially deconvoluted DNA profile able to be loaded to NCIDD for intelligence purposes. The associated barcode/unknown designation sent with this exhibit report is consistent with this partially deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this partially deconvoluted DNA profile has been assigned a sub-sample barcode number. The partially deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	
3MXLOW	3 person mix - low support for contribution	This item/sample provided a DNA profile that indicated the presence of DNA from three contributors. The DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.	Agreed	
3MXNC	3 person mix - supports non contribution	This item/sample provided a DNA profile that indicated the presence of three contributors. The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.	Agreed	
3MXND	3 person mixed DNA profile not deconvoluted	This item/sample gave a mixed DNA profile which indicated the presence of DNA from three contributors. This mixed DNA profile has been assessed and it is considered that, if the DNA profile were to be deconvoluted, it may provide sufficient information for upload to NCIDD. Deconvolution of this DNA profile has not been performed at this time. Please contact the laboratory if further interpetation is required.	Agreed	

3MXR1	3 person mix remaining - support for contrib 100 to 1000	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals	Agreed	
3MXR2	3 person mix remaining- support for contrib 1000 to 10000	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals	Agreed	
3MXR3	3 person mix rem - support for contrib 10 000 to 100 000	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals	Agreed	
3MXR4	3 person mix rem- support for contrib 100000 to 1 million	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 100 000 and 1 million times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals	Agreed	
2MXCND	NCIDD upload - conditioned contribution	The mixed DNA profile result for this sample has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and 'remaining' have been applied. The conditioned contribution described by the associated barcode has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile.	Agreed	
3MXR5	3 person rem - support for contrib 1 million to 1 billion	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 million and 1 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals	Agreed	

3MXR6	3 person rem - support for contrib 1 billion-100 billion	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is between 1 billion and 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
3MXR7	3 person mix rem - support for contribution > 100 billion	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, some or all of the components of the DNA profile from the associated barcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the assumed known contributor, this DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has also contributed to this DNA profile, rather than two unknown, unrelated individuals.	Agreed	
3MXRIN	3 per mix, intel cond, remaining intel NCIDD	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor for intelligence purposes only, some or all of the components of the DNA profile from the designated unknown sent with this exhibit report are represented within the remaining DNA profile. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only, and that any reference samples subsequently received will be compared against the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	
3MXRL	3 person mix remaining - low support for contrib	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, then the DNA profile provides low support for the proposition that the associated barcode is a contributor of DNA to this mixed DNA profile. Further information can be provided if required.	Agreed	
3MXRNC	3 person mix remaining - supports non contribution	This item/sample provided a DNA profile that indicated the presence of three contributors. If it is assumed that the barcode sent with the above exhibit report (3 contributor mixed profile, conditioned on) has contributed, the statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA profile.	Agreed	

3MXRND	3 person mixed profile, mixture remaining NCIDD	This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, a remaining contribution has been separated. This remaining contribution is a mixed DNA profile which has been deconvoluted in order to resolve any DNA profiles suitable for loading to NCIDD. In this instance, the analysis resulted in a fully deconvoluted DNA profile. The associated barcode/unknown designation sent with this exhibit report is consistent with this fully deconvoluted DNA profile and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this fully deconvoluted DNA profile has been assigned a sub-sample barcode number. The fully deconvoluted DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	
3MXRUN	3 Person Mix Rem DNA contrib unsuitable for NCIDD	The mixed DNA profile result for this sample indicates three contributors and has been deconvoluted in an attempt to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and ‘remaining’ have been applied. The remaining contribution separated after conditioning the mixed DNA profile was unsuitable for searching on NCIDD, and is therefore unable to be loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this remaining contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	
MXREMI	Remaining contribution - inconclusive	This item/sample provided a DNA profile that indicated the presence of two or three contributors. When conditioning on the assumed known contributor, the statistical interpretation in relation to the associated barcode is inconclusive.	Agreed	
2MXUNM	Mix Remaining DNA contribution indicates male origin	The remaining contribution separated after conditioning the mixed DNA profile indicates male origin	Agreed	
2MXUNS	Mix Rem DNA contrib unsuitable for NCIDD searching	The mixed DNA profile result for this sample indicates two contributors and has been deconvoluted in an attempt to resolve any DNA profiles suitable for loading to NCIDD. For ease of differentiation between the resolved contributions, the designations 'conditioned' and ‘remaining’ have been applied. The remaining contribution separated after conditioning the mixed DNA profile is of unknown origin. This remaining contribution is unsuitable for searching on NCIDD, and is therefore unable to be loaded to NCIDD. If reference evidence samples are submitted, it will be possible to compare them with this remaining contribution, the results of which will be reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary.	Agreed	

SCLNSC	Suspect check - low support or non contrib	One or more of the contributors to this DNA profile has limited information associated with it. All of the profiles from nominated reference barcodes have been compared with this DNA profile separately.The DNA profile provides limited information as to whether or not some or all of the donors are possible donors of DNA to this mixed DNA profile. Please contact the laboratory if more information is required	Agreed	
1SS9L3	Single source DNA profile < 9 loci LR 10 000 - 100 000	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual	Agreed	
1SS9L2	Single source DNA profile < 9 loci LR 1000 - 10 000	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 1000 and 10 000 times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual	Agreed	
1SS9L1	Single source DNA profile < 9 loci LR 100 - 1000	This item/sample provided a DNA profile that indicated the presence of one contributor. It consisted of less than 9 DNA loci and therefore has not obtained all of the DNA information potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode sent with this exhibit report. This DNA profile is between 100 and 1000 times more likely to have occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown, unrelated individual	Agreed	
1SSLND	Single source DNA profile < NCIDD matching stringency	The incomplete DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. The DNA profile was below the QHSS stringency for reporting a match on NCIDD, and has therefore not been loaded to NCIDD. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.	Agreed	
NHLNE	No hair located. No further examination conducte	The item/sample was examined for the presence of hair and none was located. This could be due to no hair present or item is substance other than hair. No further testing for hair was conducted on this item.	NOT TO DECOMMISSION until new lines available.	
OHPFW	On hold, pending further work	These results are currently subject to quarantine pending the completion of further quality checks. The outcome of these quality checks will be reported once complete.	Agreed	
PPSANS	Presump. PSA test positive, no sperm found	This item/sample tested positive to a presumptive test for Prostate Specific Antigen (PSA) which is a component of seminal fluid. No spermatozoa were detected by microscopy. This item was submitted for DNA testing. Results are pending.	Agreed	

PSPSRP	Presump saliva positive. Submitted-results pendi	This item/sample tested positive to a presumptive test for saliva (Phadebas) and was submitted for DNA testing. Results are pending.	Agreed	
SAC	Submitted as cells	This item/sample was submitted for general cell DNA testing.	Agreed	
SACPSP	Submitted as cells, Presump saliva test pending	This item/sample was submitted for general cell DNA testing. The item/sample will be tested with the presumptive test for saliva (Phadebas). Results are pending.	Agreed	
HLNSA	Hair located. Not suitable for analysis	Hair/s were located on this item/sample. They were observed using microscopy and deemed unsuitable for DNA testing due to no observed cellular material, or possible animal origin.	Agreed	
HAIRNFA	Hair located – not examined at this time.	During the examination of this exhibit one or more hairs were located. Based on case information available or testing requested, this has not been submitted at this time, however has been retained for potential future analysis if requested.		
1BPPSR	Presumptive blood test pos. Submitted-results pending	This item/sample tested positive to a presumptive test for blood (TMB) and was submitted for DNA testing. Results are pending.	Agreed	
PPSRP	Presump. AP test positive, submitted - results pending	This item/sample tested positive to a presumptive test for seminal fluid (AP). This item was submitted for DNA testing. Results are pending.		
ENCMDP	ENVM - Complex mixed DNA profile	This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles), and as such, no further interpretation can be conducted as this time. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.	**Decommission**	Lab clean - not reported
ENFDP	ENVM - Full DNA profile	This environmental sample gave a full DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained	**Decommission**	Lab clean - not reported
ENPDP	ENVM -Partial DNA profile	This environmental sample gave a partial DNA. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained	**Decommission**	Lab clean - not reported

ENPDPU	ENVM - Partial profile unsuitable for comparison	This environmental sample gave a partial DNA profile which was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information obtained. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds.	**Decommission**	Lab clean - not reported

Mnemonic	EXH line	Expanded Comment	Change for next version/ alternative wording	Notes	10/08/2021 JAH
CMPCE	Complex mixed DNA profile – cannot exclude	This item/sample gave a full or partial mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles) and therefore could not be loaded to NCIDD. The DNA profile obtained from the barcode sent with this exhibit report cannot be excluded as being a possible contributor of DNA to this mixed DNA profile.	no change suggested	Profiler plus result	Retain as required for old cases
CMPULN	Complex mixed DNA profile. Unable to load to NCIDD	This item/sample gave a full or partial mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could not be separated into distinct DNA contributions (e.g. major and minor DNA profiles) and therefore could not be loaded to NCIDD. This complex mixed DNA profile cannot be interpreted further as no reference sample has been received for direct comparison; or alternatively, comparison with additional reference samples may be possible if forthcoming.	no change suggested	Profiler plus result	
DPNPTP	9 loci DNA profile- NCIDD- possible sub-threshold peaks	This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. These sub-threshold peaks did not interfere with the interpretation of the reportable DNA components in the 9 loci DNA profile obtained, which has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
DPPTP	9 loci DNA profile - possible sub-threshold peaks	This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the 9 loci DNA profile obtained.	n/a	Profiler plus result	
FUPNPN	9 loci DNA profile. Uploaded to NCIDD	This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile has been selected for loading to NCIDD and will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
FUPROF	9 loci DNA profile	This item/sample gave a full 9 loci DNA profile which matches the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result	
MDPIL	Minor/Remaining DNA profile - Intel profile loaded NCIDD	This item/sample gave a mixed DNA profile, of which the minor or remaining DNA profile contained insufficient information for NCIDD matching as it was below the QHFSS stringency for reporting a match on NCIDD. The profile has been selected for loading to NCIDD for intelligence purposes only and any resulting matches will be reported in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution.	n/a	Profiler plus result	

MIPDNA	Mixed DNA profile conditioned on – NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that the DNA profile obtained from the barcode sent with this exhibit report has contributed to this mixed DNA profile. This result should always be used in conjunction with "Mixed DNA profile. Remaining profile after conditioning". This DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
MIPMAC	Mixed DNA profile. Major component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The full major DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result	
MIPMIC	Mixed DNA profile. Minor Component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The full minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result	
MIPMUN	Mixed DNA profile. Major component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile has been selected for loading to NCIDD. The full major DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
MIPPRO	Mixed profile. Remaining profile after conditioning – NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the "Mixed DNA profile conditioned on" exhibit report. The DNA profile remaining after the conditioning matches the DNA profile obtained from the barcode sent with this report. This DNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
MIRIN	Mixture Interp reqd - Intel profile loaded to NCIDD	This item/sample gave a mixed DNA profile that has been interpreted for intelligence purposes only. This interpretation may not be able to be used for evidentiary purposes. This means that we may have lowered our routine interpretational and NCIDD matching guidelines in order to assist with the generation of intelligence information. This intelligence DNA profile has been selected for loading to NCIDD and further explanation of the interpretations made will follow in an intelligence report. It should be noted that the interpretation provided within this intelligence report may not meet the stringent court reporting guidelines and therefore wording within an evidential statement may be different. The Intelligence DNA profile loaded to NCIDD will be searched against any DNA profiles currently held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this intelligence DNA profile. It will be outlined in the Intelligence report that this mixed DNA profile may be reported differently in an evidentiary statement.	n/a	Profiler plus result	

MPCMU	Mixed profile- complex minor unsuit for interp or compar.	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile indicated the presence of DNA from more than one contributor. This minor DNA profile is too complex for meaningful interpretation or comparison purposes due to the unknown number of potential contributors and/or the limited amount of information within the minor DNA profile.	n/a	Profiler plus result	
MPCO	Mixed DNA profile conditioned on	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that the DNA profile obtained from the barcode sent with this exhibit report has contributed to this mixed DNA profile. This result should always be used in conjunction with “Mixed DNA profile. Remaining profile after conditioning”	n/a	Profiler plus result	
MPMAIN	Mixed profile, major component insuff for NCIDD matching	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	
MPMC3	Mixed profile, minor comp. 3 of 18 DNA components	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 3 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	
MPMC4	Mixed profile, minor comp. 4 of 18 DNA components	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 4 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	

MPMC5	Mixed profile, minor comp. 5 of 18 DNA components	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which contained 5 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this minor DNA profile is unable to be loaded to NCIDD. This minor DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	
MPMIIN	Mixed profile, minor component insuff for NCIDD matching	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	
MPMINC	Mixed profile, minor component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile has been loaded to NCIDD. The full minor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
MPMPIM	Mixed profile,minor profile insuff– indicated male origin	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile did not contain sufficient information for comparison purposes other that to say it indicated it was of male origin.	n/a	Profiler plus result	
MPMUC	Mixed profile Minor component unsuitable for comparison	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was insufficient for comparison purposes or meaningful interpretation due to the limited amount of information obtained.	n/a	Profiler plus result	
MPNMM	Mixed profile, No major/minor – cannot exclude	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could not be separated into major and minor DNA profiles and could not be loaded to NCIDD. The DNA profile obtained from the barcode sent with this exhibit report cannot be excluded as being a possible contributor of DNA to this mixed DNA profile.	n/a	Profiler plus result	
MPNMUN	Mixed profile, No major/minor. Unable to load to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could not be separated into major and minor DNA profiles and could not be loaded to NCIDD. In the absence of reference samples, no further interpretation can be conducted; or comparison with additional reference samples may be possible if forthcoming.	n/a	Profiler plus result	
MPPMA	Mixed profile, partial major component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile. Where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result	

MPPMAN	Mixed DNA profile, partial major component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The major DNA profile was a partial DNA profile which has been selected for loading to NCIDD. Where information was obtained, the DNA components of this partial major DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile	n/a	Profiler plus result	
MPPMI	Mixed profile, partial minor component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile. Where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result	
MPPMIN	Mixed DNA profile, partial minor component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile was a partial DNA profile which has been selected for loading to NCIDD. Where information was obtained, the DNA components of this partial minor DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile	n/a	Profiler plus result	
MPRO	Mixed profile, complex mixed minor component	This item/sample gave a mixed DNA profile which indicated the presence of DNA from more than two contributors. This mixed DNA profile could be separated into major and minor DNA profiles. The minor DNA profile indicated the presence of DNA from more than one contributor. This minor DNA profile cannot be interpreted further as no reference sample has been received for direct comparison; or alternatively, comparison with additional reference samples may be possible if forthcoming	n/a	Profiler plus result	
MPRP	Mixed DNA profile. Remaining profile after conditioning	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the “Mixed DNA profile conditioned on” exhibit report. The DNA profile remaining after the conditioning matches the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result	
MPRPAC	Mixed profile. Remain profile after cond – insuff NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the “Mixed DNA profile conditioned on” exhibit report. The DNA profile remaining after the conditioning was a partial DNA profile which which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This remaining DNA profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this remaining partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	

MPRPC	Mixed profile. Remain profile after cond–unsuitable NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from no more than two contributors. This mixed DNA profile can be conditioned on the presence of a known contributor. It has been assumed that this known contributor is the barcode sent with the "Mixed DNA profile conditioned on" exhibit report. The DNA profile remaining after the conditioning was a partial DNA profile which contained insufficient information for searching on NCIDD, and therefore is unable to be loaded to NCIDD. This remaining DNA profile may contain enough information to compare to other DNA profiles for either inclusion or exclusionary purposes. Where information was obtained, the DNA components of this remaining partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	
PAPNPN	Partial DNA profile. Uploaded to NCIDD	This item/sample gave a partial DNA profile. Where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report. This partial DNA profile has been selected for loading to NCIDD and will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
PD3C	Partial DNA profile, 3 of 18 DNA components	This item/sample gave a partial DNA profile which contained 3 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable)	n/a	Profiler plus result	
PD4C	Partial DNA profile, 4 of 18 DNA components	This item/sample gave a partial DNA profile which contained 4 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable)	n/a	Profiler plus result	
PD5C	Partial DNA profile, 5 of 18 DNA components	This item/sample gave a partial DNA profile which contained 5 alleles out of a possible 18 alleles above QHFSS standard reporting thresholds. There is insufficient information for searching on NCIDD, and therefore this partial DNA profile is unable to be loaded to NCIDD. This partial DNA profile represents very limited information, however in some cases it may provide enough information to directly compare to other DNA profiles for either inclusion or exclusionary purposes. Assuming there is only one contributor to this partial DNA profile, where information was obtained, the partial DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable)	n/a	Profiler plus result	
PDNA	Partial DNA profile	This item/sample gave a partial DNA profile. Where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report.	n/a	Profiler plus result	

PDNAIN	Partial DNA profile. Insufficient for NCIDD matching	This item/sample gave a partial DNA profile which was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	
PDNPTP	Partial DNA profile- NCIDD- possible sub-threshold peaks	This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained, which has been selected for loading to NCIDD. This partial DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile.	n/a	Profiler plus result	
PDPTP	Partial DNA profile - possible sub-threshold peaks	This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained	n/a	Profiler plus result	
PIRIN	Partial profile Interp reqd – Intel profile loaded NCIDD	This item/sample gave a partial DNA profile which contained an indication of DNA at a level less than the laboratorys standard reporting threshold. This profile was submitted for further analysis below QHFSS standard reporting thresholds for intelligence purposes. The subsequent profile has been selected for loading to NCIDD for intelligence purposes only and further explanation of the interpretations made will follow in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution	n/a	Profiler plus result	
PPINPT	Partial profile, insuff NCIDD- pos. sub-threshold peaks	This item/sample gave a partial DNA profile the components of which match the corresponding DNA components of the DNA profile obtained from the barcode sent with this exhibit report; however the possible presence of additional DNA was observed. This possible DNA was not present at a sufficient level to be used for comparison purposes, as it was below QHFSS standard reporting thresholds. The sub-thresholds peaks did not interfere with the interpretation of the reportable DNA components in the partial DNA profile obtained. This partial DNA profile was below the QHFSS stringency for reporting a match on NCIDD, and therefore has not been loaded to NCIDD. This profile contains enough information to compare to other DNA profiles and where information was obtained, the DNA components of this partial DNA profile match the corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a	Profiler plus result	

PPIPL	Partial profile - Intel profile loaded to NCIDD	This item/sample gave a partial DNA profile which contained insufficient information for NCIDD matching as it was below the QHFSS stringency for reporting a match on NCIDD. This profile may also have indications of DNA at a level less than the laboratorys standard reporting threshold, therefore the profile may have been submitted for further analysis below standard reporting thresholds for intelligence purposes. The profile has been selected for loading to NCIDD for intelligence purposes only and any matches will be reported in an intelligence report. This intelligence DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this DNA profile. These results may need to be considered with caution.	n/a	Profiler plus result	
SCANM	Suspect check actioned - no match	The nominated suspect can be excluded as a potential contributor to the DNA profile obtained from this item/sample.	n/a	Profiler plus result	
SCII	Suspect check - insufficient information to compare	There was insufficient information in the DNA profile obtained from this item/sample to determine if the nominated suspect could be a potential contributor.	n/a	Profiler plus result	
SCM	Suspect check - match	The DNA profile obtained from the nominated reference barcode sent with this exhibit report matches, where information was obtained, the DNA components of this full or partial DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information and subsequent statistical calculations are required in a statement for court.	n/a	Profiler plus result	
SCMAJM	Suspect check - major profile match	The DNA profile obtained from the nominated reference barcode sent with this exhibit report matches, where information was obtained, the full or partial major DNA profile separated from this mixed DNA profile.This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information and subsequent statistical calculations are required in a statement for court.	n/a	Profiler plus result	
SCMINM	Suspect check - minor profile match	The DNA profile obtained from the nominated reference barcode sent with this exhibit report matches, where information was obtained, the full or partial minor DNA profile separated from this mixed DNA profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information and subsequent statistical calculations are required in a statement for court.	n/a	Profiler plus result	
SCCE	Suspect check - cannot exclude	The DNA profile obtained from the nominated reference barcode sent with this exhibit report cannot be excluded as a possible contributor of DNA to this mixed DNA profile. A reference evidence sample should be provided if this information is required in a statement for court. A statistical analysis may not be possible for this interpretation.	n/a	Profiler plus result	
IMAJUN	Mixed profile-no major/minor. INTEL Major loaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors and could not be clearly separated into major and minor DNA profiles. An attempt was made to separate the contributors to this mixed DNA profile in order to load intelligence information to the National Criminal Investigation DNA Database (NCIDD) for intelligence purposes only. The Intel Major DNA profile loaded to NCIDD for matching purposes will be searched against any DNA profiles currently held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this intelligence DNA profile. It is important to note that this process has been performed for intelligence purposes only, and any reference samples subsequently received which match these DNA components will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile.	n/a	Profiler plus result	

IMINUN	Mixed profile-no major/minor. INTEL Minor loaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors and could not be clearly separated into major and minor DNA profiles. An attempt was made to separate the contributors to this mixed DNA profile in order to load intelligence information to the National Criminal Investigation DNA Database (NCIDD) for intelligence purposes only. The Intel minor DNA profile loaded to NCIDD for matching purposes will be searched against any DNA profiles currently held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are uploaded to NCIDD will be searched against this intelligence DNA profile. It is important to note that this process has been performed for intelligence purposes only, and any reference samples subsequently received which match these DNA components will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile.	n/a	Profiler plus result	
IMCOU	INTEL- mix DNA profile conditioned on unknown DNA profile	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors and could not be separated into major and minor DNA profiles. For intelligence purposes only, it has been assumed that the designated unknown has contributed to this mixed DNA profile. A reference evidence sample should be provided for this individual if this information is required in a statement for court. If this assumption no longer holds, then any reference sample will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile and may include a statistical analysis. This result should always be used in conjunction with “INTEL- mix profile remaining after cond on unknown- NCIDD”	n/a	Profiler plus result	
IMROU	INTEL - mix profile remaining after cond on unknown- NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of DNA from two contributors and could not be separated into major and minor DNA profiles. When conditioning on the assumed known contributor for intelligence purposes only, a remaining DNA profile was obtained. This Intel remaining DNA profile will be searched against any DNA profiles already held on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile. It is important to note that this process is for intelligence purposes only. If the assumption for conditioning no longer holds, then any reference sample will be reported as unable to be excluded as a possible contributor of DNA to this mixed DNA profile and may include a statistical analysis. This result should always be used in conjunction with “INTEL- mix DNA profile conditioned on unknown DNA profile”	n/a	Profiler plus result	
ENMDP	ENVM - Major DNA profile	This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles, of which the major was a full or partial DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained.	n/a	Lab clean - not reported	

ENMDPU	ENVM – Minor DNA profile unsuitable for comparison	This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles, of which the minor DNA profile contained insufficient information for comparison purposes due to the limited amount of information obtained. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds		Lab clean - not reported	
ENMIDP	ENVM – Minor DNA profile	This environmental sample gave a mixed DNA profile which indicated the presence of DNA from at least two contributors. This mixed DNA profile could be separated into major and minor DNA profiles, of which the minor DNA profile was a full or partial DNA profile. It is standard procedure to analyse environmental samples below QHFSS standard reporting thresholds for quality purposes, therefore results for this sample have been interpreted and reported based on these lowered thresholds. Part of the Quality Assurance process for all environmental samples is to compare the DNA profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff DNA database. An additional quality search against the DNA Analysis Database (DAD) may be performed if required, the use of which is restricted to the DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this instance, no matches were obtained	n/a	Lab clean - not reported	

Mnemonic	EXH line	Expanded Comment	Change for next version/ alternative wordin	Notes	10/08/2021 JAH
HOIS	Hair located on the outside of an in-tube submission	A hair was located either outside the tube or partially hanging in and out of the tube. It is unclear if this hair was part of the collected item or incorrectly transferred during collection. This hair/hair portion has been stored and will only be analysed if a request is providec	no change suggested	Information sent via Examination request notification by QHFSS to SOC / SCI officer	Retain for discussion with QPS in the future
ISCB	Incorrect submission of cigarette butt	This cigarette butt was received in a tube. Items provided in a tube are intended to be submitted directly for DNA processing with minimal manual intervention. This sample required further examination as it was received as a whole cigarette butt. Please submit whole cigarette butts in a Crime Scene Sample envelope or as a sub-sample of the filter paper	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer	Retain for discussion with QPS in the future
LDIS	Labelling discrepancy	There is a labelling discrepancy (Occurrence number or sample description) between the exhibit packaging and the AUSLAB/Forensic Register interface records. This sample can not be processed until the labelling discrepancy is resolved. The discrepancy will be highlighted to the QPS Sample Management Unit for clarification in the first instance, and if unable to be resolved, will be referred to the appropriate QPS officer for resolution. Please ensure all labelling details are correct before submission to the DNA Analysis Laboratory	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer	Retain for discussion with QPS in the future
MIES	Sample required manual intervention - excess substrate	This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as excess substrate was contained within the tube. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process.	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer	Retain for discussion with QPS in the future
MIISB	Multiple items incorrectly submitted under single barcod	Multiple items, or multiple AP positive areas have been submitted under a single barcode identifier. Each item requires its own unique barcode, as the barcode is used for reporting purposes to both the forensic register and the National Criminal Investigation DNA Database. Each item will be allocated a new barcode for processing and reporting purposes	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer	Retain for discussion with QPS in the future
MISSTL	Sample required manual intervention - swab stick too lo	This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as the swab stick was too long and required shortening to enable downstream processing. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process. The ideal stick length should be no more than 24mm total length (swab stick plus swab head).	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer	Retain for discussion with QPS in the future

MITRI	Sample reqd manual intervention- tlift rolled incorrectly	This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods as the tapelift was rolled incorrectly, impeding downstream processing. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the DNA extraction process.	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer	Retain for discussion with QPS in the future
NBOS	No barcode on sample	The item/sample provided in a tube was not labelled with a barcode. A barcode is required for the processing of the item and for continuity purposes. A barcode the same as that attached to the packaging has been affixed to the item.	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer	Retain for discussion with QPS in the future
ESCD	Entire sample consumed	The entire item/sample was consumed during examination	n/a	Exhibit movement - result report not received by RMU	Retain for discussion with QPS in the future
OHII	On hold - insufficient information provided for testing	There was insufficient information provided with this submission to determine what type of analysis is required for this item/sample eg, saliva, semen. This sample is to be placed on hold until further information on the testing requirements for this sample is provided	n/a	Information sent via Examination request notification by QHFSS to SOC / SCI officer- not used since 2015	Retain for discussion with QPS in the future
SRMI	Sample required manual intervention prior to extraction	This item/sample provided in a tube required manual intervention prior to processing through QHFSS extraction methods. This necessitated additional resources to perform manipulation on the item/sample examined by QPS to ensure it was appropriate for the extraction process.		Information sent via Examination request notification by QHFSS to SOC / SCI officer - not used since 2011	Retain for discussion with QPS in the future

Possible hair located on the outside of an in-tube submission

EXHIBIT 194

[redacted]

From: Harris.LibbyA[ESC]
Sent: Wednesday, 7 September 2022 09:31
To: Neville.DavidH[OSC]
Subject: FW: Result wording for discussion

OFFICIAL

OFFICIAL

From: Allison Lloyd <[redacted]
Sent: Thursday, 9 September 2021 15:20
To: Justin Howes <[redacted] McIntyre.OliviaM[OSC] <[redacted]
Cc: Harris.LibbyA[OSC] <[redacted] Adrian Pippia <[redacted]
Subject: RE: Result wording for discussion

CAUTION: This email originated from outside of Queensland Police Service. Do not click links or open attachments unless you recognise the sender and know the content is safe.

Good afternoon,

After discussing the single source wording in the Teams meeting this afternoon with Libby and Olivia, my understanding of the result lines that QPS would prefer are as follows:

Scenario: A single source profile that is unknown or matching DNAIntel and in a blood trail for example, the first time observed will have:

1. SS
2. SS1
3. 1SSNCD

Subsequent profiles:

1. SS
2. SS1

Scenario: If it is a Single source that matches an Evid sample and is first observed:

1. SS
2. LR1 (LR1-LR8 as appropriate)
3. 1SSNCD

Subsequent profiles:

1. SS
2. LR1 (LR1-LR8 as appropriate)

Please let me know if I am misunderstanding anything or if you have any queries.

SS	Single source DNA profile	The DNA profile obtained from this item/sample indicated the presence of one contributor.

SS1	Single source DNA profile - Intel	The DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.
1SSNCD	NCIDD upload single source DNA profile	A single source DNA profile was obtained from the item/sample. This DNA profile has been selected for loading to NCIDD, and it will be searched against any DNA profiles held on NCIDD (as per the NCIDD matching rules). Further advice will be provided in the event a match is received.

Thanks,

Allison

Allison Lloyd
Senior Scientist - Intelligence Team

DNA Analysis
Prevention Division, Queensland Health

p 07 [redacted]
e [redacted] **w** www.health.qld.gov.au/fss

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From: Justin Howes <[redacted]
Sent: Wednesday, 8 September 2021 3:10 PM
To: McIntyre.OliviaM[OSC] <[redacted]
Cc: Harris.LibbyA[OSC] <[redacted] Allison Lloyd <[redacted] Adrian Pippia <[redacted]
Subject: RE: Result wording for discussion

Hi
Further edit after discussing with Olivia:

An overarching SS line is requested. This will allow SS profiles matching an evid sample to not just have an LR1 line as a result. It will also be a quick indication of a profile being Single source or Mixed.

QPS request pathway for SS matching UK/DNAIntel and another for matching Evid samples.

Scenario: A single source profile that is unknown or matching DNAIntel and in a blood trail for example, the first time observed will have:

- SS: Single Source DNA Profile: *The DNA profile obtained from this item/sample indicated the presence of one contributor.**** New line with no barcodes needed in associated barcode field***
- 1SS (expansion as below) – UK/DNAIntel barcode
- 1SSNCD

Subsequent profiles will be the same as above, without the 1SSNCD line.

If it is a Single source that matches an Evid sample and is first observed:

- SS
- 2SS: Single Source DNA Profile match to Evidence sample: *Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode.* *** New line with barcodes needed in associated barcode field***
- 1SSNCD
- LR1 - barcode

Subsequent profiles will be the same as above, without the 1SSNCD line.

I think this makes sense.

Perhaps we check again tomorrow.

Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

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

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From: Justin Howes
Sent: Wednesday, 8 September 2021 2:28 PM
To: McIntyre.OliviaM[OSC] <[redacted]
Cc: Harris.LibbyA[OSC] <[redacted] Allison Lloyd <[redacted] Adrian Pippia <[redacted]
Subject: RE: Result wording for discussion

Hi
So according to this for a profile that is unknown and in a blood trail for example, the first time observed will have:
1SS - UKx
1SSNCD

If it matches an Evid sample and is first observed:
1SS – barcode
1SSNCD
LR1 – barcode

So then subsequent SS profiles matching the same person would have:
1SS – barcode*** Note: The expansion of 1SS below mentions a statistical evaluation is not provided, but in this case a statistical interpretation is always performed. Suggest removing the last line of the 1SS expansion as written below.
LR1 - barcode

If it matches a DNA Intel sample and is first observed:
1SS- barcode*** Note: The expansion of 1SS below mentions a statistical evaluation, but in the case of DNAIntels we do not want to perform statistical interpretations. Suggest removing the last line of the 1SS expansion as written below.
1SSNCD

That is fine as long as it is all coded and automatic for us. We still don't really see the benefit of 1SSNCD when the previous NUP (NCIDD upload) was hoping to accommodate SS and MIX profiles. The NUP was never to be sent across by itself; it was to be sent with SS and MIX to give it context.

For a mix, it was thought that it could look like:
MIX
NUP (NCIDD upload) – barcode
LR1 – barcode (if applicable)

Regards
Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

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

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From: McIntyre.OliviaM[OSC] <[redacted]
Sent: Wednesday, 8 September 2021 1:44 PM
To: Justin Howes <[redacted]
Cc: Harris.LibbyA[OSC] <[redacted] McIntyre.OliviaM[OSC]
<[redacted]
Subject: Result wording for discussion

1SS	Single source DNA profile	The DNA profile obtained from this item/sample indicated the presence of one contributor. If an unknown designation is sent with this exhibit report, any reference samples associated to this case have been excluded as donors of this DNA and this DNA profile has been designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated barcode. This DNA profile has not been statistically evaluated however a likelihood ratio can be provided if required.
1SSNCD	NCIDD upload single source DNA profile	A single source DNA profile was obtained from the item/sample. This DNA profile has been selected for loading to NCIDD, and it will be searched against any DNA profiles held on NCIDD (as per the NCIDD matching rules). Further advice will be provided in the event a match is received.
NUP	Mix - NCIDD Upload	This item/sample yielded a DNA profile that matches the associated barcode, or has been designated as an Unknown profile. This DNA contribution has been uploaded to NCIDD for searching. If an Unknown profile was uploaded to NCIDD, further advice will be provided in the event a match is received.

Olivia McIntyre
DNA Management Officer
DNA Management Section, Forensic Services Group
Operations Support Command
Ph: [redacted] Mobile [redacted]
[redacted]
200 Roma Street, Brisbane
[redacted]


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EXHIBIT 195

[redacted]

From: Harris.LibbyA[ESC]
Sent: Tuesday, 13 February 2018 07:25
To: Taylor.EwenN[OSC]
Cc: McIntyre.OliviaM[OSC]
Subject: FW: FSS results identified for automation

Inspector,

Liv and I discussed this yesterday with Troy and I am supportive of this process and agree with the wording.

In regards to receiving the task in 3209, we would obviously assess this on a case by case basis dependant on if there were more exhibits to be tested or the result was on the only exhibit for that case.

Libby

From: McIntyre.OliviaM[OSC]
Sent: Monday, 12 February 2018 3:02 PM
To: Taylor.EwenN[OSC] <[redacted]
Cc: Collopen.RubenB[OSC] <[redacted] Gee Kee.KenN[OSC] <[redacted]>; Harris.LibbyA[OSC] <[redacted]
Subject: RE: FSS results identified for automation

Hi Ewen,

Further to the below email, I had a conversation with Justin Howes this afternoon in relation to another matter, and he mentioned the new process for these samples.

He has indicated that he has forwarded suggested new expanded wording to A/Inspector Troy O'Malley for the result 'DNA insufficient for further processing', and Justin advised that Troy would be liaising with DNA Management Section in relation to this wording change.

I have just spoken to Troy, and he has advised that the new wording has already been implemented into the FR, details as follows:

DNA INSUFFICIENT FOR FURTHER PROCESSING
This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling. Please contact Forensic DNA Analysis if this sample is requested to be assessed for further processing.

The following change is suggested, so that the liaison point can be through QPS DNA Management Section:

DNA INSUFFICIENT FOR FURTHER PROCESSING
This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling. Please contact the DNA Management Section if this sample is requested to be assessed for further processing via QPRIME task to Unit Code 3209.

Justin Howes was very supportive of this change.

If everyone agrees to this change, a Change Request will need to be forwarded to Forensic Technology via the Portal.

Forwarded for your information.

Kind regards

Olivia McIntyre | DNA Management Officer | Profile Management Team | DNA Management Section
Forensic Services Group| Operations Support Command | Queensland Police Service
GPO Box 1440 | Brisbane QLD 4001 | Australia
Level 4, Police Headquarters | 200 Roma Street | Brisbane QLD 4000 | Australia
ph: [redacted] | fax: [redacted]
[redacted]

From: McIntyre.OliviaM[OSC]
Sent: Friday, 9 February 2018 7:03 AM
To: Taylor.EwenN[OSC] <[redacted]
Subject: FSS results identified for automation

Hi Ewen,

As discussed, the attached spreadsheet is a list of FSS EXH results that have been identified as validated lines that could be automatically updated to QPRIME except for in the following situations:

- Previous results for exhibit have been incorrected, and the latest reviewed result falls within the category of results that would normally be automated
- The exhibit has undergone further processing / updated due to conditioning, and previous results are no longer valid, and the new result falls within the category of results that would normally be automated
- Exhibit / result has a sub-sample number (older AUSLAB results)

In the above situations, the results included on the attached spreadsheet will still need to populate into the DRMU Unit Worklist.

Forwarded for your information and further discussion with A/Inspector O'Malley.

Kind regards

Olivia McIntyre | DNA Management Officer | Profile Management Team | DNA Management Section
Forensic Services Group| Operations Support Command | Queensland Police Service
GPO Box 1440 | Brisbane QLD 4001 | Australia
Level 4, Police Headquarters | 200 Roma Street | Brisbane QLD 4000 | Australia
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[redacted]

EXHIBIT 196

De Marco.JennaL[LD]

From: McIntyre.OliviaM[OSC]
Sent: Friday, 2 March 2018 07:32
To: Justin Howes
Cc: Collopen.RubenB[OSC]; Gee Kee.KenN[OSC]; Harris.LibbyA[ESC]; Taylor.EwenN[OSC]
Subject: Changes to expanded wording comments

Good morning Justin,

Just letting you know that QPS has changed the expanded wording for the following results;

DNA INSUFFICIENT FOR FURTHER PROCESSING
This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling. Please contact the DNA Management Section if this sample is requested to be assessed for further processing via QPRIME task to Unit Code 3209.

NO STATISTICAL INTERPRETATION PERFORMED
In the absence of a reference sample/s for comparison, a statistical interpretation has not been performed. To nominate a person of interest for comparison to the mixed DNA Profile obtained from this exhibit, please contact the DNA Management Section via QPRIME task to Unit Code 3209.

If you have any questions regarding this, please let me know.

Kind regards

Olivia McIntyre | DNA Management Officer | Profile Management Team | DNA Management Section
Forensic Services Group| Operations Support Command | Queensland Police Service
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[redacted]

EXHIBIT 197

[redacted]

From: Cathie Allen
Sent: Tuesday, 20 November 2018 08:48
To: Simpfendorfer.GerardM[FDDIV]
Cc: Neville.DavidH[OSC]; McNab.BruceJ[OSC]; Collopen.RubenB[OSC]; Craig Russell
Subject: RE: Auto-Microcon process - P1 workflow

Hi Gerard

Thank you for the confirmation regarding the automatic progression of P1 samples that have not reached a threshold of 0.008ng/uL through a Microcon concentration step. As previously advised, once the microcon concentration step has been undertaken, this will completely consume the sample and no DNA extract will be available for any further testing that the QPS may wish to use.

As FR functionality for automatic progression was removed in February 2018, we now request for this functionality to be reinstated. I will request a VSTS/Azure card for this functionality to be reinstated immediately to ensure no loss of time between the quantification process and the microcon concentration process.

Cheers
Cathie

Cathie Allen
Managing Scientist

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

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From: Simpfendorfer.Gerard [redacted]
Sent: Monday, 19 November 2018 3:34 PM
To: Cathie Allen
Cc: Neville.David [redacted] McNab [redacted] Collopen [redacted] Craig Russell
Subject: Auto-Microcon process - P1 workflow
Importance: High

Good afternoon Cathie,

As per the attached document could the QPS request that all Priority 1 samples now proceed with the ‘auto-microcon’ process (paragraph 8.2.a)?

If a DNA concentration rework is required, can the Microcon process be ordered manually by the scientist.

Kind regards

Gerard

Gerard Simpfendorfer
Acting Inspector 4009415
DNA Management Section, Forensic Services Group
Operations Support Command, Queensland Police Service

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EXHIBIT 198

[redacted]]

From: Cathie Allen
Sent: Thursday, 6 December 2018 11:42
To: Simpfendorfer.GerardM[FDDIV]
Subject: RE: Removal of the Microcon step - QPS advice

Thank you

Cheers
Cathie

Cathie Allen
Managing Scientist

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

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From: Simpfendorfer.GerardM[OSC] [mailto:[redacted]
Sent: Thursday, 6 December 2018 9:23 AM
To: Cathie Allen
Cc: Craig Russell; Neville.DavidH[OSC]; McNab.BruceJ[OSC]; Collopen.RubenB[OSC]; Harris.LibbyA[OSC]
Subject: RE: Removal of the Microcon step - QPS advice

Thanks Cathie,

Yes that is correct, unless otherwise advised at P1 approval, all P1 samples are requested to go for automatic concentration that are "DNA Insufficient".

Kind regards

Gerard

Gerard Simpfendorfer
Acting Inspector 4009415
DNA Management Section, Forensic Services Group
Operations Support Command, Queensland Police Service

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From: Cathie Allen <[redacted]
Sent: Thursday, 6 December 2018 9:07 AM
To: Simpfendorfer.GerardM[OSC] <[redacted]
Cc: Craig Russell <[redacted] Neville.DavidH[OSC] <[redacted]
McNab.BruceJ[OSC] <[redacted] Collopen.RubenB[OSC]
<[redacted] Harris.LibbyA[OSC] <[redacted]
Subject: RE: Removal of the Microcon step - QPS advice

Hi Gerard

Just to confirm - The reworking options and their visibility will be available for P2 and P3 samples, as it's my assumption that the QPS still wish to keep automatic concentration for P1 samples that are 'DNA Insufficient' – is this correct?

Cheers
Cathie

Cathie Allen
Managing Scientist

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

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From: Simpfendorfer.GerardM[OSC] [mailto:[redacted]
Sent: Thursday, 6 December 2018 7:41 AM
To: Cathie Allen
Cc: Craig Russell; Neville.DavidH[OSC]; McNab.BruceJ[OSC]; Collopen.RubenB[OSC]; Harris.LibbyA[OSC]
Subject: RE: Removal of the Microcon step - QPS advice

Cathie,

Sounds like a good option, will wait and see how it looks when the first ones come through, but basically similar process to what we currently have but with Health providing the QPS more visibility around re-work options that are available before requesting any further processing which we still do via the current process.

Kind regards

Gerard

Gerard Simpfendorfer
Acting Inspector 4009415
DNA Management Section, Forensic Services Group
Operations Support Command, Queensland Police Service

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From: Cathie Allen < [redacted]
Sent: Wednesday, 5 December 2018 5:51 PM
To: Simpfendorfer.GerardM[OSC] < [redacted]
Cc: Craig Russell < [redacted] Neville.DavidH[OSC] < [redacted]
McNab.BruceJ[OSC] < [redacted] Collopen.RubenB[OSC]
< [redacted] Harris.LibbyA[OSC] < [redacted]
Subject: FW: Removal of the Microcon step - QPS advice

Hi Gerard

I've been working with the Team Leaders regarding this. We have devised wording within the expanded comments of the result lines to provide more visibility to the QPS regarding re-working options that are available. If re-working is required, the scientist would review the data available for the sample and select the most appropriate re-work option, after the QPS have advised re-work can go ahead. The process whereby the QPS send through a Request / Task to a Team Leader would be the best course of action for this.

Please let me know if you have any further queries.

Cheers
Cathie

Cathie Allen
Managing Scientist

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

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From: Cathie Allen
Sent: Friday, 30 November 2018 3:30 PM
To: 'Simpfendorfer.GerardM[OSC]'
Cc: Craig Russell; Neville.DavidH[OSC]; McNab.BruceJ[OSC]; Collopen.RubenB[OSC]; Harris.LibbyA[OSC]
Subject: RE: Removal of the Microcon step - QPS advice

Hi Gerard

I'm currently working on this with the Team Leaders in Forensic DNA Analysis.

This week, both Forensic Chemistry and Forensic DNA Analysis have had NATA technical assessments, so I've had limited opportunity for this given my commitments with the assessments.

Cheers
Cathie

Cathie Allen
Managing Scientist

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

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From: Simpfendorfer.GerardM[OSC] [mailto:[redacted]
Sent: Friday, 30 November 2018 1:51 PM
To: Cathie Allen
Cc: Craig Russell; Neville.DavidH[OSC]; McNab.BruceJ[OSC]; Collopen.RubenB[OSC]; Harris.LibbyA[OSC]
Subject: RE: Removal of the Microcon step - QPS advice

Hi Cathie,

Just wondering if you have had a chance to consider the below email?

In particular the suggestion: So, it may be that the process stays as it is, but when we send the request through to Luke Ryan (or Justin or Paula) for further processing we request advice on proceeding with Microcon step or whether some other process or testing may have a better opportunity based on the factors that have been taken into consideration to produce a usable profile, what are your thoughts on this?

I did this process recently with Justin Howes (via Luke Ryan) where I sent a request through for some assistance on options and Justin provide a good response allowing the QPS to make an informed decision. This was for a case where the investigating officer requested further processing, but when we reviewed the request we thought it better to get further advice from Health, which will hopefully prove beneficial in furthering this particular investigation. [redacted] refers.

This week I also processed through 4 requests to Luke Ryan for further processing as a result of tasks from investigators where when we reviewed the request, the reason the investigator was requesting further processing and the case decided to proceed with the Microcon step without further advice from Health.

Hope you have a good weekend.

Kind regards

Gerard

Gerard Simpfendorfer
Acting Inspector 4009415
DNA Management Section, Forensic Services Group
Operations Support Command, Queensland Police Service

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Email: [redacted]
Address: Level 4 Police Headquarters, 200 Roma St, Brisbane, Qld, 4000
Postal: GPO Box 1440, Brisbane, Queensland 4001, Australia

From: Simpfendorfer.GerardM[OSC]
Sent: Thursday, 22 November 2018 3:54 PM
To: Cathie Allen <[redacted]
Cc: Craig Russell <[redacted] Neville.DavidH[OSC] <[redacted]
McNab.BruceJ[OSC] <[redacted] Collopen.RubenB[OSC]
<[redacted] Harris.LibbyA[OSC] <[redacted]
Subject: RE: Removal of the Microcon step - QPS advice

Hi Cathie,

That wasn't really what I was chasing as I am not questioning the code of conduct or the evidence that is given in Court by the Scientist as we have no issue with this and know you and your staff always act in good faith.

It could be how I phrased the question/issue, so I'll try again.

In your email you said the following:

> There are a number of factors that would be taken into consideration regarding the balance between concentrating the sample vs preserving extract for other testing.

And then went on to describe a number of these factors in the rest of that paragraph. You also started the next paragraph with some 'key factors' and finished that paragraph with the following:

> All of these factors are taken into consideration prior to requesting a Microcon. We have assessed a large amount of data to provide the best indication of how profiles have behaved and provide this advice to the QPS to assist.

My questions around the above 2 sentences are:
- At what point of the examination process are these factors taken in to consideration?

- How do you provide this advice to QPS to assist?

I thought the line “THIS SAMPLE HAS UNDERGONE FURTHER PROCESSING” meant that either the QPS or the Scientist had requested further processing of the sample which is the rework process and that the Microcon step had commenced.

I do not believe this line provides advice on the best indication for how profiles may behave or if another of the factors you have considered may be more beneficial in obtaining a usable profile for the investigation.

Is there another option to this line to provide the QPS with this advice around your best indication in these cases besides proceeding with Microcon considering the Microcon step will consume all the available extract?

We believe the risk of deciding whether or not to Micron should not be left to the QPS solely as we do not have the expertise or access to the data about the quality and quantity of DNA in the sample. What we are chasing is some sort of decision making tree so we know what should trigger us to request further processing. At the moment it seems to be a stab in the dark for us, if we don’t request a rework we get no result. But, the chance of a result is better than nothing in certain circumstances.

So, it may be that the process stays as it is, but when we send the request through to Luke Ryan for further processing we request advice on proceeding with Microcon step or whether some other process or testing may have a better opportunity based on the factors that have been taken into consideration to produce a usable profile, what are your thoughts on this?

That way the investigating officer and the QPS can make an informed decision before authorising the consumption of all the extract.

I hope this is a little clearer.

Kind regards

Gerard

Gerard Simpfendorfer
Acting Inspector 4009415
DNA Management Section, Forensic Services Group
Operations Support Command, Queensland Police Service

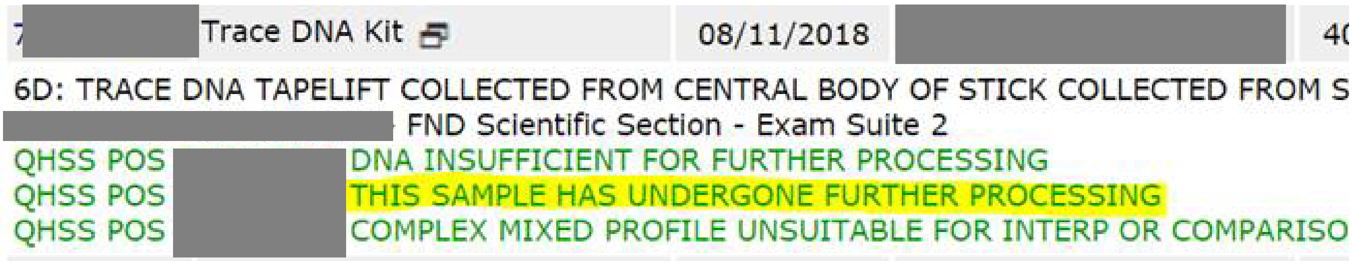
Phone: +61 7 [redacted]
Internal PHQ Extension: [redacted]
Fax: +61 7 [redacted]
Email: [redacted]
Address: Level 4 Police Headquarters, 200 Roma St, Brisbane, Qld, 4000
Postal: GPO Box 1440, Brisbane, Queensland 4001, Australia

From: Cathie Allen < [redacted]
Sent: Wednesday, 21 November 2018 12:14 PM
To: Simpfendorfer.GerardM[OSC] < [redacted]
Cc: Craig Russell < [redacted] Neville.DavidH[OSC] < [redacted]
McNab.BruceJ[OSC] < [redacted] Collopen.RubenB[OSC]
< [redacted]
Subject: RE: Removal of the Microcon step - QPS advice

Hi Gerard

Scientists in Forensic DNA Analysis apply scientific principles to processing and reworking of all samples that they review, as they are bound by the Code of Conduct for the Queensland Public Service and are committed to ensuring the best possible outcome for the Queensland Community. Reporting scientists are questioned under oath about the scientific decisions that they have made and provide answers based on scientific principles.

If the sample is reworked after a result has been released to the QPS, the QPS is advised electronically by a result line advising that the sample has undergone further processing as per the example below:



7[redacted] Trace DNA Kit 08/11/2018 [redacted] 4

6D: TRACE DNA TAPELIFT COLLECTED FROM CENTRAL BODY OF STICK COLLECTED FROM S

[redacted] FND Scientific Section - Exam Suite 2

QHSS POS [redacted] DNA INSUFFICIENT FOR FURTHER PROCESSING

QHSS POS THIS SAMPLE HAS UNDERGONE FURTHER PROCESSING

QHSS POS COMPLEX MIXED PROFILE UNSUITABLE FOR INTERP OR COMPARISO

Cheers
Cathie

Cathie Allen
Managing Scientist

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

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

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From: Simpfendorfer.GerardM[OSC] [mailto:[redacted]
Sent: Tuesday, 20 November 2018 3:35 PM
To: Cathie Allen
Cc: Craig Russell; Neville.DavidH[OSC]; McNab.BruceJ[OSC]; Collopen.RubenB[OSC]
Subject: Removal of the Microcon step - QPS advice

Hi Cathie,

And thank you for your response.

You mention there are a number of factors that would be taken into consideration regarding the balance between concentrating the sample vs preserving extract for other testing and you gave some examples including assessing the quality and quantity of the DNA as a key factor to obtaining a DNA profile.

1. Do you take these factors into consideration only when sending through the DNA Insufficient result for:
    - All exhibits?
    - P1 and P2 only exhibits?
    - P1 only exhibits?

2. Or do you take these factors in to consideration only when the QPS requests further processing of the exhibit?

3. Or do you take these factors in to consideration only when the QPS requests advice on other testing options?

If it is option 1 or 2, how do you provide this advice to the QPS to assist investigators, especially if in the Scientists expert opinion requesting a Microcon step may not be the best for obtaining a possible DNA result due to this process consuming all the available extract.

Kind regards

Gerard

Gerard Simpfendorfer
Acting Inspector 4009415
DNA Management Section, Forensic Services Group
Operations Support Command, Queensland Police Service

Phone: +61 7 [redacted]
Internal PHQ Extension: [redacted]
Fax: +61 7 [redacted]
Email: [redacted]
Address: Level 4 Police Headquarters, 200 Roma St, Brisbane, Qld, 4000
Postal: GPO Box 1440, Brisbane, Queensland 4001, Australia

From: Cathie Allen <[redacted]
Sent: Friday, 16 November 2018 4:01 PM
To: Simpfendorfer.GerardM[OSC] <[redacted]
Cc: Craig Russell <[redacted] Neville.DavidH[OSC] <[redacted]
McNab.BruceJ[OSC] <[redacted]
Subject: RE: Removal of the microcon step from P1 worflow.

Hi Gerard

The quantification values between 0.001 and 0.008ng/uL is the range for the result line of DNA Insufficient – so this is the range that prior to Feb 2018 would have automatically proceeded for concentration.

There are a number of factors that would be taken into consideration regarding the balance between concentrating the sample vs preserving extract for other testing – some examples, but limited to, – the indication within the quantification of the Y chromosome, pooling of samples from a similar area prior to concentrating as this may have a better chance of concentrating the available DNA for a 'useable' profile, preserving 1 sample and concentrating another sample from similar areas (rather than doing both in the first instance), the quantification value and if it's likely to be a mixture, the sample type (ie tapelift from a particular exhibit vs swab from a more probative area) or targeting particular samples for concentration in the context of the case (rather than all priority 1 samples).

The quality and quantity of the DNA are the key factors in obtaining a DNA profile. For these samples, whilst there was a small amount of DNA, the quality of the DNA may have been quite good, which has meant that a DNA profile was able to be generated (I haven't looked into these samples, I'm providing information on a general basis). Whilst our processes provide a quantification value, indication of degradation and indication of Y chromosome, it's the generation of DNA profile that assists in highlighting the quality of the DNA that was available. The DNA in the sample may only just be above the acceptance criteria to be called an allele, and it may generate enough alleles to provide a Likelihood Ratio of >100 billion, however its viewing the DNA profile that can show the extent of the degradation or inhibition factors that may be associated. All of these factors are taken into consideration prior to requesting a Microcon. We have assessed a large amount of data to provide the best indication of how profiles have behaved and provide this advice to the QPS to assist.

Please let me know if you have any further questions.

Cheers
Cathie

Cathie Allen
Managing Scientist

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

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

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From: Simpfendorfer.GerardM[OSC] [mailto:[redacted]
Sent: Thursday, 15 November 2018 3:24 PM
To: Cathie Allen
Cc: Craig Russell; Neville.DavidH[OSC]; McNab.BruceJ[OSC]
Subject: RE: Removal of the microcon step from P1 worflow.

Hi Cathie,

Thank you for the below advice.

Could you advise is there a quant cut off where microcon would automatically occur?

What would be the decision making advice around preserving the sample and also enhancing chances of getting a result?

Also, why did these samples yield a result and could the factors involved be used to determine future processes?

Kind regards

Gerard

Gerard Simpfendorfer
Acting Inspector 4009415
DNA Management Section, Forensic Services Group
Operations Support Command, Queensland Police Service

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Internal PHQ Extension: 66916
Fax: +61 7 [redacted]
Email: [redacted]
Address: Level 4 Police Headquarters, 200 Roma St, Brisbane, Qld, 4000
Postal: GPO Box 1440, Brisbane, Queensland 4001, Australia

From: Cathie Allen <[redacted]
Sent: Thursday, 15 November 2018 9:20 AM
To: Simpfendorfer.GerardM[OSC] <[redacted]McNab.BruceJ[OSC]
<[redacted]
Cc: Craig Russell <[redacted]Neville.DavidH[OSC] <[redacted]
Subject: FW: Removal of the microcon step from P1 worflow.
Importance: High

Hi Gerard and Bruce

I can confirm that the Microcon process has been applied to the below four sample as requested by the QPS on the dates listed below:

[redacted] – Snr Sgt Simpfendorfer requested Microcon 29/10/2018
– Snr Sgt Simpfendorfer requested Microcon 06/11/2018
- Snr Sgt Simpfendorfer requested Microcon 06/11/2018
- Snr Sgt Simpfendorfer requested Microcon 06/11/2018

During a meeting on 1st of Feb 2018, Paul Csoban (previous Executive Director for FSS) and I met with Supt Dale Frieberg to discuss the Options Paper that had previously been provided to the QPS for decision. During this meeting, the Superintendent agreed that Option 2 was the preferred option, which was later confirmed via email (as per below). During the discussion, the second part of Option 2 (section a) was discussed, which related to Priority 1 samples and the Superintendent indicated that Priority 1 samples should be processed the same as Major crime (P2) and Volume crime samples (P3), which is not to be automatically progressed through the Microcon process. After the approval from the QPS in Feb 2018, all samples have not automatically progressed through the Microcon process. The QPS or a Forensic DNA Analysis staff member can request a Microcon process for a sample at any time.

Automatic progression of samples through the Microcon process means that all available DNA extract will be consumed, so no further testing can be conducted on these samples after this step. This means that if a sample could yield a profile by specific Y chromosome testing for example, there would be no extract available for that testing to be conducted. It also means that samples that are eligible to be pooled together, as they are from the same item or area, are not able to be as there is no DNA extract left to undertake pooling. Scientists or Forensic officers reviewing results in the context of a case are able to request a Microcon process for a sample or samples.

As the decision on the automatic Microcon process was made last financial year, the budget for this financial year has been adjusted for that consumable, so this will increase the cost.

If the QPS wishes for P1 samples to automatically be processed through the Microcon process, which leaves no available extract for other testing, this process can be re-introduced. Please confirm if the QPS requires the re-introduction of this step.

The Options Paper reviewed 1449 Major crime samples that had been progressed through the Microcon process over a one year period, as this was considered to be sufficient sample numbers to demonstrate a clear trend.

The laboratory is unable to search the FR to undertake any statistical analysis regarding ‘useable’ profile numbers – this was highlighted to FSS during development that large or medium scale interrogation of the FR could only be undertaken by the QPS, as they would need to construct the search and ensure the timing of the search was undertaken so as not to add extra burden to the FR during peak operational times. If the QPS were able to generate this data, the laboratory would undertake this analysis and provide feedback. The Microcon process was no longer automatically undertaken for P1 or P2 samples from the 12th of Feb 2018.

Whilst the Microcon process has not been automatically applied to Major crime samples (P2) since mid Feb, scientists have reviewed those results and requested a Microcon process if in the context of the case it could have been of potential benefit. If the QPS undertook a search of all ‘DNA insufficient’ results on P1 and P2 samples since the 12th of Feb, the laboratory could undertake an analysis of the cases to determine if additional testing through the Microcon process is required. This would require resources and would reduce the number of results that are reviewed by the lab until this analysis was completed.

I await your advice regarding this. If you have any further questions, please let me know how I can assist.

Cheers
Cathie

Cathie Allen
Managing Scientist

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

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

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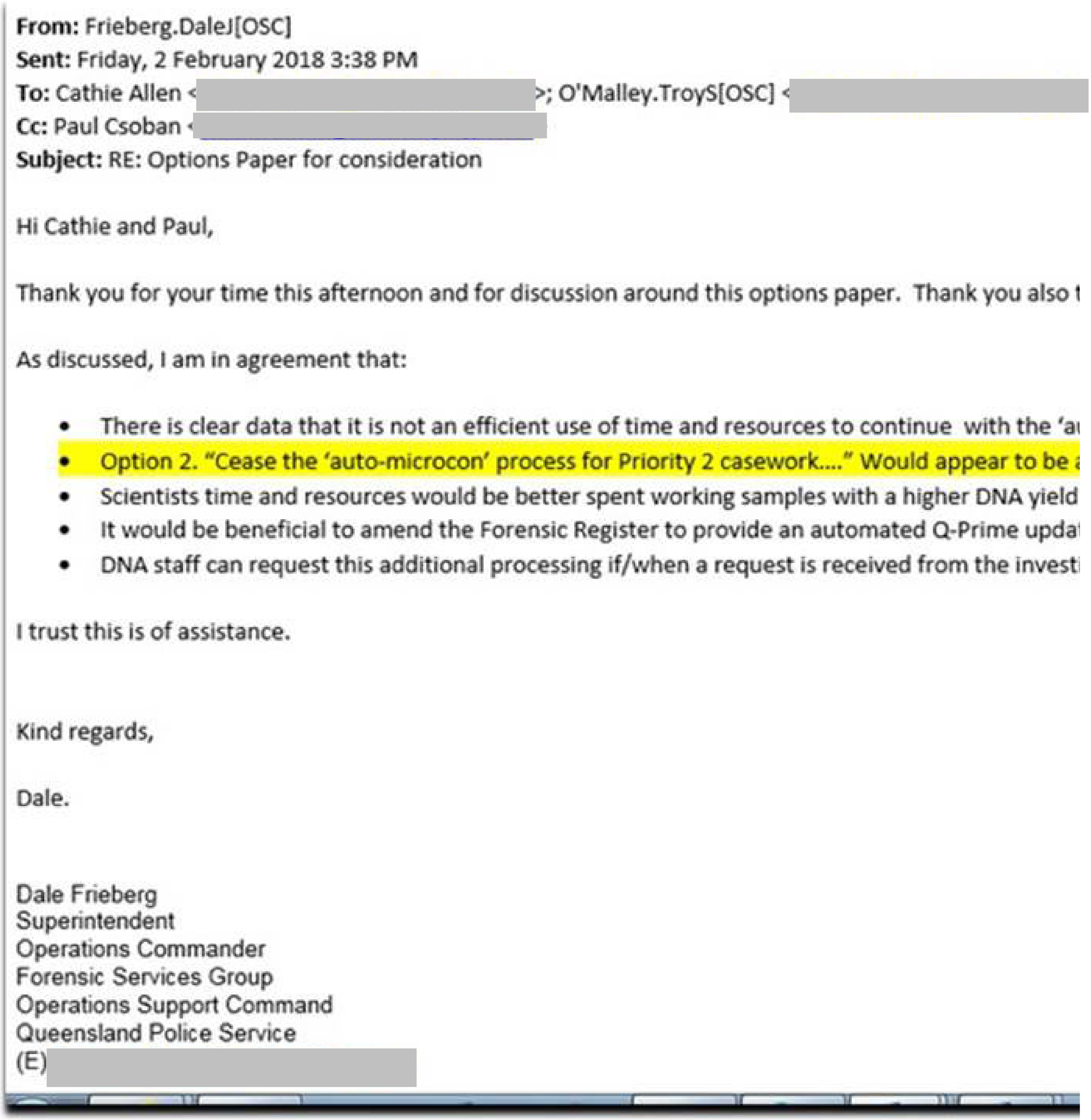
From: Neville.DavidH[OSC] [mailto: [redacted]
Sent: Wednesday, 14 November 2018 2:47 PM
To: Cathie Allen
Cc: Craig Russell; McNab.BruceJ[OSC]; Simpfendorfer.GerardM[OSC]
Subject: Removal of the microcon step from P1 worflow.
Importance: High

Dear Cathie
During the course of the investigation [redacted] over 15 samples were submitted as Priority 1. On initial testing, four samples were reported as having insufficient DNA present for further testing. Upon receipt of that result my staff requested additional testing and each of those samples yielded a result as follows:

[redacted] - SINGLE SOURCE 20 LOCI DNA PROFILE LR > 100 BILLION [redacted]; and POSSIBLE SUB-THRESHOLD INFORMATION
[redacted] - SINGLE SOURCE DNA PROFILE - ASSUMED KNOWN CONTRIBUTOR – [redacted]
[redacted] SS DNA PROFILE 9 LOCI AND ABOVE LR > 100 BILLION [redacted]
[redacted] - COMPLEX MIXED PROFILE UNSUITABLE FOR INTERP OR COMPARISON

Could you confirm if the profiles for the four samples listed above were obtained after micro-concentration was performed, please. Could you also confirm if the microcon step has been removed from the workflow as a matter of routine for P1 samples. My understanding as per the below was that this was only to occur for P2. If this process has been removed from the P1 workflow, could it please be reintroduced as it will stop delays in obtaining results that are considered urgent, please.



From: Frieberg.DaleJ[OSC]
Sent: Friday, 2 February 2018 3:38 PM
To: Cathie Allen <[redacted]>; O'Malley.TroyS[OSC] <[redacted]
Cc: Paul Csoban <[redacted]
Subject: RE: Options Paper for consideration

Hi Cathie and Paul,

Thank you for your time this afternoon and for discussion around this options paper. Thank you also t

As discussed, I am in agreement that:

- There is clear data that it is not an efficient use of time and resources to continue with the 'a
- Option 2. "Cease the 'auto-microcon' process for Priority 2 casework...." Would appear to be
- Scientists time and resources would be better spent working samples with a higher DNA yield
- It would be beneficial to amend the Forensic Register to provide an automated Q-Prime upda
- DNA staff can request this additional processing if/when a request is received from the investi

I trust this is of assistance.

Kind regards,

Dale.

Dale Frieberg
Superintendent
Operations Commander
Forensic Services Group
Operations Support Command
Queensland Police Service
(E)[redacted]

The removal of the microcon step in the process was agreed to on 2 February 2018 by Supt Frieberg based on the advice included in the attached paper. This paper estimates that there would be less than a 2% reduction in the number of useable results if the step was eliminated.

Based on the fact that 3 out of 4 samples for this case yielded a result when testing was continued, anecdotally it would seem that we may be missing out on more than 2% of results.

Since eliminating this step, has your laboratory undertaken any statistical analysis to determine if there has been a drop in the proportion of samples that give a useable profile, please.

There are other serious matters including homicides where testing has stopped once advice was received that there is insufficient DNA for further testing. Based on the results for this case (75% success rate for the ones received back so far), would you recommend that these cases be re-examined please.

Could you please direct your response to Gerard and Bruce.

David Neville
Inspector
DNA Management Unit | Forensic Services Group
Operations Support Command
QUEENSLAND POLICE SERVICE

Phone [redacted]
Email [redacted]
Address **GPO Box 1440 Brisbane 4001**

EXHIBIT 199

[redacted]

From: McLaren.ScottA[PCAP]
Sent: Thursday, 3 January 2013 12:42
To: Ayscough.DanielleM[OSC]; Holden.PatriciaM[OSC]; Simpfendorfer.GerardM[FDDIV]; Whittle.EmmaJ[OSC]; Nauschutz.MarneyS[OSC]; McIntyre.OliviaM[OSC]
Cc: Carstensen.AnthonyL[OSC]; Morgan.Ben[OSC]
Subject: Problem with DNA Result Wording - No DNA Detected

The following wording is currently attached to DNA sample that do not yield a DNA profile (and will not). It's been noted that the last sentence (in red) needs to be removed, Paula and Ben are working on that now.

This item/sample was submitted for DNA analysis; however no DNA was detected above the limit of detection at the quantitation stage. No further processing was conducted on this item. QPS can submit a request to QHFSS for a continuation of this processing if required.

However, we can't do anything about the results already released, so I would ask your assistance in ensuring that where this type of result is released that no request for additional testing is forwarded to QHSS.

Thanks

Senior Sergeant Scott McLaren | Quality Management Officer | DNA Management Section
Forensic Services Branch | Operations Support Command | Queensland Police Service
GPO Box 1440 | Brisbane QLD 4001 | Australia
Level 4 Police Headquarters | 200 Roma Street | Brisbane QLD 4000 | Australia
[redacted]

EXHIBIT 200

[redacted]

From: McNab.BruceJ[OSC]
Sent: Wednesday, 22 June 2022 16:44
To: Neville.DavidH[OSC]
Subject: RE: FSS advice regarding DNA reporting

No sign of the report mate. I'll brief up re the pending delay

Bruce McNab BM
Superintendent 7417
Forensic Services Group
OPERATIONS SUPPORT COMMAND
[redacted]
Police HQ
200 Roma Street Brisbane QLD 4000
[redacted]

From: Neville.DavidH[OSC] <[redacted]
Sent: Wednesday, 22 June 2022 09:18
To: McNab.BruceJ[OSC] <[redacted]
Subject: RE: FSS advice regarding DNA reporting

Hi Bruce
This has no impact on the operations of our staff. Perhaps it could be forwarded for their noting.

However, more importantly, the continued testing of the low concentration samples from volume crime matters is going to grind that lab to a halt. Maintenance of a .oo1 threshold for all samples probably is not practical. I would recommend that a higher threshold be used for volume crime.

Has there been any sign of the promised report from Cathie around thresholds which might be very useful in determining a threshold for volume crime matters.

Dave

From: McNab.BruceJ[OSC] <[redacted]
Sent: Wednesday, 22 June 2022 08:34
To: Neville.DavidH[OSC] <[redacted]
Subject: FW: FSS advice regarding DNA reporting

Hi Dave,
What do we need to do from our end?

Bruce McNab BM
Superintendent 7417
Forensic Services Group
OPERATIONS SUPPORT
COMMAND
[redacted]
Police HQ
200 Roma Street Brisbane QLD 4000
[redacted]

From: Lara Keller <[redacted]
Sent: Tuesday, 21 June 2022 12:12
To: McNab.BruceJ[OSC] <[redacted]
Cc: Cathie Allen <[redacted]
Subject: FSS advice regarding DNA reporting

Good afternoon Bruce

On Monday, 6th of June 2022, the Premier announced a Commission of Inquiry into Forensic DNA Testing in Queensland. The Premier also announced that, moving forward, samples that fall into the category of ‘DNA insufficient for further processing samples’ would be profiled.

On the 6th of June, the Forensic Register was amended to ensure that all crime scene samples with a quantitation value above 0.001ng/uL are amplified and results provided electronically to the QPS.

I would appreciate if you could circulate this advice to your QPS colleagues.

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

p [redacted] **m** [redacted]
a Administration, Level 1, 39 Kessels Road, Coopers Plains, QLD, 4108
e [redacted] **w** www.health.qld.gov.au/fss

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[redacted]

EXHIBIT 201

From: Matthew Rigby <[redacted]
Sent: Wednesday, 17 August 2022 19:09
To: Neville.DavidH[OSC]
Cc: David Rosengren
Subject: FSS SOP draft memo
Attachments: Extract 19.4 from SOP 17117V19.pdf; DG Memo - Required amendment to FSS SOP 17117V19 - 17 August 2022.docx

Hi Dave,

Thanks for your time today and as discussed with the Acting DG and myself this afternoon, please find attached a draft memo that has been prepared and the associated SOP extract to provide some further clarity to our staff at FSS.

Appreciate any feedback/input that you have from a QPS perspective.

Thanks Matt

Queensland Government

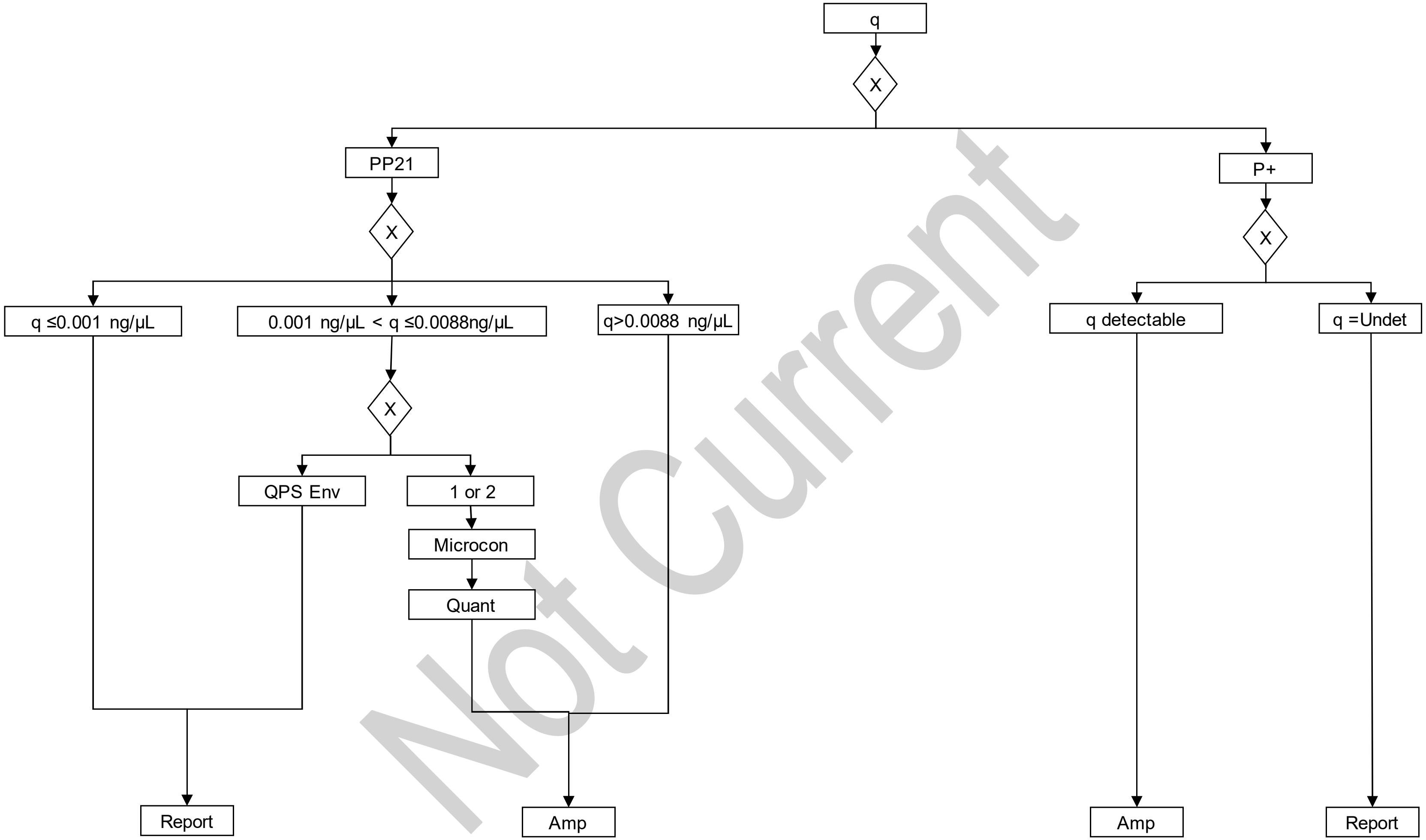
Matt Rigby
Executive Director
Office of the Director-General
Queensland Health

M [redacted]
E
W health.qld.gov.au
A Level 14, 33 Charlotte Street, Brisbane QLD 4000

****

****

19.4 Quantification workflow



Department of Health

Queensland Government

MEMORANDUM

To: Helen Gregg, A/Executive Director, Forensic and Scientific Services

Copies to: Prof Keith McNeil, Deputy Director-General and
Chief Medical Officer, Prevention Division and Chief Clinical Information

From: David Rosengren, Acting Director-General

Enquiries to: ##

07 ##

Subject: *Reversion to concentration of all Priority 2 samples in range*

Following the announcement of the DNA Commission of Inquiry, on 6 June 2022, the A/DG Shaun Drummond made a decision about the workflow relating to samples reported as '*DNA insufficient for further processing*'. This related to Priority 2 samples with a quantitation result of between 0.001ng/uL (LOD) and 0.0088ng/uL.

The A/DG's decision contemplated an option for testing that would allow a discretion for FSS Forensic DNA Analysis scientists, including in conjunction with investigating officers at QPS, to decide the merits of undertaking a concentration process for Priority 2 samples within this quantitation range, having regard to other available case information.

I appreciate that there may be grounds for the discretionary option, including a risk of the concentration process reducing residual sample quantity if it is not considered by the scientist or QPS to be beneficial. That is because reducing the sample quantity has the potential to impact future testing if requested by QPS or Defence, and could limit opportunities for results when improved processes are introduced in future. I expect this issue will be explored in detail by the DNA Commission of Inquiry.

I have reflected about options for the concentration process and for certainty pending the outcome of the DNA Commission of Inquiry, I request the workflow to revert to the concentration process for Priority 1 and Priority 2 samples stipulated in Standard Operating Procedure 17117V19 (diagram section 19.4) (**attached**). That is, the concentration process is to be undertaken automatically for <u>all</u> Priority 1 and Priority 2 samples with a quantitation result of between 0.001ng/uL (LOD) and 0.0088ng/uL.

I ask that a review of the laboratory information system be undertaken to identify any sample results within this quantitation range from 6 June 2022 to today's date inclusive. Any such samples are now to be subjected to the concentration process, if not already undertaken.

Statement confirming consultation with QPS – once feedback provided

I request that you ensure this memorandum is shared with the Forensic DNA Analysis Unit staff and ensure clarity with the approach outlined above.

Should you require further information, the Department of Health's contact is ## on telephone 07 ##.

David Rosengren
Acting Director-General
/ /

Prepared by:
Megan Fairweather
Acting Chief Legal Counsel
Legal Branch
17 August 2022

Cleared by:
Matt Rigby
Executive Director
Office of the Director-General
5 August 2022

[redacted] EXHIBIT 202

From: Neville.DavidH[OSC]
Sent: Friday, 19 August 2022 09:22
To: Matthew Rigby
Cc: McCarthy.DuncanJ[OSC]
Subject: FW: FSS SOP draft memo
Attachments: Extract 19.4 from SOP 17117V19.pdf; DG Memo - Required amendment to FSS SOP 17117V19 - 17 August 2022.docx

Hi Matt

Thank you for the opportunity to comment on the proposed change to the laboratory workflow involving automatic micro-concentration of samples in the concentration range of .001-.0088ng/uL.

The QPS agreed to the removal of this process in February 2018 following a recommendation that was initiated by the DNA laboratory and presented in an Options Paper. The QPS now has some concern about the information it was provided to make this decision including the manner in which the supporting data was derived.

In November 2018 the QPS first raised concern with the Managing Scientist that the removal of the automatic micro-concentration process may have resulted in evidence being missed. At that time the QPS was given an assurance that the success of micro-concentration was very low and that ‘automatic progression of samples through the Microcon process means that all available DNA extract will be consumed, so no further testing can be conducted on these samples after this step’. Based on this advice, the QPS continued with the arrangement.

Due to limitations of the QHFSS DNA laboratory, from time to time the QPS seeks the services of other providers to undertake alternative testing, particularly for low concentration and degraded samples. If the advice from the Managing Scientist is correct, the automatic concentration of all samples in the range of .001-.0088ng/uL could result in the opportunity being lost to use another service provider to obtain important probative evidence. This is a consequence that the QPS is unable to accept as a matter of routine.

The risk is that the proposed directive may result in a sample being exhausted making alternative testing impossible. The QPS does not have the expertise to assess the likelihood of the risk given such an assessment can only be made based on information that is exclusively within the domain of QHFSS. As a result, the QPS considers the decision to reimplement automatic micro-concentration an internal matter that QH must decide in the context that the customer (the QPS) desires to maximise the potential to obtain a profile from every sample, whether that be by services delivered by QHFSS or by another provider that can deliver a service QHFSS is not resourced to deliver.

Regards

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

From: Matthew Rigby <[redacted]
Sent: Wednesday, August 17, 2022 7:10 pm
To: Neville.DavidH[OSC] <[redacted]
Cc: David Rosengren <[redacted]
Subject: FSS SOP draft memo

Hi Dave,

Thanks for your time today and as discussed with the Acting DG and myself this afternoon, please find attached a draft memo that has been prepared and the associated SOP extract to provide some further clarity to our staff at FSS.

Appreciate any feedback/input that you have from a QPS perspective.

Thanks Matt

Queensland
Government

Matt Rigby
Executive Director
Office of the Director-General
Queensland Health

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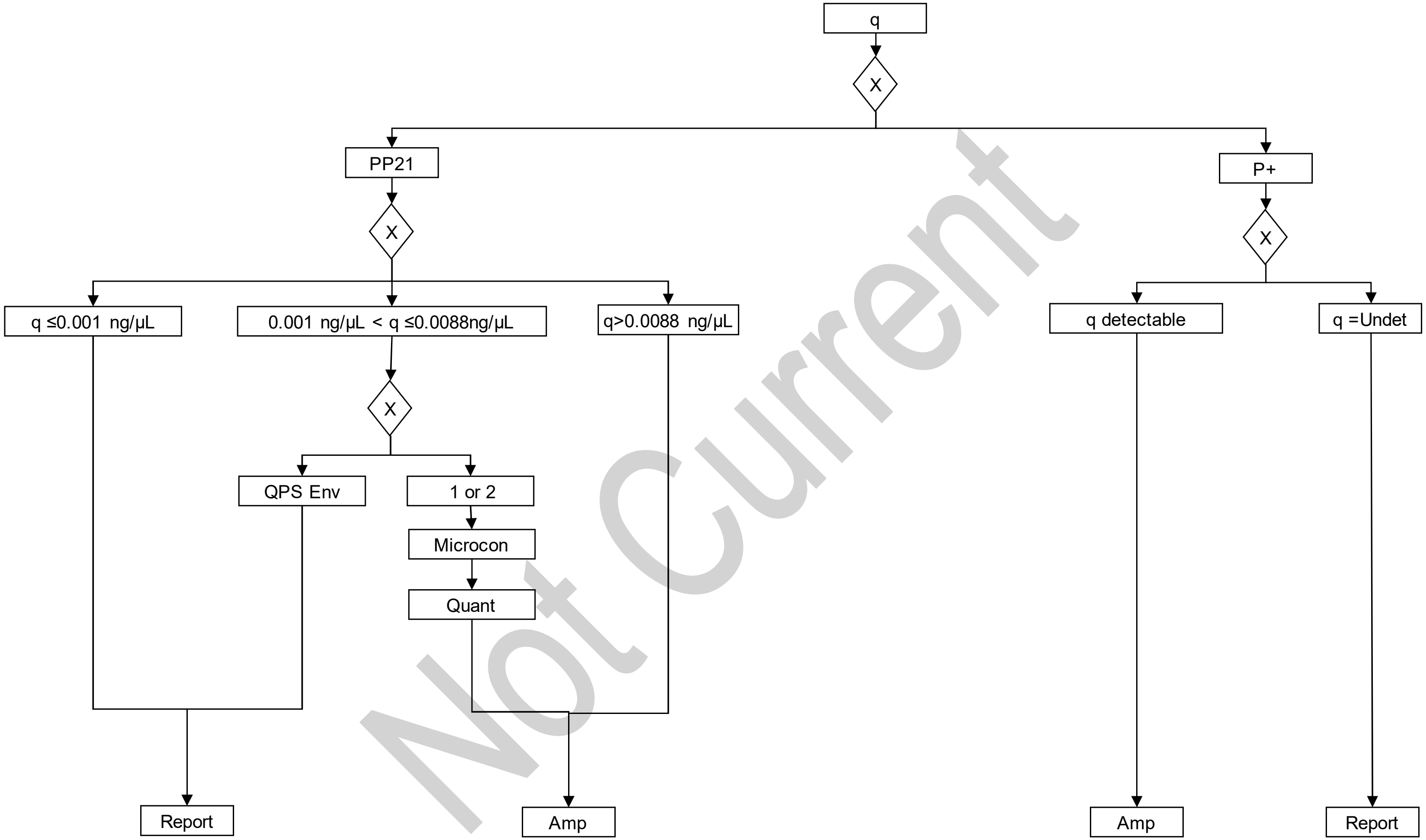
W health.qld.gov.au
A Level 14, 33 Charlotte Street, Brisbane QLD 4000

19.4 Quantification workflow



Department of Health

Queensland Government

MEMORANDUM

To: Helen Gregg, A/Executive Director, Forensic and Scientific Services

Copies to: Prof Keith McNeil, Deputy Director-General and
Chief Medical Officer, Prevention Division and Chief Clinical Information

From: David Rosengren, Acting Director-General

Enquiries to: ##

07 ##

Subject: *Reversion to concentration of all Priority 2 samples in range*

Following the announcement of the DNA Commission of Inquiry, on 6 June 2022, the A/DG Shaun Drummond made a decision about the workflow relating to samples reported as '*DNA insufficient for further processing'*. This related to Priority 2 samples with a quantitation result of between 0.001ng/uL (LOD) and 0.0088ng/uL.

The A/DG's decision contemplated an option for testing that would allow a discretion for FSS Forensic DNA Analysis scientists, including in conjunction with investigating officers at QPS, to decide the merits of undertaking a concentration process for Priority 2 samples within this quantitation range, having regard to other available case information.

I appreciate that there may be grounds for the discretionary option, including a risk of the concentration process reducing residual sample quantity if it is not considered by the scientist or QPS to be beneficial. That is because reducing the sample quantity has the potential to impact future testing if requested by QPS or Defence, and could limit opportunities for results when improved processes are introduced in future. I expect this issue will be explored in detail by the DNA Commission of Inquiry.

I have reflected about options for the concentration process and for certainty pending the outcome of the DNA Commission of Inquiry, I request the workflow to revert to the concentration process for Priority 1 and Priority 2 samples stipulated in Standard Operating Procedure 17117V19 (diagram section 19.4) (**attached**). That is, the concentration process is to be undertaken automatically for <u>all</u> Priority 1 and Priority 2 samples with a quantitation result of between 0.001ng/uL (LOD) and 0.0088ng/uL.

I ask that a review of the laboratory information system be undertaken to identify any sample results within this quantitation range from 6 June 2022 to today's date inclusive. Any such samples are now to be subjected to the concentration process, if not already undertaken.

Statement confirming consultation with QPS – once feedback provided

I request that you ensure this memorandum is shared with the Forensic DNA Analysis Unit staff and ensure clarity with the approach outlined above.

Should you require further information, the Department of Health’s contact is ## on telephone 07 ##.

David Rosengren
Acting Director-General
/ /

Prepared by:	Megan Fairweather Acting Chief Legal Counsel Legal Branch 17 August 2022
Cleared by:	Matt Rigby Executive Director Office of the Director-General 5 August 2022

[redacted]

EXHIBIT 203

From: Helen Gregg <[redacted]
Sent: Friday, 19 August 2022 15:42
To: Neville.DavidH[OSC]
Cc: Foxover.StephanP[OSC]; McCarthy.DuncanJ[OSC]
Subject: RE: Further clarification previous email: Assessment of low quant DNA samples report

Good afternoon David, Duncan and Stephan,

I am now able to confirm that all Priority 1 and Priority 2 samples with a quantitation result between 0.001ng/uL (LOD) and 0.0088ng/uL, shall be concentrated down to a volume of 35uL and undergo one amplification process.
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.

A review of the laboratory information system is being undertaken to identify any sample results within this quantitation range from 6 June 2022 to today's date inclusive. Any such samples are now to be subjected to the concentration process, if not already undertaken.

Regards
Helen

Helen Gregg
A/Executive Director

Forensic and Scientific Services
Prevention Division, Queensland Health

p [redacted] **m** [redacted]
e [redacted] **w** www.health.qld.gov.au/fss

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

From: Neville.DavidH[OSC] <[redacted]
Sent: Wednesday, 17 August 2022 8:19 AM
To: Helen Gregg <[redacted]
Cc: Foxover.StephanP[OSC] <[redacted] McCarthy.DuncanJ[OSC]
<[redacted]
Subject: FW: Further clarification previous email: Assessment of low quant DNA samples report

---

Hi Helen
I am just following up on an email sent to me by Darren Pobar. I note that all samples are run through the process now without any intial micro-con of low quant ones. The Options Paper indicated that samples below a concentration of .0088ng/uL were prone to stochastic effects. Is there a risk of profiles being missed if samples below this concentration, particularly at the lower range, are run through without micro-concentration? Is there a policy/trigger in relation to the circumstances where a sample would be reworked and what this might involve, e.g. micro-concentration. Also, was there any advantage to microconing the low quat samples before they were amplified?
Regards

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

From: Pobar.DarrenJ[OSC] <[redacted]
Sent: Wednesday, 17 August 2022 07:14
To: Neville.DavidH[OSC] <[redacted]
Subject: FW: Further clarification previous email: Assessment of low quant DNA samples report

Darren Pobar | Inspector
Scientific Section
Forensic Services Group
Operations Support Command
Queensland Police Service

[redacted] **I** [redacted]
200 Roma Street Brisbane
[redacted]

INTEGRITY PROFESSIONALISM COMMUNITY RESPECT & FAIRNESS
Our values are at the core of who we are and what we do each day

From: Helen Gregg
<[redacted]
Sent: Wednesday, 20 July 2022 12:36

To: Pobar.DarrenJ[OSC] <[redacted]
Subject: RE: Further clarification previous email: Assessment of low quant DNA samples report

CAUTION: This email originated from outside of Queensland Police Service. Do not click links or open attachments unless you recognise the sender and know the content is safe.

Hi Darren,

I have reached out to my colleagues to assist me with this response:

In 2018, an Options Paper was provided to the QPS with options regarding processing. The QPS reviewed the options and approved for the implementation of the Option where samples with a quant value between 0.0001 and 0.0088ng/ul would be advised as 'DNA Insufficient for processing' and QPS officers could request testing of these samples, which would involve a concentration step prior to amplification.

A Follow-up paper was provided to the QPS last month or so ago, regarding samples that had been concentrated prior to amplification and the outcome of those samples.

Prior to the announcement of the commission of inquiry, the DG requested options for processing that did not include the 'DNA insufficient' process. Options were provided and the Premier announced that Cabinet had decided the DNA insufficient process was no longer being used, and all samples were being processed. From this, we take it that the Premier and Cabinet did not appear to choose the option that included concentration of samples within a particular range, given potential workplace health and safety issues.

Lara advised Supt McNab of the decision and process in the attached email, given the announcement by the Premier of the Cabinet's decision.

Samples are processing through DNA profiling and upon review of the profile obtained, staff will assess if concentration of the sample would be of benefit, within the context of the case. The option of concentration is available, as it has always been since it's implementation in the late 1990's.

From a Forensic DNA Analysis perspective, the most conservative option has been chosen – in that all samples are being profiled, concentration can be done once an appropriate evaluation of the resulting profile has been reviewed, and allows the work unit to gather data on the effectiveness of the concentration step when applied to samples with low quantitation values.

Regards
Helen

From: Pobar.DarrenJ[OSC] <[redacted]
Sent: Wednesday, 20 July 2022 9:51 AM
To: Helen Gregg <[redacted]
Subject: Further clarification previous email: Assessment of low quant DNA samples report

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

Good morning Helen

Further to the below query, I am seeking further clarification of the current testing process by QHFSS announced by the Minister. With the 0.0088ng/ul threshold removed, are some samples now being processed without any microconcentration step in place. Ie those between .001 and .0088 which would potentially benefit from concentration.

Regards
Darren

Darren Pobar | Acting Superintendent
Forensic Services Group
Operations Support Command
Queensland Police Service

[redacted] **I** [redacted]
200 Roma Street Brisbane
[redacted]

INTEGRITY PROFESSIONALISM COMMUNITY RESPECT & FAIRNESS

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

---

From: Pobar.DarrenJ[OSC]
Sent: Friday, 15 July 2022 12:00
To: [redacted]
Subject: Assessment of low quant DNA samples report

Good morning Helen

I am currently relieving for a short term in Superintendent Bruce Mcnab's role in Forensic Services Group.

I refer to attached report provided by Acting Executive Director Lara Keller to Supt Mcnab on 24 June 2022 regarding a review assessment of low quant DNA samples and I thank QHFSS for compiling and providing this new report. I note that the success rate in this new review of the micro-concentration process is approximately 25%. This is considerably higher than predicted in the 2018 Options Paper that recommended the removal of the process as a matter of routine. We are still considering the material provided and hope to discuss the options with QHFSS in the near future.

I understand the Health Minister announced on 30 May 2022 the .0088ng/uL processing threshold has been removed and that all samples are now processed as a matter of routine. I am seeking clarification on the current process on testing low quant value samples. If correct that all samples from priority 1 to 3 are being processed despite low quant values, the QPS has concerns how this change will impact anticipated backlogs and turn around times of results. Should this present as a risk, could you also please advise what strategies are in place to mitigate this issue.

Thank you again for providing the report and I look forward to receiving your advice on these queries.

Regards

Darren Pobar | Acting Superintendent
Forensic Services Group

Operations Support Command
Queensland Police Service

07 [redacted] I [redacted]
200 Roma Street Brisbane
[redacted]

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****
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[redacted]

EXHIBIT 204

From: Matthew Rigby <[redacted]
Sent: Friday, 19 August 2022 16:29
To: Neville.DavidH[OSC]
Cc: McCarthy.DuncanJ[OSC]; David Rosengren
Subject: RE: FSS SOP draft memo
Attachments: DG Memo - Reversion to concentration of all Priority 2 samples in range.pdf; Extract 19.4 from SOP 17117V19.pdf

Hi Dave,

Thanks for providing your feedback below through to us.

For your information, the Acting DG has approved the attached and this has been provided through to FSS this afternoon.

Thanks Matt

Queensland Government

Matt Rigby
Executive Director
Office of the Director-General
Queensland Health

M [redacted]
E [redacted]
W health.qld.gov.au
A Level 14, 33 Charlotte Street, Brisbane QLD 4000

From: Neville.DavidH[OSC] <[redacted]
Sent: Friday, 19 August 2022 9:22 AM
To: Matthew Rigby <[redacted]
Cc: McCarthy.DuncanJ[OSC] <[redacted]
Subject: FW: FSS SOP draft memo

Hi Matt

Thank you for the opportunity to comment on the proposed change to the laboratory workflow involving automatic micro-concentration of samples in the concentration range of .001-.0088ng/uL.

The QPS agreed to the removal of this process in February 2018 following a recommendation that was initiated by the DNA laboratory and presented in an Options Paper. The QPS now has some concern about the information it was provided to make this decision including the manner in which the supporting data was derived.

In November 2018 the QPS first raised concern with the Managing Scientist that the removal of the automatic micro-concentration process may have resulted in evidence being missed. At that time the QPS was given an assurance that the success of micro-concentration was very low and that 'automatic progression of samples through the Microcon process means that all available DNA extract will be consumed, so no further testing can be conducted on these samples after this step'. Based on this advice, the QPS continued with the arrangement.

Due to limitations of the QHFSS DNA laboratory, from time to time the QPS seeks the services of other providers to undertake alternative testing, particularly for low concentration and degraded samples. If the advice from the Managing Scientist is correct, the automatic concentration of all samples in the range of .001-.0088ng/uL could result in the opportunity being lost to use another service provider to obtain important probative evidence. This is a consequence that the QPS is unable to accept as a matter of routine.

The risk is that the proposed directive may result in a sample being exhausted making alternative testing impossible. The QPS does not have the expertise to assess the likelihood of the risk given such an assessment can only be made based on information that is exclusively within the domain of QHFSS. As a result, the QPS considers the decision to reimplement automatic micro-concentration an internal matter that QH must decide in the context that the customer (the QPS) desires to maximise the potential to obtain a profile from every sample, whether that be by services delivered by QHFSS or by another provider that can deliver a service QHFSS is not resourced to deliver.

Regards

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

From: Matthew Rigby <[redacted]
Sent: Wednesday, August 17, 2022 7:10 pm
To: Neville.DavidH[OSC] <[redacted]
Cc: David Rosengren <[redacted]
Subject: FSS SOP draft memo

Hi Dave,

Thanks for your time today and as discussed with the Acting DG and myself this afternoon, please find attached a draft memo that has been prepared and the associated SOP extract to provide some further clarity to our staff at FSS.

Appreciate any feedback/input that you have from a QPS perspective.

Thanks Matt

Queensland
Government

Matt Rigby
Executive Director
Office of the Director-General
Queensland Health

M [redacted]
E [redacted]
W health.qld.gov.au
A Level 14, 33 Charlotte Street, Brisbane QLD 4000

Department of Health

Queensland Government

MEMORANDUM

To: Helen Gregg, A/Executive Director, Forensic and Scientific Services

Copies to: Professor Keith McNeil, Acting Deputy Director-General, Chief Medical Officer Chief Clinical Information Officer, Prevention Division

From: Dr David Rosengren, Acting Director-General

Enquiries to: Professor Keith McNeil

07 [redacted]

Subject: *Reversion to concentration of all Priority 2 samples in range*

File Ref: C-ECTF-22/13557

Following the announcement of the DNA Commission of Inquiry, on 6 June 2022, advice was sought on the workflow relating to samples reported as ‘*DNA insufficient for further processing’*. This related to Priority 2 samples with a quantitation result of between 0.001ng/uL (LOD) and 0.0088ng/uL.

Consideration has included an option for testing that would allow a discretion for FSS Forensic DNA Analysis scientists, including in conjunction with investigating officers at QPS, to decide the merits of undertaking a concentration process for Priority 2 samples within this quantitation range, having regard to other available case information.

I have reflected about options for the concentration process and for certainty, pending the outcome of the DNA Commission of Inquiry, I request the workflow to revert to the concentration process for Priority 1 and Priority 2 samples stipulated in Standard Operating Procedure 17117V19 (diagram section 19.4 attached).

For clarity, **all Priority 1 and Priority 2 samples with a quantitation result between 0.001ng/uL (LOD) and 0.0088ng/uL, should be concentrated down to a volume of 35uL and undergo one amplification process.**

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.

I ask that a review of the laboratory information system be undertaken to identify any sample results within this quantitation range from 6 June 2022 to today’s date inclusive. Any such samples are now to be subjected to the concentration process, if not already undertaken.

Consultation has been undertaken with the QPS on this advice.

I request that you ensure this memorandum is shared with the Forensic DNA Analysis Unit staff and ensure clarity with the approach outlined above.

Should you require further information, the Department of Health’s contact is Professor Keith McNeil, Acting Deputy Director-General on telephone 07 [redacted]

Dr David Rosengren
Acting Director-General
19/08/2022

19.4 Quantification workflow

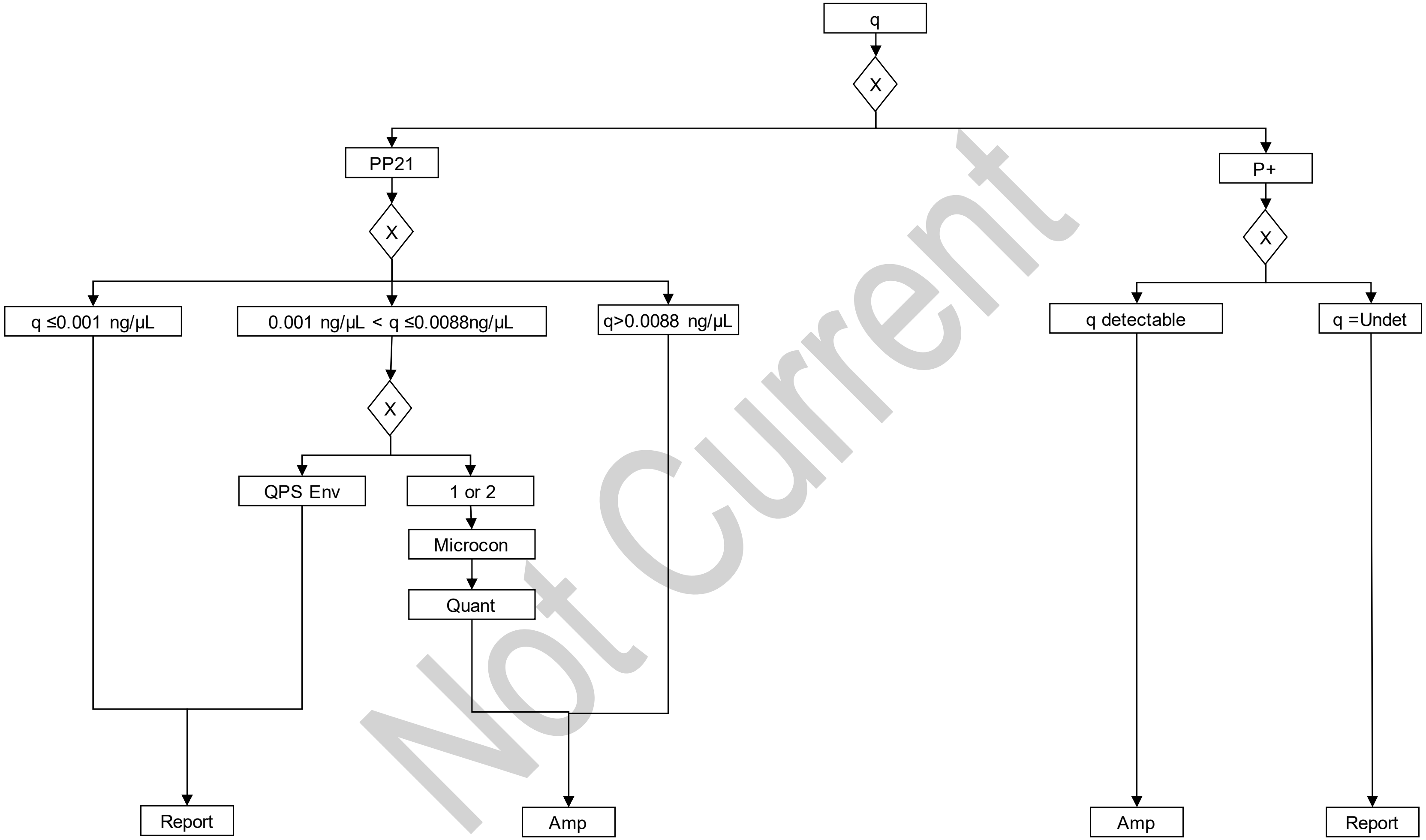

EXHIBIT 205

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[redacted]

[redacted]

[redacted]

EXHIBIT 206

From: Neville.DavidH[OSC]
Sent: Thursday, 8 September 2022 08:58
To: Matthew Rigby
Cc: McCarthy.DuncanJ[OSC]
Subject: FW: FSS SOP draft memo
Attachments: DG Memo - Reversion to concentration of all Priority 2 samples in range.pdf; Extract 19.4 from SOP 17117V19.pdf

Importance: High

Dear Matt

I refer to your email below and to the attached directive from A/Director-General Dr Rosengren to the A/Executive Director of the QHFSS that prescribes the manner in which samples in the concertation range of 0.001-0.0088ng/uL are to be processed. In particular I refer to the following instruction:

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

I have been contacted by a scientist at the QHFSS DNA laboratory who expressed concerns in relation to the attached directive.

To summarise the information provided by the scientist, I was advised that:

- The volume a sample should be concentrated to is dependent on the actual quantity of DNA present; and
- Samples with a concentration at the lower end of the 0.001-.0088ng/uL range should be concentrated to a lower volume to ensure the concentration is sufficient to develop a reliable profile; and
- For those samples at the low end of that range, adhering to the directive, results in a concentrate that is too dilute to provide a result for some samples and the process, as described, wastes half of the already diminished sample.

In short, the scientist expressed the view that by complying with the directive they were wasting evidence and potentially losing the opportunity to obtain a profile from some samples.

The scientist further stated that the scientists should make a decision on the concentration volume based on the Quant Trio data, and that a one size fits all approach is not appropriate. I was informed that other scientists hold the same view and that attempts had been made to raise these concerns with the QHFSS senior leadership team without success.

As outlined in my email response to you of 19 August 2022, the QPS desires to maximise the potential to obtain a profile from every sample, whether that be through services delivered by QHFSS, or by another provider. I mentioned my concern about the micro concentration process exhausting all samples in the context of a warning given by the Managing Scientist in 2018 when the QPS raised concern about the removal of the process. Recent information from the Managing Scientist to the effect that, after amplification, a volume of concentrate that was sufficient for further testing would remain, makes it clear that this original advice was quite incorrect.

If QHFSS is able to reliably undertake a test that has a high likelihood of yielding a useful profile, the testing should be undertaken even if it might exhaust the extract. However, if in the scientist's view the technology used at QHFSS is unlikely to yield a forensically meaningful result, consideration needs to be given to allowing the QPS the opportunity to engage the services of another laboratory that has the requisite technology. The scientist's decision should also take into account the existence and nature of any other DNA evidence already available for the particular case.

The QPS requests that attached directive be urgently reviewed in light of and having regard to the concerns raised by the scientist. Could I also be provided return advice on the result of such review, please.

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

From: Matthew Rigby <[redacted]
Sent: Friday, 19 August 2022 16:29
To: Neville.DavidH[OSC] <[redacted]
Cc: McCarthy.DuncanJ[OSC] <[redacted] David Rosengren
<[redacted]
Subject: RE: FSS SOP draft memo

Hi Dave,

Thanks for providing your feedback below through to us.

For your information, the Acting DG has approved the attached and this has been provided through to FSS this afternoon.

Thanks Matt

Queensland
Government

Matt Rigby
Executive Director
Office of the Director-General
Queensland Health

M [redacted]
E [redacted]
W health.qld.gov.au
A Level 14, 33 Charlotte Street, Brisbane QLD 4000

From: Neville.DavidH[OSC] <[redacted]
Sent: Friday, 19 August 2022 9:22 AM
To: Matthew Rigby <[redacted]
Cc: McCarthy.DuncanJ[OSC] <[redacted]
Subject: FW: FSS SOP draft memo

Hi Matt

Thank you for the opportunity to comment on the proposed change to the laboratory workflow involving automatic micro-concentration of samples in the concentration range of .001-.0088ng/uL.

The QPS agreed to the removal of this process in February 2018 following a recommendation that was initiated by the DNA laboratory and presented in an Options Paper. The QPS now has some concern about the information it was provided to make this decision including the manner in which the supporting data was derived.

In November 2018 the QPS first raised concern with the Managing Scientist that the removal of the automatic micro-concentration process may have resulted in evidence being missed. At that time the QPS was given an assurance that the success of micro-concentration was very low and that 'automatic progression of samples through the Microcon process means that all available DNA extract will be consumed, so no further testing can be conducted on these samples after this step'. Based on this advice, the QPS continued with the arrangement.

Due to limitations of the QHFSS DNA laboratory, from time to time the QPS seeks the services of other providers to undertake alternative testing, particularly for low concentration and degraded samples. If the advice from the Managing Scientist is correct, the automatic concentration of all samples in the range of .001-.0088ng/uL could result in the opportunity being lost to use another service provider to obtain important probative evidence. This is a consequence that the QPS is unable to accept as a matter of routine.

The risk is that the proposed directive may result in a sample being exhausted making alternative testing impossible. The QPS does not have the expertise to assess the likelihood of the risk given such an assessment can only be made based on information that is exclusively within the domain of QHFSS. As a result, the QPS considers the decision to reimplement automatic micro-concentration an internal matter that QH must decide in the context that the customer (the QPS) desires to maximise the potential to obtain a profile from every sample, whether that be by services delivered by QHFSS or by another provider that can deliver a service QHFSS is not resourced to deliver.

Regards

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

From: Matthew Rigby <[redacted]
Sent: Wednesday, August 17, 2022 7:10 pm
To: Neville.DavidH[OSC] <[redacted]
Cc: David Rosengren <[redacted]
Subject: FSS SOP draft memo

Hi Dave,

Thanks for your time today and as discussed with the Acting DG and myself this afternoon, please find attached a draft memo that has been prepared and the associated SOP extract to provide some further clarity to our staff at FSS.

Appreciate any feedback/input that you have from a QPS perspective.

Thanks Matt

Queensland
Government

Matt Rigby
Executive Director
Office of the Director-General
Queensland Health

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E [redacted]
W health.qld.gov.au
A Level 14, 33 Charlotte Street, Brisbane QLD 4000

Department of Health

Queensland Government

MEMORANDUM

To: Helen Gregg, A/Executive Director, Forensic and Scientific Services

Copies to: Professor Keith McNeil, Acting Deputy Director-General, Chief Medical Officer Chief Clinical Information Officer, Prevention Division

From: Dr David Rosengren, Acting Director-General

Enquiries to: Professor Keith McNeil

07 [redacted]

Subject: *Reversion to concentration of all Priority 2 samples in range*

File Ref: C-ECTF-22/13557

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Consideration has included an option for testing that would allow a discretion for FSS Forensic DNA Analysis scientists, including in conjunction with investigating officers at QPS, to decide the merits of undertaking a concentration process for Priority 2 samples within this quantitation range, having regard to other available case information.

I have reflected about options for the concentration process and for certainty, pending the outcome of the DNA Commission of Inquiry, I request the workflow to revert to the concentration process for Priority 1 and Priority 2 samples stipulated in Standard Operating Procedure 17117V19 (diagram section 19.4 attached).

For clarity, **all Priority 1 and Priority 2 samples with a quantitation result between 0.001ng/uL (LOD) and 0.0088ng/uL, should be concentrated down to a volume of 35uL and undergo one amplification process.**

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Consultation has been undertaken with the QPS on this advice.

I request that you ensure this memorandum is shared with the Forensic DNA Analysis Unit staff and ensure clarity with the approach outlined above.

Should you require further information, the Department of Health's contact is Professor Keith McNeil, Acting Deputy Director-General on telephone 07 [redacted]

Dr David Rosengren
Acting Director-General
19/08/2022

19.4 Quantification workflow