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".
- 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'.**

David Harold Neville

- 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**

- 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

David Harold Neville

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'**.

David Harold Neville

- 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.

David Harold Neville

- 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, "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." 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:

David Harold Neville

- (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.

David Harold Neville

- 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.

- 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

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

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. Traised 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 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.

**TAKEN AND DECLARED** before me at Brisbane in the State of Queensland this 14<sup>th</sup> day of September 2022

		SHUNSIONER FOR DE LARATIO
David Harold Neville	Witness	Reg.No.: IFI82 OF JUSTICE & ATTORNEY CEL





# 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.	
206.	Email from David Neville (QPS) to Matt Rigby (QH) – dated 08/09/2022

EXHIBIT 187

Notice number: 2022/ 🔊 🗸 🕉

# 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 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
Walter Sofronoff	00			

Walter Sofronoff QC Commissioner Commission of Inquiry into Forensic DNA Testing in Queensland Notice number: 2022/ Color 136 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;
  - 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.
- 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
  - 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;

- 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

<u>Mnemonic</u> SS	EXH Line Single source DNA profile	Expanded Comment The DNA profile obtained from this item/sample indicated the presence of one contributor.	Additional QPS information to be added	QPS notes 18/08/2021 To be used as an overaching line for single source results.	Analytical / Reporting teams	FSS comments New line with no barcodes needed in associated barcode field	QPS RMU Reporting Notes         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
ISS1	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	Must be received with SS, if not to come into RMU worklist for review     Z. Received with linked Unknown & ISSNCD - Auto Interface (Unless LKR previously received in case)     S. Received with linked Unknown - Auto Interface (Unless LKR previously received in case)     4. Received with Linked Intel person barcode & ISSNCD -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.					Must be received with SS & SS1 or LR1- LK8 or AC.     Must not have anything in linked field.     Received with SS and SS1 with linked unknown - auto interface     Received with SS1 with Linked person barcode - Processed by RMU (Write off line)     S. 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	Must be received with MIX     Received with linked unknown - Auto Interface (Unless LKR previously received in case)     Received with Linked Intel person barcode - Processed by RMU (Wait for LKR)     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	Received with NUP with Linked Unknown-Auto Interface     Z. Received with NUP with Linked Unknown & LKR previously received in case - Auto-update by RMU     S. Received with NLP with a Linked person barcode - Auto Update by RMU     Leceived with RLT-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	Must be received with either SS or MIX     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	Must be received with either SS or MIX     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	Must be received with MIX     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 <u>not</u> contributed to this mixed DNA profile.		Reporting	No comment	<ol> <li>Must be received with MIX</li> <li>Received with Linked evidence barcode - Process by RMU (create RMR)</li> </ol>
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	Must be received with either SS or MIX     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	Must be received with either SS or MIX     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	Must be received with either MIX     Received with Linked Unknown -     Process by RMU - auto update     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	Must be received with either MIX     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	<ol> <li>Must be received with either MIX</li> <li>Received with Linked evidence barcode - Process by RMU (create RMR)</li> </ol>

INT1	Interim result - Intel NCIDD.	A DNA contribution has been uploaded to NCIDD for intelligence		Reporting	No comment	<ol> <li>Must be received with either MIX</li> </ol>
	Rework Required.	purposes only. Final results are pending.				2. Received with Linked Unknown -
						Process by RMU - auto update
IRRFI	Intel report required for further	The results for this item/sample require further explanation which		Reporting	No comment	Processed by RMU - Intel report received
	information	will follow in an intelligence report.				via email from QHFSS.
CWBC	Consistent with being child of	The DNA profile obtained from this exhibit was consistent with		Reporting	No comment	Processed by RMU - create RMR
		being the biological child of the barcode sent with this exhibit report				
NCWBC	Not consistent with being child of	The DNA profile obtained from this exhibit is not consistent with		Reporting	No comment	Processed by RMU - create RMR
		being the biological child of the barcode sent with this exhibit				
		report.				
SC1	Suspect check - support for	The DNA profile is between 2 and 100 times more likely to have		Reporting	No comment	1. Must be received with either SS or MIX
	contribution: LR 2 to 100	occurred if the nominated suspect sent with this exhibit report has				<ol><li>Received with Linked intelligence</li></ol>
		contributed to the DNA profile, rather than has not contributed. This				barcode - Process by RMU (create RMR)
		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	This DNA profile is between 100 and 1000 times more likely to		Reporting	No comment	<ol> <li>Must be received with either SS or MIX</li> </ol>
	contribution: LR 100 to 1000	have occurred if the nominated suspect sent with this exhibit report				<ol><li>Received with Linked intelligence</li></ol>
		has contributed to the DNA profile, rather than has not contributed.				barcode - Process by RMU (create RMR)
		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	This DNA profile is between 1000 and 10 000 times more likely to		Reporting	No comment	1. Must be received with either SS or MIX
	contribution: LR 1000 to 10 000	have occurred if the nominated suspect sent with this exhibit report				2. Received with Linked intelligence
		has contributed to the DNA profile, rather than has not contributed.				barcode - Process by RMU (create RMR)
		This comparison was done for intelligence purposes only. A				
		reference evidence sample should be provided if this information is				
0.0.4	Over each also also aver a set for	required in a statement for court.		Demonstra a	N	4 Martha and site davith site an OO an MIX
504	Suspect check- support for	this DNA profile is between 10 000 and 100 000 times more likely		Reporting	No comment	Must be received with either 55 or MIX     Descived with Linked intelligence
	000	report has contributed to the DNA profile, rather than has not				2. Received with Linked Intelligence
	000	contributed. This comparison was done for intelligence purposes				baroode - 1 locess by time (create time)
		only A reference evidence sample should be provided if this				
		information is required in a statement for court				
SC5	Suspect check - support for	This DNA profile is between 100 000 and 1 million times more likely		Reporting	No comment	1. Must be received with either SS or MIX
	contribution: LR 100 000 - 1	to have occurred if the nominated suspect sent with this exhibit				2. Received with Linked intelligence
	million	report has contributed to the DNA profile, rather than has not				barcode - Process by RMU (create RMR)
		contributed. This comparison was done for intelligence purposes				
		only. A reference evidence sample should be provided if this				
000		information is required in a statement for court.				
500	Suspect check- support for	Information is required in a statement for court. This DNA profile is between 1 million and 1 billion times more likely		Reporting	No comment	1. Must be received with either SS or MIX
500	Suspect check- support for contribution: LR 1 million - 1	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		Reporting	No comment	<ol> <li>Must be received with either SS or MIX</li> <li>Received with Linked intelligence</li> </ol>
506	Suspect check- support for contribution: LR 1 million - 1 billion	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 the DNA profile, rather than has not		Reporting	No comment	Must be received with either SS or MIX     Received with Linked intelligence barcode - Process by RMU (create RMR)
506	Suspect check- support for contribution: LR 1 million - 1 billion	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 the DNA profile, rather than has not contributed. This comparison was done for intelligence purposes		Reporting	No comment	1. Must be received with either SS or MIX 2. Received with Linked intelligence barcode - Process by RMU (create RMR)
500	Suspect check- support for contribution: LR 1 million - 1 billion	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 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		Reporting	No comment	1. Must be received with either SS or MIX 2. Received with Linked intelligence barcode - Process by RMU (create RMR)
500	Suspect check- support for contribution: LR 1 million - 1 billion	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 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	Must be received with either SS or MIX     Received with Linked intelligence barcode - Process by RMU (create RMR)
SC6	Suspect check- support for contribution: LR 1 million - 1 billion Suspect check- support for	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 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. This DNA profile is between 1 billion and 100 billion times more		Reporting	No comment	Must be received with either SS or MIX     Received with Linked intelligence barcode - Process by RMU (create RMR)     Must be received with either SS or MIX
SC7	Suspect check- support for contribution: LR 1 million - 1 billion Suspect check- support for contribution:LR 1 billion- 100	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 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. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the nominated suspect sent with this		Reporting	No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence
SC7	Suspect check- support for contribution: LR 1 million - 1 billion Suspect check- support for contribution:LR 1 billion- 100 billion	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 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. 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		Reporting	No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     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 Suspect check- support for contribution:LR 1 billion- 100 billion	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 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. 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		Reporting	No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     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 million - 1 billion Suspect check- support for contribution:LR 1 billion- 100 billion	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 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. 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		Reporting	No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     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 million - 1 billion Suspect check- support for contribution:LR 1 billion- 100 billion	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 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. 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)     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 1 million - 1 billion Suspect check- support for contribution:LR 1 billion- 100 billion Suspect check - support for	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 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. 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. This DNA profile is greater than 100 billion times more likely to have		Reporting Reporting Reporting	No comment No comment No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX
SC7 SC8	Suspect check- support for contribution: LR 1 million - 1 billion Suspect check- support for contribution:LR 1 billion- 100 billion Suspect check - support for contribution: LR > 100 billion	Intornation 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 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. 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. This DNA profile is greater than 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has compared than the same than the site of the the the the theory than that this DNA profile is greater than 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has		Reporting Reporting Reporting	No comment No comment No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence     1. Must be received with either SS or MIX
SC7 SC8	Suspect check- support for contribution: LR 1 million - 1 billion Suspect check- support for contribution:LR 1 billion- 100 billion Suspect check - support for contribution: LR > 100 billion	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 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. 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. 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		Reporting Reporting Reporting	No comment No comment No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)
SC7 SC8	Suspect check- support for contribution: LR 1 million - 1 billion Suspect check- support for contribution:LR 1 billion- 100 billion Suspect check - support for contribution: LR > 100 billion	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 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. 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. 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		Reporting Reporting Reporting	No comment No comment No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)
SC7 SC8	Suspect check- support for contribution: LR 1 million - 1 billion Suspect check- support for contribution:LR 1 billion- 100 billion Suspect check - support for contribution: LR > 100 billion	Intornation 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 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. 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. 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 is ontributed 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 is on the profile is greater for court.		Reporting Reporting Reporting	No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)
SC7 SC7 SC8	Suspect check- support for contribution: LR 1 million - 1 billion Suspect check- support for contribution:LR 1 billion- 100 billion Suspect check - support for contribution: LR > 100 billion	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 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. 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. 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 Reporting Reporting	No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with UK
SC7 SC8 SC9	Suspect check- support for contribution: LR 1 million - 1 billion Suspect check- support for contribution:LR 1 billion- 100 billion Suspect check - support for contribution: LR > 100 billion Suspect check inconclusive	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 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. 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. 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. The interpretation in relation to the nominated suspect is inconclusive. As this interpretation relates only to the associated		Reporting Reporting Reporting Reporting	No comment No comment No comment No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with with Create RMR)     1. Must be received with linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with MIX     2. Received with Linked intelligence
SC8 SC9	Suspect check- support for contribution: LR 1 million - 1 billion Suspect check- support for contribution:LR 1 billion- 100 billion Suspect check - support for contribution: LR > 100 billion	Intornation 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 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. 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. 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. The interpretation in relation to the nominated suspect is inconclusive. As this interpretation relates only to the associated barcode sent with this exhibit report ocmanism. In other		Reporting Reporting Reporting Reporting	No comment No comment No comment No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with MIX     2. Received with MIX     2. Received with MIX     3. Received with MIX     4. Received with MIX
SC8 SC9	Suspect check- support for contribution: LR 1 million - 1 billion Suspect check- support for contribution:LR 1 billion- 100 billion Suspect check - support for contribution: LR > 100 billion Suspect check inconclusive	Intormation 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 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. 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. 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. 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 relates on the provident of the provident of the report.		Reporting Reporting Reporting Reporting	No comment No comment No comment No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)
SC7 SC8 SC9	Suspect check- support for contribution: LR 1 million - 1 billion Suspect check- support for contribution:LR 1 billion- 100 billion Suspect check - support for contribution: LR > 100 billion Suspect check inconclusive	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 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. 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. 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. 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 fire interpretation.		Reporting Reporting Reporting Reporting	No comment No comment No comment No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)
SC8 SC9	Suspect check- support for contribution: LR 1 million - 1 billion Suspect check- support for contribution: LR 1 billion- 100 billion Suspect check - support for contribution: LR > 100 billion Suspect check inconclusive	Intornation 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 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. 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. 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. This comparison was done for intelligence 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.		Reporting Reporting Reporting Reporting	No comment No comment No comment No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)
SC8 SC9 SC10	Suspect check- support for contribution: LR 1 million - 1 billion Suspect check- support for contribution:LR 1 billion- 100 billion Suspect check - support for contribution: LR > 100 billion Suspect check inconclusive	Intormation 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 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. 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. This DNA profile is greater than 100 billion times more likely to have courred 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. 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. The statistical interpretation provides support for the proposition		Reporting Reporting Reporting Reporting Reporting	No comment No comment No comment No comment No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with MIX     3. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with MIX     3. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with MIX
SC7 SC8 SC9 SC10	Suspect check- support for contribution: LR 1 million - 1 billion Suspect check- support for contribution:LR 1 billion- 100 billion Suspect check - support for contribution: LR > 100 billion Suspect check inconclusive	Intormation 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 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. 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. 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. 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. The statistical interpretation provides support for the proposition that the nominated suspect has not contributed to this DNA profile.		Reporting Reporting Reporting Reporting Reporting	No comment No comment No comment No comment No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)
SC7 SC8 SC9 SC10	Suspect check- support for contribution: LR 1 million - 1 billion Suspect check- support for contribution: LR 1 billion- 100 billion Suspect check - support for contribution: LR > 100 billion Suspect check inconclusive Suspect check - supports non contribution	Intormation 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 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. 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. 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. 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. 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		Reporting Reporting Reporting Reporting Reporting	No comment No comment No comment No comment No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)
SC7 SC8 SC9 SC10	Suspect check- support for contribution: LR 1 million - 1 billion Suspect check- support for contribution: LR 1 billion- 100 billion Suspect check - support for contribution: LR > 100 billion Suspect check inconclusive Suspect check - supports non contribution	Intormation 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 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. 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. 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. 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. 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. The statistical interpretation provides support for the proposition that the nominated suspect has not contributed to this DNA profile		Reporting Reporting Reporting Reporting Reporting	No comment No comment No comment No comment No comment	1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with either SS or MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     1. Must be received with MIX     2. Received with Linked intelligence barcode - Process by RMU (create RMR)     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	<ol> <li>Must be received with MIX</li> <li>Received with Linked intelligence barcode - Process by RMU (create RMR)</li> </ol>
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 proceen interpreted at this stage. QPS can submit a request to QHFSS for further work which may include the interpretation of the 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	Must be received with SS or MIX.     Received with SS or NUP with linked     unknown - Auto Interface (unless LKR     previously received in case)     Received with SS1 with a Linked     person barcode - Auto Update by RMU     Received with LR1-LR8; AC - Auto     uodate 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	<ol> <li>Must be received with MIX</li> <li>Auto updated by RMU</li> </ol>
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	This item/sample was submitted for DNA analysis. Low levels of	Please send a task to the DNA Liaison and Major		Analytical	Analytical	Auto interface
	processing	DNA were detected in this sample and it was not submitted for further DNA profiling.	Crime Unit (3211) if this sample is required to be assessed for further processing.				
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 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		Result to be reviewed by RMU
ENCMPU	ENVM- Complex mixture unsuitat	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 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	Result to be reviewed by RMU
QCFRQ	Quality control failure, refer to QF	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 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 to be reviewed by RMU

Result type	Mnemonic	Cold link line	Review by DRMU	Recommndations
Powerplex21 /	FULLCL	Full DNA profile	DNA COLD LINK - This item/sample gave a full DNA profile	New cold link line
Verifiler Plus			which matches the DNA profile obtained from Barcode Number	
			NAMES DOB **/**/**** CNI No ******** DNA Profile Number	
			LKR0000***.	
Powerplex21 /	PARTCL	Partial DNA profile	DNA COLD LINK - This item/sample gave a partial DNA profile	New cold link line
Verifiler Plus			which matches the DNA profile obtained from Barcode Number	
			AMES DOB **/**/**** CNU No. ********* DNA Brofile Number	
			LKR0000***.	
Powerplex21	MIXL	Mixed DNA profile	DNA COLD LINK - This item/sample gave a DNA profile that	New cold link line
			indicated the presence of DNA from more than one contributor.	
			Represented within the mixed DNA profile are some or all of	
			Number ******** a DNA sample obtained from SURNAME	
			GIVEN NAMES DOB **/**/**** CNI No. ******** DNA Profile	
			Number LKR00*****.	
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

# WIT.0020.0008.0026

Mnemonic	EXH line	Expanded Comment	FSS agree decommission	FR coding	QPS comments
155	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
ЗМХ	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 <u>not</u> 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	Agreed	FR code to operate for NUP
		peen selected for loading to NCIDD. This DNA profile will be searched		
		against any DNA profiles already field of NCIDD (as per the NCIDD will matching rules). Any subsequent profiles that are leaded to NCIDD will		
		The searched against this DNA profile		
MIX7	Mix - assumed contributor - Intel	For Intelligence purposes, it has been assumed that the designated	Agrood	EP code to operate for ACINIT
WIIX7		unknown has contributed to this mixed DNA profile. A reference	Agreed	rk code to operate for ACINT
		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.		
MIX8	Mix - NCIDD upload	Statistical analysis resulted in a DNA profile that was able to be loaded	Agreed	ER codeto operate for NLIP
-		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.		
MIX9	Mix - intel interp -contribution for NCIDD	The DNA profile from the designated unknown sent with this exhibit	Agreed	FR code to operate for REMINT
		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.		
MIX12	Mix - contribution consistent with unknown	Based on this assumption, a remaining DNA profile has been	Agreed	FR code to operate for CCUNK
		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.		
IVITA 13	Mix - DNA contrib < NCIDD matching stringency	Based on this assumption, a remaining DNA profile has been	Agreed	no code
		separated. This DNA profiles of unknown origin and therefore does not		
		this according DNA profiles obtained from reference samples associated to		
		In the case. This DNA contribution is below the QHF35 stilligency for		
		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 vory in this		
		instance the likelihood ratio could favour non-contribution		

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 that has been 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	This DNA profile is between 100 and 1000 times more likely to have	Agreed	No code: manual line
		occurred if the pominated suspect sent with this exhibit report has	Agreed	
	1000	contributed to this DNA profile, rather than on unknown, unrelated		
		individual/s. This comparison was done for intelligence purposes only.		
		Individual/s. This comparison was done for intelligence purposes only. A		
		reference evidence sample should be provided if this information is		
00000		Irequired in a statement for court.		
SCSC2	Suspect check - support for contribution 1000 to	This DNA profile is between 1000 and 10 000 times more likely to have	Agreed	No code: manual line
	10 000	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.		
SCSC3	Suspect check- support for contribution 10 000 to	This DNA profile is between 10 000 and 100 000 times more likely to	Agreed	No code: manual line
	100 000	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.		
SCSC4	Suspect check - support for contrib 100 000 - 1	This DNA profile is between 100 000 and 1 million times more likely to	Agreed	No code: manual line
	million	have occurred if the nominated suspect sent with this exhibit report has	, Breed	
		contributed to this DNA profile, rather than an unknown, unrelated		
		individual/s This comparison was done for intelligence purposes only A		
		reference evidence cample chould be provided if this information is		
		required in a statement for sourt		
SCSCE	Quanaat shaak, aunnant fan aantrik 4 million - 4	The DNA profile is between 4 million and 4 hillion times more likely to		
50505	Suspect check- support for contribit million - 1	This DNA profile is between T million and T billion times more likely to	Agreed	No code: manual line
	noniiion	nave 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.		
SCSC6	Suspect check- support for contrib 1 billion- 100	This DNA profile is between 1 billion and 100 billion times more likely to	Agreed	No code: manual line
	billion	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.		
SCSC7	Suspect check - support for contribution > 100	This DNA profile is greater than 100 billion times more likely to have	Agreed	No code: manual line
	billion	occurred if the nominated suspect sent with this exhibit report has	0	
		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		
SCINIMX	Suspect check inconclusive - mixed DNA profile	The statistical interpretation in relation to the nominated suspect is	Agrood	No codo: manual lino
	Cuspeer encor moonenasive - mixed Drive prome	inconclusive. As this interpretation relates only to the accessited	Agreeu	No code. manual line
		harcode cont with this exhibit report, comparison to other nominated		
		barcode sent with this exhibit report, comparison to other nonlinated		
		suspects may provide a different statistical interpretation. A reference		
		evidence sample should be provided if this information is required in a		
00010				
SUSNC	Suspect cneck - supports non contribution	i ne statistical interpretation provides support for the proposition that the	Agreed	No code: manual line
		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.		
SCANM	Suspect check Action - No Match	The nominated suspect can be excluded as a potential contributor to the	Agreed	No code: manual line
		DNA profile obtained from this item/sample.		

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).	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	1
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	1
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 DECC	MMISSION 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 will be searched against any DNA profiles already held on NCIDD (as per the 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 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 lindividual.	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 profile sobtained 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 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, 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	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	
SMACI	3 person mixea profile - conditioned on - inter	I his 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 profile 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 as usb-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	Agreed	
01111 11 10		three contributors. The statistical interpretation provides support for the	Agreed	
		proposition that the associated barcode has not contributed to this		
		mixed DNA profile.		
3MXND	3 person mixed DNA profile not deconvoluted	This item/sample gave a mixed DNA profile which indicated the	Agreed	
		presence of DNA from three contributors. This mixed DNA profile has	5	
		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.		
3MXR1	3 person mix remaining - support for contrib 100	This item/sample provided a DNA profile that indicated the presence of	Agreed	
	to 1000	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.		
3MXR2	3 person mix remaining- support for contrib 1000	This item/sample provided a DNA profile that indicated the presence of	Agreed	
	to 10000	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.		
3MXR3	3 person mix rem - support for contrib 10 000 to	This item/sample provided a DNA profile that indicated the presence of	Agreed	
	100 000	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.		
3MXR4	3 person mix rem- support for contrib 100000 to	This item/sample provided a DNA profile that indicated the presence of	Agreed	
	1 million	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.		

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 profile 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 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 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 DECO	MMISSION 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 pendir	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	no change suggested	Profiler plus result	Retain as required
		presence of DNA from at least two contributors. This mixed DNA profile could not			for old cases
		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.			
CMPULN	Complex mixed DNA profile. Unable to load to NCIDD	This item/sample gave a full or partial mixed DNA profile which indicated the	no change suggested	Profiler plus result	
		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.			
	A lasi DNA profile NCIDD, possible sub threshold posto	This item/complexes a full 0 last DNA sysfile which matches the DNA sysfile	~/~	Drafilar plus result	
DENETE	19 loci DNA profile- NCIDD- possible sub-tifiestiolo peaks	This item/sample gave a full 9 loci DNA profile which matches the DNA profile	n/a		
		processes of additional DNA was observed. This possible DNA was not process at			
		a sufficient level to be used for comparison purposes, as it was below OHESS			
		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 unloaded to NCIDD will be			
		searched against this DNA profile			
DPPTP	9 loci DNA profile - possible sub-threshold peaks	This item/sample gave a full 9 loci DNA profile which matches the DNA profile	n/a	Profiler plus result	
		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.			
FUPNPN	9 loci DNA profile. Uploaded to NCIDD	This item/sample gave a full 9 loci DNA profile which matches the DNA profile	n/a	Profiler plus result	
		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.			
		This item/sample gave a full 9 loci DNA profile which matches the DNA profile	n/a	Profiler plus result	+
	a loci DNA prome	obtained from the barcode sent with this exhibit report			
MDPIL	Minor/Remaining DNA profile - Intel profile loaded NCIDD	This item/sample gave a mixed DNA profile, of which the minor or remaining DNA	n/a	Profiler plus result	
		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.			

MIPDNA	Mixed DNA profile conditioned on – NCIDD Mixed DNA profile. Major component	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. 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	n/a n/a	Profiler plus result Profiler plus result	
MIPMIC	Mixed DNA profile. Minor Component	profile obtained from the barcode sent with this exhibit report. 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	n/a	Profiler plus result	
MIPMUN	Mixed DNA profile. Major component uploaded to NCIDD	Trom the barcode sent with this exhibit report. 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 MPCO	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. 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	n/a n/a	Profiler plus result Profiler plus result	
	Mixed wefile main companyation of fee NCIDD matching	this mixed DNA profile. This result should always be used in conjunction with "Mixed DNA profile. Remaining profile after conditioning"	-	Drofilor plus result	
MPMAIN	INIXed profile, major component insuff for NCIDD matching	In its 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).	nza	Pronier plus result	
МРМСЗ	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 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 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 dave a partial DNA profile the components of which match the	n/a	Profiler plus result
		corresponding DNA components of the DNA profile obtained from the barcode	104	
		contesponding DNA components of the DNA profile obtained from the balcode		
		sent with this exhibit report, nowever 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)		
PPIPI	Partial profile - Intel profile loaded to NCIDD	This item/sample gave a partial DNA profile which contained insufficient	n/a	Profiler plus result
		information for NCIDD matching as it was below the OHESS stringency for	104	
		reporting a match on NCIDD. This profile may also have indications of DNA at a		
		Inepoliting a match on NCIDD. This prome may also have indications of DNA at a		
		nevel 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.		
SCANM	Suspect check actioned - no match	The nominated suspect can be excluded as a potential contributor to the DNA	n/a	Profiler plus result
		profile obtained from this item/sample.		
SCII	Suspect check - insufficient information to compare	There was insufficient information in the DNA profile obtained from this	n/a	Profiler plus result
		item/sample to determine if the nominated suspect could be a potential		
		contributor.		
SCM	Suspect check - match	The DNA profile obtained from the nominated reference barcode sent with this	n/a	Profiler plus result
00111		exhibit report matches where information was obtained the DNA components of	in a	
		this full or partial DNA profile. This comparison was done for intelligence		
		This full of 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.		
SCMAJM	Suspect check - major profile match	The DNA profile obtained from the nominated reference barcode sent with this	n/a	Profiler plus result
		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.		
SCMINM	Suspect check - minor profile match	The DNA profile obtained from the nominated reference barcode sent with this	n/a	Profiler plus result
		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		
SCCE	Suspect check cannot evolude	The DNA profile obtained from the peripated reference baracde cost with this	n/o	Profiler plue recult
SUCE	Cuspect check - calliot exclude	avhibit report cannot be evaluated as a pessible contributor of DNA to this mixed	1%a	
		Exhibit report carinot be excluded as a possible contributor of DINA to this mixed		
		Diva 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.		

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	n/a	Lab clean - not	
		presence of DNA from at least two contributors. This mixed DNA profile could be		reported	
		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.			
ENMDPU	ENVM – Minor DNA profile unsuitable for comparison	This environmental sample gave a mixed DNA profile which indicated the		Lab clean - not	
		presence of DNA from at least two contributors. This mixed DNA profile could be		reported	
		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.			
ENMIDP	ENVM – Minor DNA profile	This environmental sample gave a mixed DNA profile which indicated the	n/a	Lab clean - not	
		presence of DNA from at least two contributors. This mixed DNA profile could be		reported	
		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			
		1			

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	no change suggested	Information sent via Examination	Retain for
		hanging in and out of the tube. It is unclear if this hair was		request notification by QHFSS to SOC	discussion with QPS
		part of the collected item or incorrectly transferred during		/ SCI officer	in the future
		collection. This hair/hair portion has been stored and will			
		only be analysed if a request is provided.			
ISCB	Incorrect submission of cigarette butt	This cigarette butt was received in a tube. Items provided	n/a	Information sent via Examination	Retain for
		in a tube are intended to be submitted directly for DNA		request notification by QHFSS to SOC	discussion with QPS
		processing with minimal manual intervention. This sample		/ SCI officer	in the future
		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			
		Ifilter paper.			
LDIS	Labelling discrepancy	There is a labelling discrepancy (Occurrence number or	n/a	Information sent via Examination	Retain for
		sample description) between the exhibit packaging and the		request notification by QHFSS to SOC	discussion with QPS
		AUSLAB/Forensic Register Interface records. This sample		/ SCI officer	in the future
		Ican not be processed until the labelling discrepancy is			
		Comple Management Unit for elevification in the first			
		instance, and if unable to be received will be referred to			
		the appropriate OPS officer for resolution. Please ensure			
		all labelling details are correct before submission to the			
		DNA Analysis Laboratory			
MIES	Sample required manual intervention - excess substrate	This item/sample provided in a tube required manual	n/a	Information sent via Examination	Retain for
		intervention prior to processing through QHFSS extraction		request notification by QHFSS to SOC	discussion with QPS
		methods as excess substrate was contained within the		/ SCI officer	in the future
		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.			
MIISB	Multiple items incorrectly submitted under single barcod	Multiple items, or multiple AP positive areas have been	n/a	Information sent via Examination	Retain for
		submitted under a single barcode identifier. Each item		request notification by QHESS to SOC	discussion with QPS
		requires its own unique barcode, as the barcode is used		/ SCI officer	in the future
		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			
MICOTI	Communication of the second	Treporting purposes.		Information contain Examination	Detain fan
MISSIL	Sample required manual intervention - swab stick too lo	intervention prior to proceeding through OHESS extraction	11/a	Information sent via Examination	
		methods as the sweb stick was too long and required		/ SCL officer	in the future
		Includes as the swap slick was too long and required			
		necessitated additional resources to perform manipulation			
		In the item/sample examined by OPS to ensure it was			
		appropriate for the DNA extraction process. The ideal stick			
		length should be no more than 24mm total length (swab			
		Istick plus swab head)			
			1		

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
ОНІІ	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** 

From:Hoffman.CarolynP[OSC]Sent:Wednesday, 7 September 2022 08:55To: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:								
PHQ ext:								
Email:								
DNA banner_v3_FA								

From: Justin Howes < Sent: Wednesday, July 20, 2022 11:20 am To: Hoffman.CarolynP[OSC] < Cc: Paula Brisotto < 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



Team Leader - Forensic Reporting and Intelligence Team
Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health
p
m
a 39 Kessels Road, Coopers Plains, QLD 4108

w www.health.gld.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.



Wash your hands regularly to stop the spread of germs.

From: Hoffman.CarolynP[OSC] < Sent: Wednesday, 20 July 2022 6:58 AM To: Justin Howes < 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 DNA Management Section

Police Headquarters 200 Roma Street Brisbane QLD 4000

**DNA Management Section website** 

The DNA you take from an offender today could be the *missing link* in solving a serious crime.



CONFIDENTIALITY: The information contained in this electronic mail message and any electronic files attached to it may be confidential information, and may also be the subject of legal professional privilege and/or public interest

Always check/take offender's DNA.

immunity. If you are not the intended recipient you are required to delete it. Any use, disclosure or copying of this message and any attachments is unauthorised. If you have received this electronic message in error, please inform the sender or contact <u>1300.psaict@police.qld.gov.au</u>. This footnote also confirms that this email message has been checked for the presence of computer viruses.

### 

Disclaimer: This email and any attachments may contain legally privileged or confidential information and may be protected by copyright. You must not use or disclose them other than for the purposes for which they were supplied. The privilege or confidentiality attached to this message and attachments is not waived by reason of mistaken delivery to you. If you are not the intended recipient, you must not use, disclose, retain, forward or reproduce this message or any attachments. If you receive this message in error, please notify the sender by return email or telephone and destroy and delete all copies. Unless stated otherwise, this email represents only the views of the sender and not the views of the Queensland Government.

Queensland Health carries out monitoring, scanning and blocking of emails and attachments sent from or to addresses within Queensland Health for the purposes of operating, protecting, maintaining and ensuring appropriate use of its computer network.

 From:Harris.LibbyA[ESC]Sent:Wednesday, 7 September 2022 09:30To:Neville.DavidH[OSC]Subject:FW: Review of proposed changes to EXH linesAttachments:Copy of EXH\_Proposed changes\_draft copy JAH working on\_March 2021 (003).xls

## OFFICIAL

### OFFICIAL

From: McIntyre.OliviaM[OSC] < Sent: Thursday, 1 July 2021 11:45 To: Paula Brisotto < Cc: Harris.LibbyA[OSC] <

Justin Howes < Foxover.StephanP[OSC]

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: Mobile

200 Roma Street, Brisbane



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

Manager	- EXH line	Encoded Comment	Devices by DDMU	Natas	De commendations	Formation and the statement	Maxamete	16/03/20	21 Comments	46/02/2024 Notes	Manageria	EXH Line	RMU review 01/07/2021	AURTINOM Netre DMU
155	Single source DNA profile	The DNA profile obtained from this item/sample indicated the presence of one contributor.	The DNA profile obtained from this item/sample indicated the presence of	PP21 - reported -	Recommend this is only used	Changes recommended	SS1	Single source	The DNA profile obtained from this	Needs further QPS discussion	SS1	Single source DNA	The DNA profile obtained from this	Further discussion required re moving
		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	one contributor. This profile has been designated as UNKNOWN MALE / FEMALE		when single source unknown results are being validated. Nil			DNA profile	tem/sample indicated the presence of one contributor. This profile has been designated			profile	item/sample indicated the presence of one contributor. This profile has been	away from receiving intelligence links, instead receiving all results as
		designated as an unknown. Alternatively, if a barcode is sent with this exhibit report, where			value in continuing to validate				as UNKNOWN MALE / FEMALE.				designated as UNKNOWN MALE / FEMALE	unknowns where applicable.
		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.			the 'intel' link results as these are not reported by RMU RMU									
		evaluated however a likelihood ratio can be provided if required.			waits for confirming cold link									
10000	Circle annual 20 Inci DNA ann fa 10	This issues and a considered a CAM another that indicated the assessment of one contributes it	This item formula provided a complete DNA profile that is directed the	0001 secondad	result	Nil shares are seen and at her OMU	104	Comment for	This DNA section is section then 100 billion		1.04	Connection	This DNA sector is second to these 400 billion	Connect above
TOOLOL	> 100 billion	obtained all of the DNA information potentially available. This DNA profile matched the	presence of one contributor. This DNA profile matched the corresponding	1121-Tepotes	include information that it	in charge recommended by remo	LICI	contribution: LR	times more likely to have occurred if the			contribution: LR	times more likely to have occurred if the	oupport change
		corresponding information in the DNA profile from the associated barcode sent with this	information in the DNA profile from the associated barcode sent with this		matched the person sample.			>100 billion	barcode sent with this exhibit report has			>100 billion	barcode sent with this exhibit report has	
		If the barcode sent with this exhibit report is the donor of the DNA rather than an unknown.	occurred if the barcode sent with this exhibit report is the donor of the DNA		Por discussion.				not contributed.				has not contributed.	
		unrelated individual.	rather than an unknown, unrelated individual.											
1S9L10	SS DNA profile 9 loci and above LR	This item/sample provided a DNA profile that indicated the presence of one contributor. It	This item/sample provided a DNA profile that indicated the presence of	PP21 - reported	I think it is important that we	Changes recommended	DECOMMISSION				1S9L10	SS DNA profile 9		Decommission - agree with OHFSS
	> 100 billion	consisted of at least 9 DNA loci, however it has not obtained all of the DNA information	one contributor. Where information was obtained, this DNA profile		include information that it							loci and above LR	>	
		potentially available. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the associated bacode part with this	matched the corresponding information in the DNA profile from the associated barcode sent with this report. This DNA profile is greater than		matched the person sample.							100 billion		
		exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred	100 billion times more likely to have occurred if the barcode sent with this											
		if the barcode sent with this exhibit report is the donor of the DNA rather than an unknown,	exhibit report is the donor of the DNA rather than an unknown, unrelated											
1SS9L9	SS DNA profile 9 loci and above LR	This item/sample provided a DNA profile that indicated the presence of one contributor. It	This item/sample provided a partial DNA profile that indicated the presence	PP21 - reported	I think it is important that we	Changes recommended	LR2	Support for	This DNA profile is between 1 billion and 100		LR2	Support for	This DNA profile is between 1 billion and	Support change
	billion- 100 billion	consisted of at least 9 DNA loci, however it has not obtained all of the DNA information	of one contributor. Where information was obtained, this DNA profile		include information that it			contribution: LR	billion times more likely to have occurred if the			contribution: LR 1	100 billion times more likely to have	
		corresponding information in the DNA profile from the associated barcode sent with this	associated barcode sent with this report. This DNA profile is between 1		For discussion.			billion	contributed to the DNA profile, rather than has			billori to 100 billori	report has contributed to the DNA profile.	
		exhibit report. This DNA profile is between 1 billion and 100 billion times more likely to have	billion and 100 billion times more likely to have occurred if the barcode						not contributed.				rather than has not contributed.	
		occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an	sent with this exhibit report is the donor of the DNA rather than an											
1SS9L8	SS DNA profile 9 loci and above LR	This item/sample provided a DNA profile that indicated the presence of one contributor. It	This item/sample provided a partial DNA profile that indicated the presence	PP21 - reported	I think it is important that we	Changes recommended	LR3	Support for	This DNA profile is between 1 million and 1		LR3	Support for	This DNA profile is between 1 million and 1	Support change
	million - 1 billion	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	of one contributor. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the		include information that it matched the person sample			contribution: LR	billion times more likely to have occurred if the barroute sent with this exhibit report has			contribution: LR 1	billion times more likely to have occurred if the barrode cent with this exhibit report has	
		corresponding information in the DNA profile from the associated barcode sent with this	associated barcode sent with this report. This DNA profile is between 1		For discussion.			billion	contributed to the DNA profile, rather than has				contributed to the DNA profile, rather than	
		exhibit report. This DNA profile is between 1 million and 1 billion times more likely to have	million and 1 billion times more likely to have occurred if the barcode sent						not contributed.				has not contributed.	
		unknown, unrelated individual.	unrelated individual.											
1SS9L7	SS DNA profile less than 9 loci LR >	This item/sample provided a DNA profile that indicated the presence of one contributor. It	This item/sample provided a partial DNA profile that indicated the presence	PP21 - reported	I think it is important that we	Changes recommended	DECOMMISSION				1SS9L7	SS DNA profile less	5	Decommission - agree with QHFSS
	100 billion	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	at one contributor. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the		matched the person sample.							than 9 loci LR > 10	0	
		corresponding information in the DNA profile from the associated barcode sent with this	associated barcode sent with this report. This DNA profile is greater than		For discussion.									
		exhibit report. This DNA profile is greater than 100 billion times more likely to have occurred	100 billion times more likely to have occurred if the barcode sent with this											
		unrelated individual.	individual.											
1SS9L6	SS DNA profile < 9 loci LR 1 billion -	This item/sample provided a DNA profile that indicated the presence of one contributor. It	This item/sample provided a partial DNA profile that indicated the presence	PP21 - reported	I think it is important that we	Changes recommended	DECOMMISSION				1SS9L6	SS DNA profile < 9		Decommission - agree with QHFSS
	TOU DINION	consisted or resistant 9 DNA loci and therefore has not obtained at of the DNA information potentially available. Where information was obtained, this DNA profile matched the	matched the corresponding information was obtained, this DNA profile		matched the person sample							100 billion		
		corresponding information in the DNA profile from the associated barcode sent with this	associated barcode sent with this report. This DNA profile is between 1		For discussion.									
		exhibit report. This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the bacode and with this archibit report is the doors of the DNA rather than an	billion and 100 billion times more likely to have occurred if the barcode											
		unknown, unrelated individual.	unknown, unrelated individual.											
1SS9L5	SS DNA profile < 9 loci LR 1 million -	This item/sample provided a DNA profile that indicated the presence of one contributor. It	This item/sample provided a partial DNA profile that indicated the presence	PP21 - reported	I think it is important that we	Changes recommended	DECOMMISSION				1SS9L5	SS DNA profile < 9		Decommission - agree with QHFSS
	1 billion	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	at one contributor. Where information was obtained, this DNA profile matched the corresponding information in the DNA profile from the		matched the person sample.							billion		
		corresponding information in the DNA profile from the associated barcode sent with this	associated barcode sent with this report. This DNA profile is between 1		For discussion.									
		exhibit report. This LINA 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	with this exhibit report is the donor of the DNA rather than an unknown.											
		unknown, unrelated individual.	unrelated individual.											<b>N</b> -
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.	This item/sample provided a partial DNA profile that indicated the presence of one contributor. Where information was obtained this DNA profile.	PP21 - reported	I think it is important that we include information that it	Changes recommended	LR4	Support for contribution: LB	This DNA profile is between 100 000 and 1 million times more likely to have occurred if the		LR4	Support for contribution: LB	This DNA profile is between 100 000 and 1 million times more likely to have occurred if	Support change
		potentially available. Where information was obtained, this DNA profile matched the	matched the corresponding information in the DNA profile from the		matched the person sample.			100 000 to 1	barcode sent with this exhibit report has			100 000 to 1 million	the barcode sent with this exhibit report has	
		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	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		For discussion.			million	contributed to the DNA profile, rather than has not contributed				contributed to the DNA profile, rather than bas not contributed	
		occurred if the barcode sent with this exhibit report is the donor of the DNA rather than an	with this exhibit report is the donor of the DNA rather than an unknown,										ing not controlated.	
ICCAVN	Sinde Source DNA profile - argumer	unknown, unrelated individual. This item/sample provided a DNA profile that indicated the presence of one contributor. The	unrelated individual. This item/rample provided a DNA profile that indicated the presence of	DD21 - reported		Nil change recommended by PMI	DECOMMISSION: rea AC				1CCAVN	Single Source DNA		Decommission - agree with OHESS -
IDDANN	known contributor	associated barcode matches this DNA profile. Based on information provided to the	one contributor. The associated barcode matches this DNA profile. Based	rrzi - reporteu		Nit change recommended by Kino	DECONNIGSION: SEE AC	1			IGGANN	profile - assumed		see AC
		laboratory, it has been assumed that the associated barcode is the donor of this DNA.	on information provided to the laboratory, it has been assumed that the									known contributor		
		Given alls assumption, no saassical interpretation has been performed.	statistical interpretation has been performed.											
1SSNCD	NCIDD upload single source DNA	A single source DNA profile was obtained from the item/sample. This DNA profile has been	This item/sample yielded a DNA profile that has been uploaded to NCIDD	PP21 - auto update if received with	1	Changes recommended	NUP	NCIDD Upload	This item/sample yielded a DNA profile that		NUP	NCIDD Upload	This item/sample yielded a DNA profile that	Further discussion with QHFSS. How
	profile	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.	for searching. Further advice will be provided in the event a match is received	unknown / written off if receive with evidence result					has been uploaded to NCIDD for searching. Further advice will be provided in the event a				has been uploaded to NCIDD for searching. Europerative will be provided in the event	is this going to work with mixture unknown results
		to NCIDD will be searched against this DNA profile.							match is received.				a match is received.	
MIX	Mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from at least	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		MIX	Mixed DNA	This item/sample provided a DNA profile that indicated the presence of DNA from at least		MIX	Mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from at least	t Support use of this for all mixtures
			Diversion in these we contributed.		to get the Four person mixed			prome	two contributors.				two contributors.	
284.9	Two percen mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from two	This item/sample provided a DNA profile that indicated the presence of	DD21 - reported	DNA profile line	Nil change recommended by PMI	DECOMMISSION: rea M				244	Two person mixed		Decommission - same with OUESS
L.M.A.	The person mixed brief prome	contributors.	DNA from two contributors.	(12) - Tepower	No change suggested	in change recommended by forio	DECOMINIOUNT. SEC IN	~			21101	DNA profile		becommander agree war on a co
3MX	Three person mixed DNA profile	This item/sample provided a DNA profile that indicated the presence of DNA from three	This item/sample provided a DNA profile that indicated the presence of DNA from three analyticulars	PP21 - reported	No change suggested	Nil change recommended by RMU	DECOMMISSION: see MI	x			3MX	Three person mixed	d	Decommission - agree with QHFSS
new	Mix - Support for contribution 2 to	New Result line	This DNA profile is between 2 and 100 times more likely to have occurred if	FOR DISCUSSION: Original LR	New Result	New Result	LR7	Support for	This DNA profile is between 2 and 100 times		LR7	Support for	This DNA profile is between 2 and 100 times	Support change
	100		the barcode sent with this exhibit report has contributed to this DNA	brackets as follows:				contribution: 2 to	more likely to have occurred if the barcode			contribution: 2 to	more likely to have occurred if the barcode	
			prome, namer mani has not contributed.	100-1000				100	the DNA profile, rather than has not			100	to the DNA profile, rather than has not	
				1000-10,000					contributed.				contributed.	
				10,000-100,000										
				1 million - 1 billion										
				1 billion - 100 billion										
				> 100 billon										
new	Mix - Support for contribution 100 to	New Result line	This DNA profile is between 100 and 1000 times more likely to have		New Result	New Result	LR6	Support for	This DNA profile is between 100 and 1000		LR6	Support for	This DNA profile is between 100 and 1000	Support change
	1000		DNA profile, rather than has not contributed.					to 1000	barcode sent with this exhibit report has			1000 1000	barcode sent with this exhibit report has	
									contributed to the DNA profile, rather than has				contributed to the DNA profile, rather than	
new	Mix - Support for contribution 1000 to	New Result line	This DNA profile is between 1000 and 100 000 times more likely to have		New Result	New Result	LR5	Support for	This DNA profile is between 1000 and 100 000		LR5	Support for	This DNA profile is between 1009 and 100	Support change
	100,000		occurred if the barcode sent with this exhibit report has contributed to this					contribution:	times more likely to have occurred if the			contribution: 1000	000 times more likely to have occurred if the	
			UNA protile, rather than has not contributed.					1000 to 100 000	parcoge sent with this exhibit report has contributed to the DNA profile, rather than has			10 100 000	parcode sent with this exhibit report has contributed to the DNA profile, rather than	
									not contributed.				has not contributed.	
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	This DNA profile is greater than 100 billion times more likely to have occurred if the barrode sent with this exhibit report has contributed to this	PP21 - reported		NII change recommended by RMU	see LR1				MIX3	Mix - support for contrib > 100 billion		Decommission - agree with QHFSS - see LB1
		contributed.	DNA profile, rather than has not contributed.									100 200		
MIX4	Mix - inconclusive	The statistical interpretation in relation to the associated barcode is inconclusive. As this interpretation relates only to the associated barcode set with this exhibit event.	The statistical interpretation in relation to the associated barcode is	PP21 - reported		Nil change recommended by RMU	LR8	LR inconclusive	The statistical interpretation in relation to the		LRŚ	LR inconclusive	The statistical interpretation in relation to the	Further discussion with QHFSS re EXH
		comparison to other reference samples may provide a different statistical interpretation.	sent with this exhibit report, comparison to other reference samples may						interpretation relates only to the associated				interpretation relates only to the associated	www-wygeson(moniciosive)
			provide a different statistical interpretation.						barcode sent with this exhibit report,				barcode sent with this exhibit report,	
									provide a different statistical interpretation.				provide a different statistical interpretation.	
				0001										
MIX5	Mix - supports non contribution	The statistical interpretation provides support for the proposition that the associated barcode has not contributed to this mixed DNA omfile	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 becode		LR9	Supports non contribution	The statistical interpretation provides support for the proposition that the	Support change
									has not contributed to this mixed DNA profile.				associated barcode has not contributed to	
new	Mix - Assumed contributor	Based on information provided to the laboratory it has been assumed that the according	Based on information provided to the laboratory, it has been assumed that	PP21 - reported		Nil change recommended by RMU	AC	Assumed	Based on information provided to the		AC	Assumed	this mixed DNA profile. Based on information provided to the	Support change
		barcode has contributed to this DNA profile. Given the assumption for this person, no	the associated barcode has contributed to this DNA profile. Given the					Contributor	laboratory, it has been assumed that the			Contributor	laboratory, it has been assumed that the	
		statistical interpretation has been performed.	assumption for this person, no statistical interpretation has been						associated barcode has contributed to this				associated barcode has contributed to this	
			pursuines.						person, no statistical interpretation has been				person, no statistical interpretation has been	
10000	NCIDD unland annual	The second section developed by the second start becaute has by	The second end in the described by the second state is	ODD1 this secult first is to 1		Nil shares an end of her DMI	OF COMBERSION		performed.		10010	NCIDDuralant	performed.	Presented Income forther of
MILK10	contribution	loading to NCIDD. This DNA profile will be searched against any DNA profiles already held	selected for loading to NCIDD. This DNA profile will be searched against	and not reported to QPRIME		the crashye recommended by KMU	Course NUMBER					assumed		<ul> <li>we will need to ensure QHFSS are</li> </ul>
		on NCIDD (as per the NCIDD matching rules). Any subsequent profiles that are loaded to	any DNA profiles already held on NCIDD (as per the NCIDD matching									contribution		still using the linked barcode of the
		NCIDD will be searched against this DNA profile.	rules). Any subsequent profiles that are loaded to NCIDD will be searched against this DNA profile.											assumed known contributor on mixtures so we known who the MCIDD
			- Proventing and Proventing											upload relates to

MDC7	Mix - assumed contributor - I	Intel For Endigence purposes, Trais been assumed hat the designated unknown has the induced of the intermediation is registered on a datement for control of the analysis that induced and the intermediation is registered for a datement for control of the assumption longer holds, then any references sample will be attitutionally evaluated against the measure without a contribution being assumed and the result reported as a likelihood ratio.	For Intelligence purposes, if has been assumed that the dissipated transmission of the state of the state of the state of the state analyse should be provided for this individual of the information is regarded in a statement for court. If this assumption no longer holds, then any determines ample the statestacky evaluated against the instance without a contribution being assumed and the result reported as a likelihood rate.	PP21 - reported	Further discussion, appears this result has not been received	Nil change recommended by RMU	ACINT	Assumed contributor - lintel	For Intelligence purposes, it has been assumed that the designated unknown has contributed to this DNA profile. A reference widence sample should be provided for this evidence that any example and the relationship of the sample should be relationed 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 wirkness sample should be provided for this evidence sample should be provided for this statement for court. If this assumption no longer holds, hen 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
MIXB	Mix - NCIDD upload	Biolistical analysis resulted in a DMA profile fract use all the bio bioder 56 NECOD. The contribute to the inner DMA profile fract uses all the bioder 56 NECOD. The contribute to the inner DMA profile all the sectored against and DMA profile the are isolated in DECOD with a sectored against and DMA profile all the sectored against and DMA profile the are isolated in DECOD with a sectored against and DMA profile all the sectored against and DMA profile takes all the DMA profile and DMA profile all the sectored against and DMA profile, with the samples subsequently increased will be compared with the order mease DMA profile, with the starting of the subsequently concerning and in a DMA profile, with the starting of the subsequently increased and and the sectore mease DMA profile, with the starting of the subsequently concerning will also any decoding of the subsequently and the sectore mease DMA profile, with the starting of the subsequently increased and any of the mease DMA profile, with the starting of the subsequently and the subsequent and the mease DMA profile.	Statistical analysis smulled in a DMA profile that was also be taken which is not be associated on the DMA profile that was also be taken which is not it as possible contribute the time mixed DNA profile. The DNA profile will be searched against any DNA profiles already hold on NDDD age in the NEGDO strateging using All your profiles already hold on NDDD by and that this process has been performed for intelligence purposes why, and that any reference samples absolution to intelligence purposes hashingtone calls. The DNA profile has all be hashingtone calls. Depending on the nature of the mixed DNA profile, the strateging of the support to contribution will way.	PP21 - reported		Ni change recommended by RMU	DECOMMISSION see N	9			MIX8	Mix - NCIDD uploar	d	Further discussion with OHPSS 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 II is next to single source line not the NCIDD line
MIX9	Mix - Intel Interp -contribution	Ver The DNA profile from the designated unknown serve with this exhibit report could be a the profile of the designation of	The DNA parolle from the designated unincome sent with this activity regre- tory operations of the sentence sentences across the transformation reactivity of the sentence of	PP21 - reported		Nil change recommended by RMU	REMINT	Contribution for NCIDD - Intel purposes	The DNA profile from the designated unknown ent 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, with the strength of the support for contribution will pary.		REMINT	Contribution for NCIDD - Intel purposes	The DNA profile from the designated unknown sent with this achibit 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 netligence purposes only, and that any reference samples subsequently necessed Will be compared against the entire mixed DNA profile, with the result reported as a Method ratio. Depending on the nature of the mixed DNA profile, the strength of the apport for contribution will vary.	Support change
MIX12	2 Mix - contribution consistent unknown	Will Bland on this assumption, a minimizing OMA potelle has been separated. This is exceeded that are also assumption, a minimizing OMA potelle has been separated. This is exceeded that are with this address ranks are also than and been performed at the time. Any reference analysis addressampting revealed by the addressamption of a universam as a likelihood ratio. Depending on the nature of the minimizing of a universam as a likelihood ratio. Depending on the nature of the minimizing of a universam as a likelihood ratio. Depending on the nature of the minimizing of the likelihood ratio will vary in this instance the likelihood ratio could lever run-contribution.	Effect of the security/law, a remaining DNA profile has been sequence within the case and solution to the second second second second within the case and solution to have other with the exhibit negret. It is important to note that this information is provided for initializance purposes by and a statistical evaluation is and other performed at the time. Any without component will be compared against the entire initial for the profile, with the rest increded as a liability of all other and the time of the profile, with the rest increded as a liability of all other and the time of the instance the likelihood ratio could feature non-contribution.	PP21 - reported	Is this currently only used for PT cases? This result has only been received once (18/12/2020) do we need this line?	Ni change recommended by FMU	COUNK	Remaining contribution consistent with unknown	Based on the assumption, a freemaning UMA with the unknown designation (previously dentified within this case and loaded to VCICD) serve the lise and/bit speart. It is provided for intelligence purposes only and a statistical evaluation has not been participant autoequery proceeds for the destification of autoequery proceed for the destification of application and the entities mixed DNA profile, with the autoequery proceed for the destification of application of the entities mixed DNA profile, with the entities mixed DNA profile, the hashed cat and could be are not encombuting.	is all the wording required? It could end before "it is important?	CCUNK	Remaining contribution consistent with unknown	Based on the assumption, a remaining DVA provides that been benefacial. This is upper the second of the second of the second (previcuous) sterified within this case and based to INCIDD) sent with this exhibit report.	Suppot change - removed wording from it is important*
MIX13	3 Mix - DNA contrib < NCIDD : stringency	matching Based on this assumption, a semanting DNA pottle matching based on this assumption. The DNA pottle of unknown organ and therefore does a rankin any DNA pottle additional from reference recording a match on NoIDD and has beneficien and the semantic processing matching and the NoIDD and has beneficien and the semantic processing readers as any semantic and NoIDD and has beneficien and the semantic processing matching in the next the semantic processing and the semantic processing matching and the next the semantic processing and the semantic processing matching and the semantic processing of the support to combinition will way, in the instance of the matching of the support of combinition will way, in the instance the file-theory and file-to-ordination.	Based on the assumption, a remaining DNA profile has been separated into IDNA profiles and unchanon origin and enveloped dear and much any trime DNA contribution in believe the CHFMS attragency by transition This DNA contribution in believe the CHFMS attragency by transition and analtari on NODD and the therefore not beaded to NCDD. If reference evidence samples are submitted, if will be possible to compare any with the DNA contribution, the result of which will be properties as a through of the subport to contribution will way. In bits relations the littlehead ratio could fease runs contribution.	PP21 - reported		Nil change recommended by RMU	QPS will consider whethe	er there is ongoing	need for this		MIX13	Mix - DNA contrib < NCIDD matching stringency	¢	Decommission
MIX14	4 Mix - DNA contrib unsuitable NCIDD searching	for Based on this assumption, a remaining DMA policit has been separated. This DMA policies and the interfere smallest be to is based to INCOUT, if BUDA contribution, the results of which will be reported as a liketihood ratio. Depending on the nature of the mixed DMA policy the strength of the support for contribution, will vary, is the instance the liketihood ratio could favour non-contribution.	Based on this assumption, a remaining DNA profile has been separated. This DNA profile is unsuitable for searching on NCIOD, and is therefore unable to be loaded to NCIDD. If reference evidence samples are subwritted, it will be possible to concept 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 stength of the support for contribution will vary. In this instance the likelihood ratio could favour nen- contribution.	PP21 - reported		Nil change recommended by RMU	QPS will consider whethe	er there is ongoing	need for this		MIX14	Mix - DNA contrib unsuitable for NCIDD searching		Decommission
EVDE	XC Single evidence sample exc	used This item/sample gave a mixed DNA profile that indicated the presence of DNA from two o three contributors. The statistical interpretation shows that the associated barcode sent wit this sublikit 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 repor 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
INTER	15 Interim result- maxed profile - NCIDD. Rework Regd	Heff This is not a final result, sengels are currently undergoing results. Reservit, can mean that part of the process to obtain a LVM public teri repeated or addictional lenging b imports the heat public senses to obtain a LVM public teri repeated or addictional lenging b imports the process of the longing of the process of the lenging of the longing of the process or DMA from it establic controllutions. A matter plan lase mean deal lenging term more DVA profiles within the immod DVA profile in order to lase 0 kDDD for intelligence purposes only intelligence and the lenging of the lenging of the lenging of the lenging with the lenging of the lenging of the lenging of the lenging of the lenging with the lenging of the lenging of the lenging of the lenging of the longing of the NDDD (with heat and line) and set lenging of the longing of the lenging of the enging of the NDDD mathing releasing releasing and the DVA popelle in order to enging on the longing of the lenging of the lenging of the lenging of the lenging of the NDDD (with heat and lenging releasing and the longing of the lenging of the lenging of the lenging of the enging of the lenging of the enging of the lenging of the enging of the lenging of the lengi	This is not a final result, samples are currently undergoing revolv. Hench can make that part of the process to coldina JDM profile a Meenon contrast and the process to coldina JDM profile induced the presence of DMA from all least two contributors. An attempt has been the presence of DMA from all least two contributors. An attempt has been the presence of DMA from all least two contributors. An attempt has been added to any other and the presence of the second the presence of DMA from all least two contributors. An attempt has been contrast to separate many one of micro CMA profiles which this max DDM. DMA profiles has been leaded to NACIDD and further interpretations are conjunct. The DMA profile will be searched contrasting number, Any babequerget profiles that equipables to ALCDO (which Austandary line assess) which are supported by CDC (which Austandary line and the presence of the second babe explanates by statement in order to carby interpretations assumptions. Frant caubias are profiles. At the second babe presentable by statement in order to carby interpretation assumptions. Frant caubias are profiles.	PP21 - reported (used for P1 cases	5)	Nil change recommended by (RMU	INT1	Interim result - Intel NCIDD. Rework Required.	A DNA contribution has been uploaded to NGID for trielingence purposes only. Final results are pending.	new expanded comment.	INT1	Interim result - Intel NCIDD. Rework Required.	A DNA contribution has been uploaded to MCIDD for initiatione purposes only. Final results are pending.	Support change
INTSS	SR Interim Result- incomplete s source: Rework reqd	Ingle 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 revork. Rework can mean that part of the process to obtain a DNA profile is repeated or additional testing t improve the DNA profile is being undertaken. Final results are pending.	The interim result obtained from this sampleittem was an incomplete single source DNA profile. This is not a final result and the sampleits are currently o 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	5)	Nil change recommended by RMU	DECOMMISSION: see IF	RSUR			INTSSR	Interim Result- incomplete single source. Rework reqd		Decommission
IRRFI	Intel report required for furth information	er 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	IRREI	Intel report required for further information	d The results for this item/sample require further explanation which will follow in an intelligence report.	QPS agree
CWBC	C Consistent with being child o	If 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 the obtaint is exhibit to be a set of the obtaint	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
EXPE	mother Excluded as biological father	The UNA profile obtained from this exhibit report. The DNA profile obtained from the barroote sent with this exhibit report is exhibit report is 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				EXRE	being biological mother Excluded as		Decommission
NCM	RC Not consistent with being ch	a biological father of the DNA profile obtained from the exhibit report is excluded as being in the exhibit of the DNA profile obtained from the exhibit was not consistent with heine the historical child	excluded as being a biological father of the DNA profile obtained from the exhibit. The DNA profile obtained from this exhibit is not consistent with being the	PP21 reported		Changes recommended	NCWBC	Not consistent	The DNA profile obtained from this exhibit is	no change	NOWBO	biological father	The DNA profile obtained from this whihit is	OPS agree
		of the barcode sent with this exhibit report.	biological child of the barcode sent with this exhibit report.					with being child of	not consistent with being the biological child of the barcode sent with this exhibit report.			being child of	not consistent with being the biological child of the barcode sent with this exhibit report.	a Ngruu
NCWE	BM Not consistent with being bio mother	In 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
NEXB	IN IN IN INVERSE IN INVERSE IN INVERSE IN INVERSE IN INVERSE INTO INVERSE INVERSE INVERSE INVERSE INVERSE INVERSE INVERSE INVE	I ne unva prome 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.	I ne LNA prome 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	December of the second s	Changes recommended	DECOMMISSION	C	The DNA staffs is het		NEXBF	Not excluded as biological father	The DMA surfices by	Decommission
SCLÖ	<ul> <li>Suspect check - low support contribution</li> <li>Suspect check - support for contribution 2 to 100</li> </ul>	tor the use process provides to support the propolation that the intrinsitied august is a peoplet is not only to this in the market process to the propolation that the intrinsitied august is a peoplet should be provided if this element or support of the statement or support of the statement or court.	The survey prome is between 2 and 50 times more 100 more likely to have concred if the nonexide suppert care with the additr report has individually. This comparison was done for intelligence purposes only. A required in a statement for court.	HY-21 - reported	Necontimend change to EXH line as well as expanded wording.	unanges recommended	501	suspect check - support for contribution: LR 2 to 100	The unve profile is between 2 and 100 times more likely to ave occurred if the nominated suspect sent with this exhibit report has contributed to the DNA profile, rainer 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		801	support check - support for contribution: LR 2 to 100	Ine unw protie is between 2 and 100 times more likely to have occurred if the nominated suspect sent with this exhibit report has contributed to the DAR 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.	eupport change

	Comment alongly assessed for	This DAIA surface is between 400 and 4000 times more likely to be a second if the	This CALL surfly is habitan 400 and 4000 times may likely to have	0004 second d	Nil shares a second ad by OMU	200	Comment should	This DNA sanfils is habered 100 and 1000		800	Property all all and	This DNA seefle is between 100 and 1000	0.00
30301	contribution 100 to 1000	nominated suspect sent with this exhibit report has contributed to this DNA profile rather	occurred if the nominated suspect sent with this exhibit report has	PP21 - Teponeu	Nil change recommended by Rwo	302	support for	times more likely to have occurred if the		302	support for	times more likely to have occurred if the	urs agree
		than an unknown, unrelated individual/s. This comparison was done for intelligence	contributed to this DNA profile, rather than an unknown, unrelated				contribution: LR	nominated suspect sent with this exhibit report			contribution: LR	nominated suspect sent with this exhibit	
		purposes only. A reference evidence sample should be provided if this information is	individual/s. This comparison was done for intelligence purposes only. A				100 to 1000	has contributed to the DNA profile, rather than			100 to 1000	report has contributed to the DNA profile,	
		required in a statement for court.	reference evidence sample should be provided if this information is					has not contributed. This comparison was				rather than has not contributed. This	
			required in a statement for courc.					reference evidence sample should be provided				purposes only. A reference evidence sample	
								if this information is required in a statement for				should be provided if this information is	
								court.				required in a statement for court.	
80802	Surpect check - support for	This DNA profile is between 1000 and 10,000 times more likely to have occurred if the	This DNA profile is between 1000 and 10 000 times more likely to have	PP21 - reported	Nil change recommended by PMU	903	Surnect check -	This DNA profile is between 1000 and 10 000		603	Surpert check -	This DNA profile is between 1000 and 10	OPS agree
30302	contribution 1000 to 10 000	nominated suspect sent with this exhibit report has contributed to this DNA profile, rather	occurred if the nominated suspect sent with this exhibit report has	PP21 - reported	Nil change recommended by Raro	363	support for	times more likely to have occurred if the		363	support for	000 times more likely to have occurred if the	uro agree
		than an unknown, unrelated individual/s. This comparison was done for intelligence	contributed to this DNA profile, rather than an unknown, unrelated				contribution: LR	nominated suspect sent with this exhibit report			contribution: LR	nominated suspect sent with this exhibit	
		purposes only. A reference evidence sample should be provided if this information is	individual/s. This comparison was done for intelligence purposes only. A				1000 to 10 000	has contributed to the DNA profile, rather than			1000 to 10 000	report has contributed to the DNA profile,	
		required in a statement for court.	reference evidence sample should be provided if this information is					has not contributed. This comparison was				rather than has not contributed. This	
			required in a statement for court.					done for intelligence purposes only. A				comparison was done for intelligence	
								if this information is required in a statement for				should be provided if this information is	
								court.				required in a statement for court.	
SCSC3	Suspect check- support for	This DNA profile is between 10 000 and 100 000 times more likely to have occurred if the	This DNA profile is between 10 000 and 100 000 times more likely to have	PP21 - reported	Nil change recommended by RMU	SC4	Suspect check-	This DNA profile is between 10 000 and 100		SC4	Suspect check-	This DNA profile is between 10 000 and 100	QPS agree
	contribution 10 000 to 100 000	nominated suspect sent with this exhibit report has contributed to this DNA profile, rather	occurred if the nominated suspect sent with this exhibit report has				support for	000 times more likely to have occurred if the			support for	000 times more likely to have occurred if the	
		numoses only. A reference evidence sample should be provided if this information is	individual/s. This comparison was done for intelligence purposes only. A				10 000 to 100	has contributed to the DNA profile rather than			000 to 100 000	report has contributed to the DNA profile	
		required in a statement for court.	reference evidence sample should be provided if this information is				000	has not contributed. This comparison was			00010100000	rather than has not contributed. This	
			required in a statement for court.					done for intelligence purposes only. A				comparison was done for intelligence	
								reference evidence sample should be provided				purposes only. A reference evidence sample	
								if this information is required in a statement for				should be provided if this information is	
								court.				required in a statement for court.	
SCSC4	Suspect check - support for contrib	This DNA profile is between 100 000 and 1 million times more likely to have occurred if the	This DNA profile is between 100 000 and 1 million times more likely to	PP21 - reported	Nil change recommended by RMU	SC5	Suspect check -	This DNA profile is between 100 000 and 1		SC5	Suspect check -	This DNA profile is between 100 000 and 1	QPS agree
	100 000 - 1 million	nominated suspect sent with this exhibit report has contributed to this DNA profile, rather	have occurred if the nominated suspect sent with this exhibit report has				support for	million times more likely to have occurred if the			support for	million times more likely to have occurred if	-
		than an unknown, unrelated individual/s. This comparison was done for intelligence	contributed to this DNA profile, rather than an unknown, unrelated				contribution: LR	nominated suspect sent with this exhibit report			contribution: LR	the nominated suspect sent with this exhibit	
		purposes only. A reference evidence sample should be provided if this information is	individual/s. This comparison was done for intelligence purposes only. A				100 000 - 1	has contributed to the DNA profile, rather than			100 000 - 1 million	report has contributed to the DNA profile,	
		required in a statement for court.	required in a statement for court				million	done for intelligence purposes only. A				comparison was done for intelligence	
								reference evidence sample should be provided				purposes only. A reference evidence sample	
								if this information is required in a statement for				should be provided if this information is	
								court.				required in a statement for court.	
80908	Surnect check, support for earthin 4	This DNA profile is between 1 million and 1 billion times more likely to have account if the	This DNA profile is between 1 million and 1 billion times more films to have	PP21 - reported	Nil change recommended by PMU	908	Surpect check	This DNA profile is between 1 million and 1		sca	Surpert chech	This DNA profile is between 1 million and 1	OPS agree
acaca	million - 1 billion	nominated suspect sent with this exhibit report has contributed to this DNA nonfile rather	occurred if the nominated suspect sent with this exhibit report has	seponed	in change recommended by Rato		support for	billion times more likely to have occurred if the		000	support for	billion times more likely to have occurred if	a. o ag. de
		than an unknown, unrelated individual/s. This comparison was done for intelligence	contributed to this DNA profile, rather than an unknown, unrelated				contribution: LR	nominated suspect sent with this exhibit report			contribution: LR 1	the nominated suspect sent with this exhibit	
		purposes only. A reference evidence sample should be provided if this information is	individual/s. This comparison was done for intelligence purposes only. A				1 million - 1	has contributed to the DNA profile, rather than			million - 1 billion	report has contributed to the DNA profile,	
		required in a statement for court.	reference evidence sample should be provided if this information is				billion	has not contributed. This comparison was				rather than has not contributed. This	
			required in a statement for court.					done for intelligence purposes only. A				comparison was done for intelligence	
								reference evidence sample should be provided				purposes only. A reterence evidence sample	
								court.				required in a statement for court.	
SCSC6	Suspect check- support for contrib 1	This DNA profile is between 1 billion and 100 billion times more likely to have occurred if the	This DNA profile is between 1 billion and 100 billion times more likely to	PP21 - reported	Nil change recommended by RMU	SC7	Suspect check-	This DNA profile is between 1 billion and 100		SC7	Suspect check-	This DNA profile is between 1 billion and	QPS agree
	billion- 100 billion	nominated suspect sent with this exhibit report has contributed to this DNA profile, rather	have occurred if the nominated suspect sent with this exhibit report has				support for	billion times more likely to have occurred if the			support for	100 billion times more likely to have	
		than an unknown, unrelated individual's. This comparison was done for intelligence	considuated to this DNA profile, rather than an unknown, unrelated				contribution:LR 1	nominated suspect sent with this exhibit report			contribution:LR 1	occurred if the nominated suspect sent with	
		purposes only. A reference evidence sample should be provided if this information is	individualis. This comparison was done for intelligence purposes only. A				billion- 100	has contributed to the DNA profile, rather than			billion- 100 billion	this exhibit report has contributed to the	
		required in a statement for court.	reference evidence sample should be provided if this mormation is				Dimon	done for intelligence numores only. A				This comparison was done for intelligence	
			required in a statement of court.					reference evidence sample should be provided				purposes only. A reference evidence sample	
								if this information is required in a statement for				should be provided if this information is	
								court.				required in a statement for court.	
00007	a					0.04		6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		0.00		D DI	0.00
susu/	contribution > 100 billion	I his LINA profile is greater than 100 billion times more likery to have occurred if the nominated suspect sent with this exhibit report has contributed to this DNA profile, rather	I his DNA profile is greater than 100 billion times more likely to have occurred if the nominated suspect sent with this exhibit report has	PP21 - reported	NII change recommended by RMU	SUS	support for	times more likely to have occurred if the		SUB	Suspect cneck - support for	times more likely to have occurred if the	uPS agree
	contribution > roo billion	than an unknown unrelated individual/s. This comparison was done for intelligence	contributed to this DNA profile rather than an unknown unrelated				contribution: LR	nominated suspect sent with this exhibit report			contribution: LB >	pominated suspect sent with this exhibit	
		purposes only. A reference evidence sample should be provided if this information is	individual/s. This comparison was done for intelligence purposes only. A				> 100 billion	has contributed to the DNA profile, rather than			100 billion	report has contributed to the DNA profile.	
		required in a statement for court.	reference evidence sample should be provided if this information is					has not contributed. This comparison was				rather than has not contributed. This	
			required in a statement for court.					done for intelligence purposes only. A				comparison was done for intelligence	
								reference evidence sample should be provided				purposes only. A reference evidence sample	
								if this information is required in a statement for				should be provided if this information is	
								COUL.				required in a suscement for court.	
SCINMX	Suspect check inconclusive - mixed	The statistical interpretation in relation to the nominated suspect is inconclusive. As this	The interpretation in relation to the nominated suspect is inconclusive. As	PP21 - reported	Nil change recommended by RMU	SC9	Suspect check	The interpretation in relation to the nominated		SC9	Suspect check	The interpretation in relation to the	Support change
	DNA profile	interpretation relates only to the associated barcode sent with this exhibit report,	this interpretation relates only to the associated barcode sent with this				inconclusive	suspect is inconclusive. As this interpretation			inconclusive	nominated suspect is inconclusive. As this	
		comparison to other nominated suspects may provide a different statistical interpretation. A	exhibit report, comparison to other nominated suspects may provide a					relates only to the associated barcode sent				interpretation relates only to the associated	
		reference evidence sample should be provided if this information is required in a statement	different interpretation. A reference evidence sample should be provided if					with this exhibit report, comparison to other				barcode sent with this exhibit report,	
		fan Caust	this information is considered in a statement for Count					THE REPORT OF A DESCRIPTION OF A DESCRIPTION OF A DESCRIPTION				semical and the other semicated succession	
		for Court.	this information is required in a statement for Court.					internetation A reference mideoce cample				comparison to other nominated suspects	
		for Court.	this information is required in a statement for Court.					interpretation. A reference evidence sample should be provided if this information is				comparison to other nominated suspects may provide a different interpretation. A reference evidence sample should be	
		for Court.	this information is required in a statement for Court.					interpretation. A reference evidence sample should be provided if this information is required in a statement for Court.				comparison to other nominated suspects may provide a different interpretation. A reference evidence sample should be provided if this information is required in a	
		for Court.	this information is required in a statement for Court.				-	interpretation. A reference evidence sample should be provided if this information is required in a statement for Court.				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.	
SCSNC	Suspect check - supports non	for Court.	this information is required in a statement for Court.	PP21 - reported	 Nil change recommended by RMU	SC10	Suspect check -	Interpretation. A reference evidence sample should be provided if this information is required in a statement for Court. The statistical interpretation provides support	slight change to suggested	SC10	Suspect check -	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. The statistical interpretation provides uncertainty in representation by the the	Support change
SCSNC	Suspect check - supports non contribution	for Court. The statistical interpretation provides support for the proposition that the nominated support as not contributed to this mixed DNA profile. This comparison was done for intelligence	this information is required in a statement for Court. The statistical interpretation provides support for the proposition that the nominated suppet has not contributed to his mixed DNA profile. This commarison was not not initiationen purposes out, A reference evidence	PP21 - reported	 Nil change recommended by RMU	SC10	Suspect check - supports non	Interpretation. 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 DNA profile. This	slight change to suggested wording. Removed 'mixed'.	SC10	Suspect check - supports non	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. The statistical interpretation provides support for the proposition that the nominated sursect has not contributed to	Support change
SCSNC	Suspect check - supports non contribution	for Court.  The statistical integretation provides support for the proposition that the nominated support as not contributed to the meed DNA profile. This comparison was down for intelligence purposes only. A reference evidence sample should be provided if this information is regurated in a statement for court.	this information is required in a statement for Court. The statistical interpretation provides support for the proposition that the normatide auspect has not contributed to this make DNA profile. This comparison was done for intelligence purposes only. A reference evidence ample should be provided if this information is required in a statement for	PP21 - reported	Nil change recommended by RMU	SC10	Suspect check - supports non contribution	Interpretation. 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 DNA profile. This comparison was done for intelligence pursoes	slight change to suggested wording. Removed 'mixed'.	SC10	Suspect check - supports non contribution	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. The statistical interpretation provides support for the proposition that the nominated suspect has not contributed to this DNA profile. This comparison was done	Support change
SCSNC	Suspect check - supports non contribution	for Court the statistical interpretation provides support for the proposition that the nominuted support the statistical interpretation provides applied to the companion was done for intelligence properties of a Adventity of the output of the information is equivalent in a adventity for court.	this information is required in a statement for Court. The statistical interpretation provides support for the proposition that the nominated support has not contributed to this mixed DMA profile. This mample should be provided if this information is required in a statement for court.	PP21 - reported	 Nii change recommended by RMU	SC10	Suspect check - supports non contribution	Interpretation. 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 DAA profile. This comparison was done for intelligence purposes only. A reference evidence sample schuid be	slight change to suggested wording. Removed 'mixed'.	SC10	Suspect check - supports non contribution	comparison to other nominated suspects may provide a different interpretation. A reference evidence sample should be provided diffus 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 DNA profile. This comparison was done for intelligence purposes only. A reference	Support change
SCSNC	Suspect check - supports non contribution	for Court. The adaptical interpretation provides apport for the proposition that the nonnotated assessed than not controllated to this make OMA profile. This companions was done for intelligence approase any Anternoor exidence assigns about the provided if this information is required in a statement for court.	this information is required in a statement for Court. The statistical interpretation provides support for the proposition that the norminated suspect has not contributed to this mixed DNA profile. This comparison was also for intrilligione propositions of X-informer evidence sample aloud 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	Interpretation 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 normated 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	slight change to suggested wording. Removed 'mixed'.	SC10	Suspect check - supports non contribution	comparison to other nominated suspects may provide a filterent interpretation. A reference evidence sample should be provided if this information is required in a line statistical interpretation provides susport for the proposition that the nominated suspect has not contributed to inis IDAN profile. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this	Support change
SCSNC	Suspect check - supports non contribution	for Court The statistical interpretation provides support for the proposition that the nominuted support and combinated in the means DNA profile. This comparison was done for intelligence propriorat city. A reference exclones sample should be provided if this information is expand in a submet for round.	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 samples should be provided if this information is required in a statement for court.	PP21 - reported	NII change recommended by RMU	SC10	Suspect check - supports non contribution	Interpretation. 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 normated support has not contributed to this DAM provides. This comparison was done for intelligence purposes only. A reference evidence sample should be provided if this information is required in a salament for court.	slight change to suggested wording. Removed 'mixed'.	SC10	Suspect check - supports non contribution	comparison to other norminated suspects may provide a difficient interpretation. 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 norminated suspects has not contributed to this DNA profile. This comparison was done in intelligence purposes only. A reference evidence sample should be provided if this offormation is regurided in a statement for homan because in the statement for provide in a statement for the provide in a statement for provide in a statement for the provide in a statement for provide in a statement for provide in a statement for provide in the statement for provide in the statement provide if this provide in a statement provide in a statement for provide in a statement provide in a statement for provide in a statement provide in a statement for provide in a statement provide in a s	Support change
SCSNC	Suspect check - supports non contribution Suspect check Action - No Materix	for Court The aduation integration provide apport to the proposition that the nominoted suspect takes not contributed to the mass CMA profile. This comparison was done for intelligence approases only. American evidence asympte should be provided if this information is required in a statement for court. The nominated suspect can be excluded as a control contributor to <sup>the on</sup> TMA - m/m	this information is required in a statement for Court. The statistical interpretation provides support for the procession that the nominated support for the procession of the the state DNA profile. This comparison was done for intelligence purposes and A reference enforms angle is table to provide if this information is required in a statement for court. The commander support can be excluded as a dotted provide way to the	PP21 - reported	Ni change recommended by RMU	SC10 SC11	Suspect check - supports non contribution Suspect cherk -	Integration. An elemente avidence sample houde be provided if this information is required in a statement for Court. The statistical interpretation provides support to the proposition that the nominated suspect has not combinated to this DMA profile. This outpartion was done for intelligence purposes only. A reference endence sample should be provided if this information is requeried in a statement for court.	slight change to suggested wording. Removed 'mixed'. slight change to description	SC10	Suspect check - supports non contribution	comparison to other norminated suspects may provide a different interpretation. A reference evidence sample should be provident of thromismics required in a submitted to the structure of the the statistical interpretation provides support for the proposition that the norminated suspect has not contributed to the interpretation provides submitted to the structure of the taken the structure of the taken sample structure as the advance sample should be provided if this submitted in the norminate statement for the norminate structure structure as the norminate structure as the structure as the structure of the statement and the structure of the norminate structure as the structure of the s	Support change Support change
SCSNC SCANM	Suspect check - supports non contribution Suspect check Action - No Match	for Cent: The statistical interpretation provides acquort for the proposition that the nominated suggest have not extracted to the instead DMA prefile. This comparison was done for intelligence acquired in its adversest for courts acquired in its adversest for courts the instead of the instead of the instead of the instead of the the instead of the instead of the instead of a patiential contribution to the DMA profile distanced than the instead one.	this information is required in a statement for Court. The statistical interpretation provides support for flar proposition that the normalised support has not contributed to this instead DNA profile. This support should be provided if this information is required in a statement for court. The instead support can be insteaded as a pointed contribute to the DNA profile databation to the alternative of the antibility of the theory of the provided in the statement of the other statement support can be enabledged as a pointed contribute to the DNA profile databation the alternative of the statement of the provided statement of the statement	PP21 - reported	 NII change recommended by RMU	SC10	Suspect check - supports non contribution Suspect check - Excluded	Integration. A reference evidence sample house be provided if this information is required in a statement for Court. The statistical integration provides support for the proposition that the normatox isagent as not contributed to his DNA profile. This comparison was done for helitigence 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'. slight change to description	SC10	Suspect check - supports non contribution Suspect check - Excluded	comparison to other norminated suspects may provide a different interpretation. A provide of this information is required in a datament for Court. The statistical interpretation provides apport for the providen that the to this ISNA profile. This comparison was done this ISNA profile. This comparison was done intelligence purposes only. A reference evidence sample should be provided if this formation is required in a statement for The somethated suspect can be excluded as a potential contributor to the DNA confile.	Support change Support change
SCSNC SCANM	Suspect check - supports non contribution Suspect check Action - No Match	for Court.  The individual Integration provides apport for the proposition that the commission seasons takes not controllated to this make IDM profile. This companies was done for intelligence approase sity, American evidence amplies abruid be provided if this information is required in a statement for court.  The institutional suspect can be excluded as a patential contributor to the DNA profile channel from this terrorampte.	this information is required in a statement for Court. The statistical interpretation synchron support for the projection that the nominate output that out combustor that means DNA portion. This comparison was done for infollinging purposes and the American evidence sample shaded be provided if this information is required in a statement for court. The nominated support can be excluded as a primitial combustor to be DNA profile advanced from this fermioampie.	PP21 - reported	 Nil change recommended by RMU	SC10 SC11	Suspect check - supports non contribution Suspect check - Excluded	Integration. A reference enderine sample house be provided if this information is required in a statement for Court. The statistical integration provides support for the proposition that the norminated support for the proposition that the norminate disupport provided if this information is required in a statement for court. In mominated support can be encluded as a potential contributor to the DMA profile abatement.	slight change to suggested wording. Removed 'mixed'. slight change to description	SC10 SC11	Suspect check - supports non contribution Suspect check - Excluded	comparison to other norminated suspects reference evidence sample should be provided if this information in required in a subarrent for Countinear provides support for the proposition that the norminated suspect has not contributed to this DNA profile. This comparison was done without the support of the statement for existing the support of the statement for existing the support of the statement for exat a potential combuter to the DNA profile attained from the ternisangle.	Support change Support change
SCSNC SCANM 18PPSR	Suspect check - supports non contribution - Suspect check Action - No Match Presumptive blood test pos.	for Court.  The statistical Interpretation provides apport for the proposition that the nominated support has not controllated to this mixed DMA profile. This comparison was done for intelligence approace sign, American evidence ample total de provided if this information is required in a subannet for court.  The nominated support can be excluded as a potential contributor to the DNA profile distance from this information;  The formation the information;  The formation the information;  The formation the information;  The mominated support can be excluded as a potential contributor to the DNA profile distance from this information;  The formation the information	this information is required in a statement for Court. The statistical interpretation provides apport for the proposition that the nominated suspect has not combudied to this inset DNA profile. This comparison was done with informac purposes only. A reference evidence court: The nominated suspect can be excluded as a potential combinition to the DNA profile dozened from this inclusion.	PP21 - reported	 Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU	SC10 SC11	Suspect check - supports non contribution Suspect check - Excluded	Integration. A inference and/article sample house be provided if this information is sequine in a statement for Court. The statistical integration provides support for the proposition that the normalised support to the proposition that the normalised support comparison was denoted for the thigment purposes only. A neterence endence sample should be provided if this internation is negative in a subsemble for court. Support of the normalised and advanted for the statement of the the normalised statement of the third support of the Normalised statement of the the normalised statement statement of the statement of the the normalised statement of the statement of th	slight change to suggested wording. Removed 'mixed'. slight change to description not discussed	SC10 SC11	Suspect check - supports non contribution Suspect check - Excluded	comparison to other nominated suspects may provide a different imprentation. A provided of their information is request provided of their information is request in a datement for Court. The statistical integratation provides aspect of the proposation that the support for the proposation that the support of the support of the support information is request on a statement for a portential contribution the IOM profile calaries from this itemisampte.	Support change Support change Refer to Paula Briscoto
SCSNC SCANM 18PPSR	Buspots check - supports non contribution Suspect check Action - No Match Presumptive blood test pos. Submitted results pending	for Cost: The additional interpretation provides apport for the proposition that the extended interpretation provides apport for the proposition was done for intelligence purposes only. Arternation evidence arraying should be provided if this information is required in a statement for court. The nominated suspect can be actualed as a potential contributor to the DNA profile distance from this leminample. This leminample back positive tax presumptive test for bood (TMB) and was submitted to DNA water, Reveals an pending	this information is required in a statement for Court. The statistical interpretation provides acquest for the representation from the temperature interpretation and the temperature interpretation acquest that the information is required in a statement for court. The normalized subject can be included as a potential contributor to the ONA profess determined that the reducted as a potential contributor to the ONA profess determined the forwards. This information taken, "Seaking Seaking Seaking Seaking Seaking Seaking" (TMB) and a submitted TMB) and the statement of profession activity of the ONA profession of the Information is required in a statement of the Seaking S	PP21 - reported	 Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU	SC10 SC11	Suspect check - supports non contribution Suspect check - Excluded	relepation. A reference evidence surger advacable provided framinstration as require in a statistment for Court provide the statistical frequency of the statistical reference of the statistical reference purposes provided fraministration is regarded in a statement for court. The normalization statistical fraministration statement for court.	slight change to suggested wording. Removed 'mixed' slight change to description not discussed and discussed	SC10 SC11	Suspect check - supports non contribution Suspect check - Excluded	comparison to other nominated suspects methods and an expected of the second second second second periodical of this information is required in a determined includes the periodical of the second second the sublication encounter of the second second the DNA periodic that the methods and the DNA periodic that the method has DNA periodic that the second second the DNA periodic that the second second information is required in a statement for card. The method combined on the method second that DNA periodic to the DNA periodic detailed from this iterritange.	Support change Support change Refer to Paula Bristoto Refer to Paula Bristoto
SCSNC SCANM 1BPPSR AINT CMPU	Suspect check - supports non contribution Suspect check Action - No Match Presumptive blood test pos. All term now tested Omplex media police susualidate	for Court.  The statistical interpretation provides apport for the proparties that the nonnotate inspect has not contributed to this mass DMA profile. This comparison was done for intelligence approase only. American evidence analysis about the provided if this information is nequired in a statement for court.  The nonnotated support can be excluded as a patential contributor to the DNA profile datamet down this informance.  The nonnotated support can be excluded as a patential contributor to the DNA profile datamet down this informance.  The nonnotated support can be excluded as a patential contributor to the DNA profile datamet down this informance.  The nonnotated support can be excluded with the to Socid (TMB) and was submitted to DMA mating. Results are performed.  The informance parameters complex Mass DMA profile with multiple contributors.  The nonnotate	this information is required in a statement for Court. The statistical interpretation provides apport for the proposition had the nominated suspect has not contributed to this mixed DNA profits. This comparison was done to interflapport process of the provides of the interpret of the statement for court. The nominated suspect can be excluded as a potential contributor to the DNA profits doctimed to this itemation. The nominated suspect can be excluded as a potential contributor to the DNA profits doctimed to the this manufacture. This itemation of the DNA hadron, the provides with the totood (TMB) and are advanted to DNA hadron, then are perform. The itemation previous compared was done provides the the totood (TMB) and the itemation previous compared was done provides with the totood (TMB) and the itemation previous compared was done provides with the totood (TMB) and the itemation previous compared was done provides with the totood (TMB) and the itemation previous compared was done provides with the totood (TMB) and the itemation previous compared was done provides with the totood (TMB) and the itemation previous compared was done and the itemation of the itematic of the itemation of the itemation of the itematic of the itema	PP21 - reported	 Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU	SC10 SC11 CPU	Suspect check - supports non contribution Suspect check - Excluded	Integration, A reference evidence surgel acade to provide the information is waiter in a statisticari for Court. The statistical mercentarism provides susport for the proposition that the normalized suspect comparison was done to information provides and comparison was done to information provides and automation in equired in a statement for court. The normating suspect can be excluded as a potential conduct to the CNA profile and the statematic of the CNA profile and the statematic of the CNA profile. The termination provides and profiles and the provides of the information.	slight change to suggested wording. Removed "mixed". slight change to description not discussed not discussed not discussed	SC10 SC11 CPU	Suspect check - supports non contribution Suspect check - Excluded	comparison is other mominated supports interview of the information is required in a distancer lar Court information existence and the information is revealed supported for the proposition that the important of the proposition that the mominate auguest rule and contributed by the information and the contributed by the information and the provided frag- tion and the proposition is a statement of the mominate auguest rule of the statement of the mominate auguest rule and the provided proposition and the provided frag- al potential communities of the DMA public automation and the interview of the DMA automation and the interview of the Interview of the DMA automation and the interview of the Interview of the IDMA automation and the interview of the IDMA automation and th	Support change Support change Refer to Paula Brisotto Refer to Paula Brisotto
SCSNC SCANM 1BPPSR AINT CMPU	Suspect sheek - supports non contribution Suspect check Action - No Match Presumptive blood feet pos Subantited - could pending Complex mode panding Complex mode panding	for Cost. The statistical integration provides asport for the proposition that the nominate support has not contributed to the mess DM profile. This comparison was done for intelligence support of a substrained for court. The intermediate support court any substrained by provided if this information is expanded in a substrained for court. The intermediate support court any substrained as a patiential contributor to the DMA profile advanced to mit the intermanipie. This intermanipie isotatic patient to a second of the substrained for the DMA profile advanced to mit the intermanipie. This intermanipie isotatic patients as personageive test for blood (TMB) and was submitted by DMA substrip, Research as personage.	The information is required in a statement for Court. The statistical relegonitation provides august for the proposition that the normalised support has not combusted to this mines (DNA profile. This support should be provided if this information is required in a statement for court. The normalised support can be encluded as a prioritial contribution to be CMA profile databates the statement and the provided in the statement of the normalised support can be encluded as a prioritial contribution to be CMA profile databates the statement and the statement of the This technologies listed profiles to a prioritized with the foreign of (TMB) performance all statements for the statement and the statement of the control of the stateM content is a prioritized with the foreign of (TMB) performance all states for the stateM content is not auble for the managing in implicit profile and performance.	PP21 - reported prefilm - auto update Automatically field on FR PP21 - reported	 NE change recommended by RMU NE change recommended by RMU NE change recommended by RMU NE change recommended by RMU NE change recommended by RMU	SC10 SC11 CPU	Suspect check - supports non contribution Suspect check - Excluded Complex profile	Integration, A reference endorse analysis and action is provided the information is marked in a statement for Court in admitted in regulation provides support that actional information provides support has not constructed to this DNA profile. This comparison was able to information analysis abud to activate the constructed to the DNA profile statement for court. The normalitie support can be excluded as a potential controllated to the DNA profile. This terminantial pages a complex DNA profile.	slight change to suggested wording. Removed 'mixed'. slight change to description not discussed replace with this line which has already been created.	SC10 SC11 CPU	Suspect check - supports non contribution Suspect check - Excluded	comparison to john roomvaled asynchro methods to john roomvaled asynchro methods and the second second second provided of the information is required in a The statistical information provides aspect for the proposition that the the statistical information provides in the DNA profile. This comparison was done for intelligence purposes only. A reference information is required in a statement for continuation is required in a statement for continue of the information of the DNA profile content of the information of the DNA profile. The DNA profile on the statement profile. This DNA profile on not stated be the	Support change Support change Refer to Paula Biscoto Support change
SCSNC SCANM 1BPPSR AINT CMPU	Supped check - supports non contribution Supped check Action - No Match Presumptive blood test pos Substitution deventing participa Substitution deventing participa Substitution deventing participation Substitution deventing participation of the Substitution deventing participation of the Substitution of the Substitution of the Substitution Substitution of the Substitution of the Substitution of the Substitution of the Substitution of the Substitution of the Substitution of the Substitution of the Substitution of the Substitution of the Substitution of the Substitution of the Substitution of the Substitution of the Substitution of the Substitution of the Sub	for Cost: The statistical interpretation provides apport for the proposition that the networked have been approached by the mass DMA profile. This comparison was done for intelligence approaches that approximate without approximation to provided if this information is required in a statement for court. The noninstated support can be excluded as a patential contributor to the DNA profile datamatic from this itembrane): The Internative protocols approximate the for block (TMB) and was submitted to DMA being required and the approximation of the DMA profile datamatic from this itembrane): The Internative protocols approximate the for block (TMB) and was submitted to DMA being required and the approximation of the Internative protocols approximation on the other than the oppolocy relating to the internative protocols and the internation and the interlation and of all internative protocols and the interlation of the other than and of all shortsman approximative protocols and the interlation and the interlation and other interlation and other interlations and the interlation approximation of the other than and of all the Internative protocols and the interlation of the Interlation and the interlation and the interlation approximation of the interlation of	this information is required in a statement for Court. The statistical interpretation provides aspect for the proposition that the nominated suspect has not contributed to this maked DNA profile. This comparison was done for interplance proposed by a frequency device angular shall be provided if the information is required in a statement for court. The nominated suspect can be excluded as a potential contributor to the DNA profile obtained from this terminative. This isometry and the torus the statement be into DNA profile obtained for the statement. The nominative terminative terminative term for block (TMB) and and largers for the state bits for particular profile. The statement is not subled for maningful interplation date contributors. This initiate is not subled for maningful interplation date contributors.	PP21 - reported	 NE change recommended by RMU NE change recommended by RMU NE change recommended by RMU NE change recommended by RMU NE change recommended by RMU	SC10 SC11 CPU	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsuitable for interp or	Interpretation, A reference evidence sample advalche provided für information in waylier din a statistimetti for Court in the advalce information provides support for the proposition that the normalised surgest approximation and the normalised surgest interpretation successful or traditional provides regulated für information in expande an a statistimet for court. The normalistic support can be excluded as a potential contribute to the DNA profile. The DMA profile is not suitable for meximplicity provides in the information.	slight change to suggested wording. Removed 'mixed'. slight change to description not discussed rol discussed rol discussed already been created	SC10 SC11 CPU	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsultable for inter	comparison to other mominated supports comparison to other mominated supports interview with the support of the information is required in a discussion of or Courts support of the proposition that the mominated suspect has not contributed to the information of the provided the the mominated suspect in the contributed to the information is required in a statement for mominated suspect in the contributed to the information is required in a statement for mominated suspect in the statement for mominated suspect in the statement of the information is required in a statement for mominated suspect in the statement of the information of the INM profile advanted for the humanges.	Support change Support change Refer to Paula Broots Refer to Paula Broots Support change
SCSNC SCANM 18PPSR AINT CMPU	Susped check - supports non carditudion Suspect check Action - No Match Precomption blood test proc Advantable resulting profile anticable for entry or companion	for Cost: The statistical interpretation provides support for the proposition that the nominated support has not contributed to this mixed DMA profile. This comparison was done for intelligence appropring only. A reference on other camples should be provided if this intermetion is required in a substantial for much the nominative statement for much the nominative statement of much the nominative statement of the anticipation of the statement of the nominative statement of the statement of the statement of the nominative The nominative statement of the statement of the statement of the nominative the nominative statement of the statement of the nominative statement of the nominative statement of contributions and/or the interled amount of moment of the statement of contributions and/or the interled amount of moments with the VMA profile.	The information is required in a statement for Court. The statistical interpretation provides apport for the proposition that the normabile appeortance of contributed to this instead DAA profile. This interpretation that the provides of this information and the provides of the information of the provides of the information and the provides of the information of	PP21 - reported pretim - auto spotne Automatically Ned on PR PP21 - reported	 NI change recommended by RMU NII change recommended by RMU NII change recommended by RMU NII change recommended by RMU NII change recommended by RMU	SC10 SC11 CPU	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsuitable for interp or comparison	Integration. A reference existence analysis aduated to a provided the information is magning that a statistimum for Court to statistical responsibility of the statistical responsibility of the test statistical responsibility of the statistical response comparison was done for the DNA profiles. This comparison was done for the DNA profiles thatment of occurs. The normalized studyed can be enabled on a patiential done of the DNA profiles thatmend for occurs.	slight change to suggested working. Removed 'mixed' slight change to description not discussed replace with this line which has already been created	SC10 SC11 CPU	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsuitable for interp or comparison	comparison to give momentation supports intervence evidence sample should be provided if this information is required in a the statistical interpretation provides support for the proposition that the the statistical interpretation provides to statistical interpretation provides to statistical interpretation provides to statistical interpretation provides to statistical interpretation and the statistical interpretation and the statistical interpretation of the SNA profile. The statistical interpretation to the SNA profile cost. This membranelity part a constraint SNA membranelity in the statistical statistical cost of the statistical statistical statistical statistical statistical cost of the statistical statistical statistical statistical statistical cost of the statistical statistical statistical statistical statistical statistical cost of the statistical statistical statistical statistical statistical statistical statistical cost of the statistical statistical statistical statistical statistical statistical cost of the statistical s	Support change Support change Refer to Paula Briosto Refer to Paula Briosto Support change
SCSNC SCANM 1BPPSR AINT CMPU	Supped check - supports non contribution Supped check Action - No Match Presumptive blood bed nos Submitties desured produce Complex mixed profile usuable fo etemp or comparison	for Cost: The initiality integration provide apport for the proposition that the initiality apport taxe not contributed to this make DMA profile. This comparison was done for intelligence approase only, American evidence analysis apported in this information is required in a statement for court. The monimum data support can be excluded as a potential contributor to the DMA profile charanse from this iteminangle. The monimum data apport can be excluded as a potential contributor to the DMA profile charanse from this iteminangle. The initializing freedule to a possimption tent for blood (TMB) and was submitted the DMA profile contributor to the contributor. This induces watchman and potential upon number of contributors and/or the limited amount of information within the DMA profile.	this information is required in a statement for Court. The statistical interpretation provides support for the proposation that the normated support for a contributed to this maked DNA profile. This comparison was done for interplance purposes and A reference enforms angle shall be provided if this information is required in a statement for court. The normated support can be excluded as a potential contributor to the DNA profile accepted can be excluded as a potential contributor to the DNA profile accepted can be excluded as a potential to the interplance to the statement of the top of the profile of the was adverted for DNA service. Reveals are pending. This itemation particular to a pre-supervised with the top of the profile.	IP21 - reported preter - auto update Approximation field or PT Approximation field or PT P21 - reported	 Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU	SC10 SC11 CPU	Suspect check - supports non contribution Suspect check - Excluded Complex profile Complex profile nutration for interp or comparison	Integration, A reference encloses assigned aduction is provided the information is a square in a statement for Carut the aduction provides assigned the the aduction and enclose provides assigned than end contributed to this DNA profiles. This comparison was also for the IMMA profile. This comparison was also for the IMMA profile. This advanced to carute a statement to carut advanced to carute a statement to carut advanced to carute a statement to carute advanced to carute a statement to carute advanced to carute a statement to carute advanced to carute advanced to the statement to carute the the IMMA profile. The functionality advanced to compare DMA profile. The functionality advanced to compare DMA profile. The functionality advanced to compare DMA profile.	slight change to suggested wording. Removed traxed: alight change to description not discussed replace with this line which has already been created	SC10 SC11 CPU	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsuitable for inter or comparison	comparison to other mominated supports comparison to other mominated supports provided Pf this information is required in a distancent for Control and the support of the support of the support support of the proposition that the mominated support has not contributed to the DNA profile. This comparison was done without the support of the support of the proposition that the information is required in a statement for the comparison of the support of the support algorithm of the support of the support of the comparison of the comparison of the other comparison of the the comparison of comparison and comparison of the the other other other comparison of the other other other other other other other comparison of the other other other other other other comparison of the other other other other other other other comparison of the other other other other other other other other other comparison of the other othe	Support change Support change Refers to Partial Bitototo Support change
SCSNC SCANM 18PPSR AINT CMPU	Suspect check - supports non contribution Suspect check Action - No Match Presumptive blood test pos. Butmittle - exust panchog Butmittle - exust pa	for Cost: The Mathield Helepretation provides apport for the propulsion that the nonmated sequent has not contributed to this mused DMA profile. This comparison was done for intelligence approprises only. American evidence analyse should be provided if this information is required in a seasometh for could. The nonmated support can be excluded as a potential contributor to the DNA profile claimed for this information. This intervanging leaguest can be excluded as an appendix of this information the data and the season of the season of the season of the season of the the limit of the season of the season of the season of the limit of the season of the limit of the season of the season of the limit of the season of the information within the DNA profile.	The information is required in a statement for Court. The statistical interpretation provides apport for the proposition has the nominated suspect has not contributed to this mixed DNA profits. This comparations will doe the intelligence purposes of the statement for court. The nominated suspect can be excluded as a potential contributor to the CMA profile address of this information. In require in a statement for CMA profile address of the statement of the total total total total The nominated subject can be excluded as a potential contributor to the CMA profile address of the statement of the total of (TMB) and are submitted to DNA testing. Result as a product, the limited amount of the statement of the total of (TMB) and contributors. This minutes is not stated for manifold interpretational contributors. This minutes is not stated for manifold interpretational combinets of combinations and of the limited amount of information within the DNA profile.	PP21 - seponed protein - such specifie protein - such specifie Automatically Net on PP PP21 - reported	 Nii change recommended by RMU Nii change recommended by RMU Ni change recommended by RMU Ni change recommended by RMU	SCI9 SCI1 CPU	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsuitable for interp or comparison	Integration, A reference existence surger aduated to exposed of the information is equilated in a subtainer for Court. The aduated memory of the existence of the existence of the proceeding the existence of the existence or the existence existence asingle should be aduated and the existence of the existence of the existence of existence existence of the existence of the existence of existence of the existence of the existence of existence on any potential signs of the existence of existence on any potential signs and the existence of existence on any potential signs of the existence of existence on the the DM potential signs of the existence o	slight chunge is suggested working. Removed Instead slight chunge is description rel discussed rol discussed rol discussed rol discussed is law which has almady been created	SC10 SC11 CPU	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsuitable for interp or comparison	comparison is other mominated surgests interview of the information is required in a difference existence sample should be provided if the information is required in a difference existence and a solution on provide support of the proposition that the mominated augues if the oric contributed be provided in the provided the provided fraction for initiation purposes only. A reference existence sample submittance to a setundated or initiation of the provided fraction of the reaction of the momenta of the provided fraction could be contributed to provided fraction a pointed contribution to the DNA profile and a pointed contribution to the DNA profile. This DNA profiles and statuble for complexity relating the unknown and patientially they number of contributions patients the DNA profile.	Support change Support change Refer to Paula Brochto Refer to Paula Brochto Support change
SCSNC SCANM 1BPPSR AINT CMPU	Suspect check - supports non contribution Suspect check Action - No Match Presumption blood test pos Automated-enable particip All ferm now tested wherp or comparison	For Cost. The statistical integration provides asport for the proposition that the nominate asport has not contributed to this most DM profile. This comparison was done for intelligence suggested in a distance of the cost. The intermediate suggest can be excluded as a potential contribute to the DMA profile association of the intermediate suggest can be excluded as a potential contribute to the DMA profile association of the intermediate suggest can be excluded as a potential contribute to the DMA profile association of the intermany is a potential contribute to the DMA profile association of the intermany is a potential contribute to the DMA profile and the intermany is and a porting. 20 Interms to the excluded are parameterized as the intermediate contributes. The network to the subscience and potentially length and one there is completely poly contributions. The network is not subscient for many of the contributions and/or the initial amount of elements when the DMA profile.	The information is required in a statement for Court. The statistical interpretation provides apport for the proposition that the memory of the statement of the statement (DAA profit. This maniput studied is provided if this information is required in a statement for court. The instructional surged can be enabled as a potential contributor to be CMA profile statement on the isometament. This technologies that courted is a statement for the index a statement of the statement of the enabled is an expension of (HBI) werk as automatic of the statement of the statement of the court of the statement of the statement of the statement of the statement of the statement of the statement of the statement of a statement of the DAA profile.	19921 - reported	 NE change recommended by RMU NE change recommended by RMU NE change recommended by RMU NE change recommended by RMU NE change recommended by RMU	SC10 SC11 CPU	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsutable for comparison	Integration. A reference existence ample disadles to provided the information is trading to a statement for Caul- trading and the statement of Caul- trading and the statement of Caul- trading and the statement of Caul- har of controllated to this DNA profile. This organization was done to the BMA profile attement for caul- terial cardination is sparse and a statement of could be DNA profile. The termination state of the DNA profile attement of could be autiliated for an angle attement of could be autiliated for the statement of could be autiliated for the statement attement of could be autiliated for manipular integrations also define atto complex DNA profile. The terminative gave a complex DNA profile.	sight charge to suggested wording Removed inseed. Sight charge to description not discussed indicases with the line which has almostly been created	SC10 SC11 CPU	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsuitable for interp or comparison	comparison to give roomvaled asynchronia methods of the second s	Support change
SCSNC SCANM 1BPPSR AINT CMPU	Support check - supports non contribution Support check Action - No Match Presumptive blood test pos Submitted-could pending Submitted-could pending s	for Cost: The abstituted interpretation provides apport for the preparation that the nonnotect sequent has not contributed to this mass DMA profile. This comparison was done for intelligence approase only. Arrestment the coult approace only. Arrestment the coult the nonnotated subject can be excluded as a patential contributor to the DNA profile datamet down this deminance. The nonnotated subject can be excluded as a patential contributor to the DNA profile datamet down this deminance. The nonnotated subject can be excluded as a patential contributor to the DNA profile datamet down this deminance. The nonnotated subject can be excluded as a patential contributor to the DNA profile datamet down the data as participants that for toxic (TMB) and was submitted to DMA tangets. The analysis are completed toxic DNA profile with multiple contributors. The matures is not subled for meaningula integrated to due to the intel precisively relating to the information within the DNA profile.	The information is regulard in a statement for Court. The statistical interpretation provides apport for the proposition had the noninvalued support has not contributed to the mixed DAA profits. This comparison was done to interflamon as negative in a statement for non-the statement of the information is negative in a statement for court. The noninvalued acapted if the information is negative in a statement for DAA profits deatment from this termination. In negative is a statement for the information of the information is negative in a statement for DAA profits deatment from this termination. The noninvalue statement of the information is not to be informed and account of the information of the information of the block (TMB) and and the information is not stated for manifold integrated on data contributors. This minitian is not stated for manifold integrated on data contributors. This minitian is not stated for manifold integrated on data to the for complete the provider that the provider the information within the DAA profits.	PP21 - seponted protein - suits opdate Cutomatically field on TRC PP21 - reported	 Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU	SCI9 SCI1 CPU	Suspect check - contribution Suspect check - Excluded Complex profile unsultable for interp or comparison	Interpretation, A reference evidence sample aduation be provided the information is regarilled in a substimet for Court. The adatability encounter that the constrained suspect of the proposition that the constrained suspect is the substitution of the substitution of the sub- trained substitution of the substitution of the proposition in substitution is regarded an a substitution of the court. The termination subsect can be excluded as a calculated from their semicondination calculated from their semicondination that the termination and their semicondination runnel of internation and/or the limited amount of internation within the DMA profile.	slight change to suggested wording. Removed Imaed - slight change to description and discussed ord discussed ord discussed already been created	SC10 SC11 CPU	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsuitable for inter or comparison	comparison to other mominated supports interference existence sample should be provided if this information is required in a disearch for Could support of the proposition that the support of the proposition that the mominated suggest in two contributed be the information of the contributed be the information of the contributed be the information provides only. A reference widence anying beaution that the energy of the mominated suggest in a statement for the mominate suggest the statement for advance of the information of the OMA public exists. DNA profiles and statement patiential page number of contributes patiential page number of contributes advance the DNA public.	Support change Support change Refer to Paula Broots States to Paula Broots States to Paula Broots
SCSNC SCANM 18PPSR AINT CMPU	Suspect check - supports non contribution Suspect check Action - No Match Preservices Under Action - No Match Preservices Under Action - No Match All Seam A	for Cent:	The information is required in a statement for Court. The statistical interpretation provides augort for the proposition that the normated assages than out contributed to this manked DAA priority. This interprets should be provided if this information is repared in a statement for court. The provided suggest can be reached as a potential contributor to the Court of the provided if this information is repared in a statement for court. This information suggest can be reached as a specified contributor to the Court of the provided if the information is repared in the statement of the provided suggest can be reached as a specified contributor to the Court of the provided suggest can be reached as a specified contributor to the Court provided assignment on the information is information. This information part of the courts of the provided in	PP21 - reported PP21 - rep21 - reported PP21 - reported PP21 - rep01 - rep21 -	 Ni change recommended by RMU Ni change recommended by RMU Ni change recommended by RMU Ni change recommended by RMU Change recommended by RMU	SC10 SC11 CPU DSP1	Suspect check - suspects non contribution	Interpretation. A reference existence assigned aducative a provided the information in sur- traparties in a aductment for Court. The datability interpretation provides subport that and control the court of the court and the control the court of the annexes of information within the DNA profile. The court of the court of the court of the court of the court of the court of the cour	sight change to suggested working. Removed traved: alight change to description not discussed ord discussed provides with the line which has aliesdy been coasted description and the set of has aliesdy been coasted	SC10 SC11 CPU DIFP1	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsuitable for inter or comparison	comparison to other monitories supports improve a start of the information is required in a the statistical integration provides support of the proposition that the the statistical integration provides support of the proposition that the the statistical integration provides integration of the proposition that the the statistical integration is a statistical to the integration provides and the statistical to the integration of the statistical to the statistical integration is a statistical to control. This methylamic and support on the integration obtained in integration due to the IOM profile integration of the interviewer. This methylamic and support on the interviewer interviewer integration of the statistical to the another interviewer in the statistical to the statistical to the statistical to the statistical to the statistical to the statistical to the statistical to the statistical to the statistical to the statistical to the statistical to the statistical to the statistical to the statistical to the statistical to the statistical to the statistical to the sta	Support change Support change Role to Paula Brocks Support change Role to Paula Brocks Support change Role to Paula Brocks - sight changes
SCSNC SCANM IBPPSR AINT CMPU	Suspect check - supports non contribution Suspect check Action - No Match Presumptive blood ted post advantited creatibility particip Complex mode profes usuable for ellerp or comparison OMA insufficient for further processing	for Cost:      the statistical interpretation provides apport for the investment that the interivated interpretation provides apport for the investment that the interivated is asserted than not contributed to the investment that the provided if this information is magnited in a statement for court.      The noninstated suspect can be excluded as a patential contributor to the DNA profile channel from the information.      The noninstated suspect can be excluded as a patential contributor to the DNA profile channel from the information.      The interivative the provides approximately test for block (TMB) and was submitted to DNA testing. Results are performed in the information is not abundle for manipulation on the entermined in modple contributors. The matter is not abundle for manipular interpretation can be effer in contributors of the information in the information with the DNA profile.      This listicative approximation for DNA analysis. Low levels of DNA were detected in the information with the DNA profile.      This listicative approximation for DNA analysis. Low levels of DNA were detected in the DNA modple.	This information is required in a statement for Court. The statistical interpretation provides apport for the proposition that the normatical support has not contributed to this maked DNA profile. This comparison was done for interpretation area and the statement for court. The normatical provides if the information is required in a statement for court. The normatical provides if the information is required in a statement for court. The normatical support can be excluded as a potential contributor to the DNA profile obtained from this terminante. This instruction between the court of the transmitter of the DNA profile obtained from the terminante. This instruction between the court of the transmitter of the DNA profile contributors. This instruct is not statelled for maningful interplation date to other bots of courts by the hardwoen and potential larger marked of contributors and/or the limited amount of information within the Court of the sample and/or the not observe and the information within the Court observe and the limited amount of information within the Court observe and the limited amount of information within the Court observe and the limited amount of information within the Court observe and the sample and it can not abstimited for CMA analyses. Line levels of DMA wave decision in this sample and it can not abstimited for CMA analyses.	IPP21 - reported	 NE change recommended by RMU NE change recommended by RMU NE change recommended by RMU NE change recommended by RMU Change recommended by RMU Change recommended including task information.	SC10 SC11 CPU	Suspect check - susports non contribution Suspect check - Excluded Complex profile unsultable for interp or comparison	Interpretation, A reference on extension assumption doubles to provide the two formation on the second trademic to a substantian for Gaussian and the second trademic to the substantian of the second trademic trademic has not constructed to this DNA profiles. This comparison was also not trademic to a substantiant of to could provided of their information is equated in a substantiant to could advantiant to could be DNA profiles. The comparison was also substantiant to could be an extended on a substantiant to could be advantiant to could be approximated to substantiant to could advantiant to could be advantiant to could be advantiant to could be advantiant to could be advantiant to could advantiant to could be advantiant to could be advantiant the benchmarked provides DNA profiles. The the benchmarked provides advantiant to could advantiant to could be advantiant to could be advantiant the advantiant to could be advantiant to could be advantiant the advantiant to could be advantiant to could be advantiant the advantiant to could be advantiant to could be advantiant the advantiant to could be advantiant to could be advantiant the advantiant to could be advantiant to could be advantiant to the advantiant to the the top advantiant to the top advantiant the advantiant to the advantiant to the top advantiant to the advantiant to the top advantiant to the top advantiant to the advantiant to the top advantiant top	Sight change to suggested wording Removed Interd" Sight change to description of discussed or discussed or discussed indicates with the line which has alwedy been created change in exp comment	SC10 SC11 CPU	Suspect check - support non contribution Suspect check - Excluded Complex profile to-sustable for interp or comparison MA insufficient for Mather processing	comparison to other mominated supports comparison to other mominated supports provided Pfiles information is required in a disearch of Crockin support of the information is required in a support of the proposition that the mominated suspen than the contributed by the information of the provided Pfiles to intelligence purposes only. A reference evidence sample should be provided Pfiles to intelligence purposes only. A reference evidence sample should be provided Pfiles the international evidence on the excluded and a potential combutor to the DNA profiles and and the the international evidence and profile. This DNA profiles not statisticate for mainting of the the internation and the the Internation due to their the complexity relating by the unknown and addre the limited ancul of information within the DNA profiles.	Support change Support change Refers to Paula Brocks Support change Support change Refer to Paula Brocks - slight changes recommended
SCSNC SCANM 1BPPSR AINT CMPU	Suspect check - supports non contribution Suspect check Action - No Match Presumptive blood test pos All term source tested and post tested seter per companion seter per companion	for Cost: The Atabilitied Interpretation provides apport for the proposition that the norm-last aspect than not contributed to this muse DMA profile. This comparison was done for intelligence approares only, Alternative evidence analyses that be provided if this information is required in a setainment for could. The normitated august can be excluded as a potential contributor to the DNA profile datamatic times and the provides of this information is the limit time of the analysis of the provides of the information is the limit time of the provides of the provides of the information of the limit time of the provides of the provides of the other than the profile of the limit time of the provides and provides and the provides of the limit time of the time limit time of the provides and provides and the limit time annual of information within the DNA profile. This leminicating beam provides approximation and the limit time annual of and the limit time of the time DNA profile. The contract of DNA were detected in the sequence of the work advected for DNA analysis. Low locks of DNA were detected in the lamit time of the use of advected based contract the DNA profile database of the limit time DNA profile. The sec orticat the DNA profile database of the limit time of the limit time of DNA were detected in the lamit time of the use of advected time DNA profile. The lamit time of DNA were detected in the lamit time of the use of advected time of the lamit time of DNA were detected in the lamit time of the use of advected time of the lamit time of the lamit time of the DNA profile database of the lamit time of the DNA profile.	This information is required in a statement for Court. The statistical interpretation provides apport for the proposition has the nominated suspect has not combudied to this instead DNA profile. This comparison was done with informer purposes only. A reference evidence court: The nominated suspect can be excluded as a potential combinition to the DNA profile advanced from the instruments. This communities and the combined of the total of (1MB) and the submitted total provides in a practice in the block (1MB) and the submitted total provides in a practice in the block (1MB) and the submitted total provides in a practice in the block (1MB) and the submitted total provides in a practice in the block (1MB) and the submitted total provides in a practice in the block (1MB) and provides in the block in the block (1MB) and the block combinets. The ministra is not statisfied to maximple interpretation and market of combinations and the blinked amount of information when the DNA profile. This stample and it are not abundhed for there DNA works advanced to the stample in the statistical block of the block (1MB) and profile. This stample was submitted for OMA analyses. Low levels of DNA work prediction of the stample and its assess of further movements.	PP21 - seponted pretter - such specified pretter - such specified pretter - such specified pP21 - reported pP21 - reported pP21 - reported pP21 - seponted pP2	 Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU Change recommended scluding lask information.	SC10 SC11 CPU CPU	Suspect check - supports non contribution Suspect check - Excluded Complex profile unlerg or comparison	Integration. A reference existence surgel aduated to exposed of the information is sequired in a statististic for Court. The statistical responsibility of the courter of the production of the courter of the courter of the courter of the courter of the courter of the courter of the courter of the courter of the courter of the courter of the courter of the courter of the courter of the courter of the courter of the courter of the courter of the courter of the courter o	sight change to suggested worting Removed Insect - sight change to description and discussed and discussed assay been created disciple in any comment change in any comment	SC10 SC11 CPU	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsuitable for interp or comparison DNA insufficient for further processing	comparison is other mominated surgeds interference existence sample should be provided if this information is required in a the statistical and the surged should be supported for the proposition that the the statistical and the concentrations be the statistical and the provided fractions and the statistical and the provided fractions that statistical and the statistical term initial program and the statistical data and the surgest the statistical between the statistical concentrations between the statistical concentration and the concentration of the statistical between the statistical between the statistical between the statistical between the statistical between patientially targe number of contributions with the DMA profiles are statistical the DMA profiles are statistical between the DMA profiles are statistical between the statistical between the theory of the profiles are statistical between the the theory of the profiles are statistical between the profiles are statistical between the theory of the profiles are statistical between the profiles are statistical between the theory of the profiles are s	Support change Support change Refer to Paula Brocks Support change Refer to Paula Brocks Support change Refer to Paula Brocks - slight changes
SCSNC SCANM 1BPPSR AINT CMPU	Suspect check - supports non contribution Suspect check Action - No Match Presumption blood for proc. All Rem none tested all Actionated even bending all Rem none tested and actionated for the subscription of the processing	for Cost:               The statistical integration provides acquort for the proposition that the normalized suspect	The information is required in a statement for Court. The additional interpretation provides augent for the proposition that the manimated suggest has not contributed to this missed DNA profile. This maniput should be provided if this information is required in a distinct for court. The nontroverse suggest can be excluded as a prioritid contribution to be- DNA profile distortion to be ambunding to the prioritid contribution to be- DNA profile distortion to be ambunding to the prioritid contribution to be- DNA profile distortions in the ambunding of the prioritid contribution to be- DNA profile distortions in the ambunding of the prioritid contribution to be- DNA profile distortions in our adable for more segment all forms for the adable DNA to the to be more and potentially streng DNA profile. This temperature is not adable for more approximation them the DNA profile. This temperature is not adable for more approximation them the DNA profile. This temperature is not adable for more approximation them the DNA profile. This temperature is not adable for more approximation them the DNA profile. This temperature is not adable for more approximation them the DNA profile. This temperature is not adable for more approximation them the DNA profile. This temperature is not adable for more approximation them the DNA profile. This temperature is not adable for more approximation the more of the temperature is not adable for more approximation the temperature is the temperature is the temperature is the temperature in the more the temperature is th	19721 - reported prater - such spelate Custometach field on PT - PTP1 - reported	 NE change recommended by RMU NE change recommended by RMU NE change recommended by RMU NE change recommended by RMU Change recommended including task information.	SC10 SC11 CPU CRP1	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsustable for interp or comparison DNA insufficient for further processing	Integration, A reference encloses sample disculta la provided the information is separate in a statement for Cause the admitted integration provides support that admitted integration provides support has not controlled to this DNA profile. This comparison was adress to the INMA profile. This comparison was adress that the INMA profile. The monitorial support can be excluded a a particular distribution is signal as advected and the INMA profile. The the INMA profile is the DNA profile advected to this there also that provides the advected to this there also the INMA profile. The thermative game a complex DNA profile.	slight change to suggested wording Removed tread? alight change to description ord discassed for discassed annualy been onated in a change in exp comment	SC10 SC11 CPU DIFP1	Support next outports next contribution Support check - Excluded Complex profile installable to 'http: contribution DMA neutricient for turbe processing	comparison by other momentation supports in the second sec	Support change Support change Refer to Paula Brocks Support change Support change Refer to Paula Brocks - slight changes
SCSNC SCANM 18PPSR AINT CMPU	Suged check - supports non contribution Surgest check Action - No Match Presumptive blood test pos Submittle - counts particing submittle - counts particing submittle - counts particing eterp or comparison	for Cost:               In additional interpretation provides apport for the proparation ban the non-node sequence	This information is required in a statement for Court.  The statistical interpretation provides apport for the proposition has the noninelistic support for the proposition. This comparison we did the traditional provides apport for the proposition. This comparison we did the traditional provides apport for the proposition has the most of the statement for court.  The noninelistic support can be excluded as a potential contributor to the DNA profile document for the traditional provides in appoint in a statement for the proposition with the provides appoint of the observations in require it is a statement for the traditional provides appoint the traditional provides appointed in the traditional provides appointed by the statement.  This is interpret to a statement is not stated for manifold interprotection date to the tradition of the state of the tradition of the tradition of the tradition of the state of the tradition of the tradition of the state of the state of the tradition of the tradition of the state of the state of the tradition of the state of the	1921 - seponed pritin - such opdate Submitted II Bed on 197 P921 - reported	 Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU Change recommended including task information:	SC10 SC11 CPU DRP1	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsultable for interp or comparison	Integration, A reference evidence surgel aduated to eposted efficiency and a substantiant regard of the substantiant for Court. The statistical mergeneous provides suggest of the proposition that the normalism surgest comparison was done to integrate a particular to the proposition that the normalism surgest of the proposition of the surgest of a surgest of an exploration surgest of the surgest of an exploration surgest of the surgest of an exploration of the surgest of the surgest of an exploration of the surgest of the surgest of the surgest of the surgest of the surgest of the surgest frage the provide surgest of the surgest of the surgest of the surgest of the surgest of the surgest frage the bar substantiant for DMA were detected in the surgest of the surgest of the surgest of the surgest frage. The surgest of the surgest of the surgest of the surgest frage the bar surgest of the surgest of the surgest of the surgest frage the bar surgest of the surgest of th	sight change to suggested wording. Removed 'mated'. sight change to description and discussed of discussed analy been created damps in exp comment	SC10 SC11 CPU	Burgach sheek - sapports non contribution Burgach sheek - Backaded Complex profile or comparison Statute processing	comparison is other mominated surgests interference existence sample should be provided if this information is required in a disearch for Court statement in the court of the sample should be supported the proposition that the support of the proposition that the mominated auguest that no contributed be for intelligence purposes only. A reference widence asingle back to provided from the contributed be provided from the contributed on the sectioned as potential contributor to be DNA profile. This terminantly tage number of contributors and/or the final section of a section of potential types number of contributors and/or the final section of a section potential types number of contributors and/or the final section of a section of the sample and or the DNA profile. This terminantly and the section of a formation to the sample and or both the top the sample and the section of the DNA analysis. Low levels of DNA works and a believels to the back and the section of the DNA analysis. Low levels of DNA works and the final contribution of the profile of the top the contribution and the back and the section of the top the the back halo and the back back and the top the termination of the top the section of the top the termination of the section of the top the termination of the top the top the top the top the top the termination of the top the top the top the top the top the termination of the top the top the top the top the top the top the termination of the top	Support change Support change Refer to Paula Brooto Support change Support change Refer to Paula Brooto - sight changes recommended
SCSNC SCANM 1BPPSR AINT CMPU	Suspect check - supports non contribution Suspect check Action - No Match Preservices I and a support All Seam conservations and professional and a support and professional and a support and professional and a support and professional and a support processing	for Cost: The statistical integration provides support for the proposition that the normality asserts have not contributed to this muse DMA profile. This comparison was done for intelligence proposes only. A method was not been assessed to provided if this internation is required in a submitted to cost: The normality is an example should be provided in this internation is assessed to a submitted to cost. The normality is annual pro- sidence of the solid base of the solid of an appendix the for blood (TMB) and was submitted for the normality is annual pro- tical framework and provides the for blood (TMB) and was submitted for the normality large names of costs and the provided in the provided in the solid of them to the solid base on the scattered of the normality large names of costs and the base can be an excepted on the solid base on the scattered of the normality large names of costs and the limited amount of information with the DMA profile. The DMA area (see a for the formation of the limited mount of the solid base on the solid base can be can be assessed This limited and pointered to be a solid base on the limited amount of information with the DMA profile. The DMA area (see a control This limited and pointered to be a solid base on the limited amount of the simulation of the scattered to be assessed for the the operation of the scattered and the limited and limited and the limited and t	The information is required in a statement for Court.  The information is required in a statement for Court.  The statistical interpretation provides august for the proposition that the normalical august has not contributed to this mance DAA profile. This interprets include the provided if this information required in a statement for court.  The control of this information is not a statement of the august in the august in the august in the august in the august include the provided if this information required in a statement for court.  The control of this information is not august in the august information  August and august in the august and a statement for court.  This information august and the august and august and the august and  August and august and august and august and august and  August and august and august and august and august and  August and august and the limited august and potential provides the  This information august and the limited august and potential provides the  Court product  This information august and the limited august and potential provides the  Phases and a state the DUA Results Management on the  Court product  This information august and the DUA Results August and  This information august and the binded august and  August and august and  Dual product  This information august and the DUA Results August and  Au	PP21 - reported pretim - such spidele Appretim - such spidele Appretim - such spidele PP21 - reported PP21 - rep21 - reported PP21 - rep21 - r	 Ni change recommended by RMU Ni change recommended by RMU Ni change recommended by RMU Ni change recommended by RMU Change recommended by RMU Change recommended including lask information.	SC10 SC11 CPU D#P1	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsuitable for interp or comparison DNA insufficient for further processing	Integration, A reference existence sample disculta les provided frain information in super- magnetic in a astamment for Court. The admitted integration provides support that and courter of the court of the admitted information and the court of the court of the court provides and the court of the court of the court of the court of the court of the court of the court of the admitted support can be excluded as a protocol and the court of the court of the court of admitted support can be excluded as a court of the court of the court of the court of the admitted support can be excluded as a court of the court of the court of the admitted of the the court of the court of the admitted of the court of the court of the admitted of the court of the court of the annexes of information with the follow profile. This temperature is not one of the follow of the court of the court of the court of the annexes of information with the DDM profile. This temperature is not observed of the the the court of the court of the second of the court of the court of the court of the court of the annexes of information with the DDM profile. This temperature is not observed of the the the court of the court of the second of the the the court of the court of the second of the the the court of the court of the second of the the the court of the court of the second of the the the court of the court of the second of the the the court of the court of the second of the the the court of the court of the second of the the the court of the court of the court of the the court of the second of the court of the court of the second of the the the the court of the court of the court of the second of the the the court of the court of the court of the second of the the the court of the court of the court of the the court of the second of the the the court of the cour	sight change to suggested wording Removed Intend". Slight change to description not discussed of discussed made been coulded descript in any comment change in any comment	SC10 SC11 CPU DFP1	Bugent sheek - supports non contribution Bugent sheek - Excluded Complete profile or comparison NAA madificient for further processing	comparison is other monwaled supports memory of the information is required in a movie of the information is required in a the statistical integration provides support of the proposition that the the statistical integration provides to statistical integration provides to information in the statistical of the transformer purposes only. A reference without the statistical integration is a statistical to control integration of the statistical of the control integration is a statistical of the meaning of integration on the IOM profile integrating integration on the IOM profile meaning of integration of the statistical of the meaning of the statistical of the statistical of the meaning of the statistical of the statistical of the meaning of the statistical of the statistical of the statistical of the statistical of the meaning of the statistical of the	Support charge Support charge Side to Paula Brocks Disport charge Rate to Paula Brocks Disport charge Refer to Paula Brocks - sight charges montmanded
SCSNC SCANM 1BPPSR AINT CMPU DIFP	Suspect check - supports non contribution Suspect check Action - No Match Presumptive blood test poss advantated creatility panding Complex mode profes usualize for eterp or comparison ONA multificant for further processing Name Scalable for surgicity Part Incolated Not suitable for analysis	for Cost:	The information is required in a statement for Court. The statistical interpretation provides apport for the proposition had the nonmatical support has not contributed to the inmed DAA portion. This comparison was done to interflow particular of the proposition. That has many the statement of the interpretation of the provide in a statement for court. The nonmatical provides if the information is negline if in a statement for court. The nonmatical support can be excluded as a potential contributor to the DAA potie dealmed from the termination. The information because of the information of the toto of (108) and are scientification of the information of the proposition of the information are scientification of the information of the information of the information contributors. This mutuate is not statistical for manifold integration due to align the complex proposition (108) and provides the tradition of the DAA poties. This benchmarphic and calculated for DAA and provides the information within the DAA poties. The benchmarphic and calculated for DAA and provides the information within the bases send a lask to DAA Results despendent by (200 profile) fra- sample in regulated to the taxesses for future sciences of the these taxes for the provides the calculated for the processing. The benchmarphic and calculated for the processing. The science of the processing and the integration of the another the top of the science of the processing. The base top is a lask to provide the top of the processing.	PP21 - reported protein - auto opdide protei	NE change recommended by RMU Change recommended including task information. NE change recommended by RMU	SC10 SC11 CPU DSP1	Suspect check - susports non contribution Suspect check - Excluded Complex profile unsultable for interp or comparison DMA insufficient for finality	Integration, A reference existence sample double to provide the information is an equariant in a subsemption for Guide the additional provides subsemption. The additional control of the subsemption of the han end control and the the Subsemption of the han end control and the subsemption of the subsemption in the subsemption on a subsemption of the subsemption provided of the information is equated in a subsemption on a subsemption of the subsemption provided of the information is equated in a subsemption on a subsemption of the subsemption additional for control and the formation additional for the subsemption of the subsemption additional for the subsemption of the subsemption and the subsemption of the subsemption and the formation and potential for DRA provides and the subsemption of the subsemption and the formation with the DRA public the Benchmanism was automatical for DRA public additional to a subsemption of the subsemption and the formation and potential for DRA public additional to a subsemption of the subsemption and the formation and potential for DRA public additional to a subsemption of the subsemption and the formation and potential for DRA public additional to a subsemption of the subsemption and the subsemption of the subsemption of the subsemption of the subsemption and the subsemption of the subsemption of the subsemption of the subsemption and the subsemption of the	sight change to suggested wording Removed Interf. sight change to description of discussed indicated change in say comment change in say comment change in say comment	SC10 SC11 CPU DIFP1	Busset thek - support non contribution Excluded Complex profile unsatisfies for inter complex profile unsatisfies for inter complex profile unsatisfies for inter complex profile	comparison is other mominated supports momentum is other mominated supports memory and the information is required in a disease of the information is required in a disease of the proposition that the mominated auguest that no contributed by support of the proposition that the mominated auguest that no contributed by the information and the provided frag- tion of the proposition that the information any product to a statement for advance any product calls are excluded as a potential contributor to the DNA profile advanced fram the transmission. The information appendix contributor to the DNA profile advanced fram the transmission. The information potential upper number of contributors and/or the limits are of advanced and potential upper number of contributors and/or the limits are of advanced potential upper number of contributors and/or the limits are on dustributed for frammation are and advanced and a state of Limits UNA profiles are quarked as a last of 2014 of the simulation are subscheduted assessed for further processing.	Support change Support change Refer to Paula Brocks Support change Refer to Paula Brocks - slight changes Refer to Paula Brocks - slight changes Refer to Paula Brocks
SCSNC SCANM 1BPPSR AINT CMPU	Suspect check - supports non contribution Suspect check Action - No Match Presumption blood set pos- al area non trained Complex miced gradie unsubble for webp or companion or companion of watcher processing Name Tooland Not subble for analysis	for Cost.  In the statistical interpretation provides apport for the proposition that the norm-lated sequent than not contributed to this mixed DMA profile. This comparison was done for intelligence proposes only, Alvertisme evidence and provides of this information is experted in a statement for out.  The norm-lated subject can be excluded as a potential contributor to the DMA profile The information is experient in a statement for out.  The norm-lated subject can be excluded as a potential contributor to the DMA profile The information is the information.  The norm-lated subject can be excluded as a potential contributor to the DMA profile datamet for information is denotating in the information is denoted in the information when the information when the information is denoted in the information when	This information is required in a statement for Court. The information is required in a statement for Court. The initiation interpretation provides apport for the proposition that the normatical suspect has not contributed to this initiated DAA profile. This comparison was done to initiation as provide in a submitted to Court. The normatical suspect can be excluded as a potential contributor to the DAA profile advanced from the excluded as a potential contributor to the DAA profile advanced from the excluded as a potential contributor to the DAA profile advanced from the excluded as a potential contributor to the DAA profile advanced from the excluded by an excluded to the exclusion of the excluded by an exclusion of the block (1MB) and All senses for the advanced from the exclusion of the block (1MB) and All senses for the advanced by the initial amount of information within the CMA profile. This flomituating base advanced for DAA analysis. Low levels of DAA were detected in the surgery and it as not advanced by the block (1MB) and the surgery and its assessed for further processing. This flomituating base advanced for the processing.	PP21 - seponted profilm - auto spolate Automatically list or PF PP21 - reported PP21 - reported PP21 - reported	Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU Nil change recommended by RMU Change recommended probability for the second Change recommended including test information.	9010 S011 CPU CPU	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsultable for integration Complex profile unsultable for comparison	Integration, A reference existence surgel adapted to a provided the information is surged to adapte and the information is supported to the statistical responses approximately and the statistical responses of the information is support of the providence existence analyse is total of the information and the information is supported in the information is supported in the information of the information is supported in the information is and the information is supported in the information and the Information is an information and the Information is an information in the information is an information and the information is an information within the DNA profile. This information within the DNA profile manual of information within the DNA profile ansaudic of the information within the DNA profile ansaudic of information within the DNA profile. This information within the DNA profile ansaudic of information within the DNA profile ansaudic of information within the DNA profile.	eight change to suggested worting Removed Interd. Sight change to description not discussed ond discussed disards with the line which has alloady been created change in easy comment.	SC10 SC11 CPU DIFP1	Bugect check - supports non contribution Bugect check - Excluded Complex profile ar comparison Units processing	comparison is other mominated surgeds interference existence sample should be provided if this information is required in a the statistical and existence of the statistical support of the proposition that the the statistical and existence of the statistical support of the proposition that the the statistical and existence of the statistical transformer purposes only. An effective transformer purposes only. An effective transformer purposes only and the statistical transformer purposes only and the statistical dataset of the the statistical transformer of continue of the statistical transformer of existing the statistical transformer of existing the statistical transformer of purposes that the statistical transformer of the CDM particle. These statistical transformer and the CDM particle parts and the statistical transformer of contributions and the CDM parts of the statistical to the CDM parts of the statistical to the statistical transformer of contributions of the statistical transformer of the statistical to the statistical to the CDM parts of the statistical to the statistical transformer of the statistical to the statistical to the CDM parts of the statistical to the statistical to the CDM parts of the statistical to the statistical to the the CDM parts of the statistical to the statistical to the statistical transformer of the statistical to the statistical to the statistical transformer of the statistical to the statistical to the statistical transformer of the statistical to the stati	Support change Support change Refer to Paula Briocito Refer to Paula Briocito Refer to Paula Briocito - slight changes recommended
SCSNC SCANM 18PPSR AINT CMPU DFP FENSA HESRP	Suspect check - supports non contribution Suspect check Action - No Match Presumption blood for proc. All Rem none tested and remaining and remaining and all rem none tested and remaining and remaining and remaining and remaining and remaining and remaining and remaining and remaining and remainin	for Cost:	The information is required in a statement for Court. The additional interpretation provides augent for the proposition that the manual suggest has not contributed to this make DMA profile. This manual suggest has not contributed to this make DMA profile. This manual suggest strategies are the interpretation is required in a distinct for court. The interpretation suggest can be enabled as a prioritid contribution to be DMA profile distances that the enabled is a split- strate interpretation of the interpretation of the profile and the profile distances in the alemandary of the profile and the strategies in the split strategies are approximated in the strategies interpret to the simulation of the profile of the the DMA profile distances in our studies for monoral profile and the the the DMA profile distances in our studies for monoral profile and the profile and and the the DMA family is being a strategies. The beside of DMA aver- detection is not acaded for monoral and potentially gives DMA profile. The DMA based being and annotation the DMA aver- detection is not acaded for monorant of the DMA aver- based at this to be DMA Results being and average and the Prate temportagies are statistical for DMA average is a may be DMA based based for the statistical based on the langement of the DMA average distances and detection consultable for DMA average is a statistication of the statistication is a monoranged and the DMA based based and the statistication is the statistication of the statistication	PP21 - reported prilin - sulta update PP21 - reported PP21 - r	NE change recommended by RMU NE change recommended by RMU NE change recommended by RMU Change recommended by RMU Change recommended by RMU Change recommended by RMU NE change recommended by RMU	SC10 SC11 CPU DRP1	Support non support non contribution Support check - Excluded Complex profile unsutable for interp or comparison	Integration, A reference encloses sample disculta la provided framiliarity in terms of the square in the automation provides support that and the automation provides support that automation integration provides support has not controlled to this DNA profile. This comparison was able to integration provides and a provided of their information is equated a automation support of the DNA profile automation sub-to the DNA profile automation sub-to their the CMA profile automation sub-to their the company and automation of automation and for the hindle automation of the automation of the hindle of the form automation of the automation of the hindle of the form automation of the automation of the hindle of the form automation of the automation of the hindle of the automation automation of the automation of the hindle of the automation	sight change to suggested wording Removed travel. adjust change to description ord discussed of discussed change in exp comment change in exp comment ord discussed	SC10 SC11 CPU	Supert dieck - support non contribution Excluded Complex profile insulatie for integr comparison DAA neuralitient for Laffer processing	comparison to give momentation supports interpretention of the second second second second second provided of the individual in required in a the statistical interpretention provides sequent for the proposation that the the the statistical interpretention that the second sequent for the proposation that the second second for intelligence purposes only. A reference interpretention of the second second second second for intelligence purposes only. A reference interpretention of the second second second second for intelligence purposes only. A reference interpretention of the second second second second for intelligence purposes only. A reference interpretention of the second second second protection of the second second second second reference of the second second second reference of the second second second reference of the second second second second reference of the second second second second reference of the second second second reference of the second second reference of the second second second reference of the second second reference of the second second reference of the second second second reference of the second second reference of the second second second reference of the second second second reference of the second second second second reference of the second second second second reference of the second second second second second reference o	Support change Support change Support change Support change Support change Support change Support change Support changes Support chang
SCSNC SCANM 18PPSR AINT CMPU DIFP HENSA HESRP	Suspect check - supports non contribution Suspect check Action - No Match Presumptive blood test pos. 2018 Emission and and and and and 2018 Emission and and and and anterp or comparison processing 104A multificant for further processing 104F located. Not suituate for analysis 104F located. Submitted results	for Cost: The Adatabal Helepretation provides apport for the propatition bat the nonmatic secret. The Adatabal Helepretation provides apport for the propatition bat the nonmatic secret. The notice that is not the second provide a third the provide of this information is requeries in a seasoner to could an apportant contributor to the DNA profile chained in the information. The nonmatic support can be excluded as a potential contributor to the DNA profile chained in this information. The information bate and the provide of this information is information this information. The information bate contributor to the DNA profile of the information bate and the provide of the information of the the information bate contributor of the third profile on the bates. The information bates contribution of the other information and of information within the DNA profile. This internation bates and profile that DNA profile and the appropriately relating to the amplies of it was not admitted for DNA analysis. Low levels of DNA wave addicated in the sample and it was not admitted for DNA analysis. Low levels of DNA wave addicated in the amplies and it was not admitted for DNA analysis. Low levels of DNA wave addicated in the sample and it was not admitted for DNA analysis. Low levels of DNA wave addicated in the and contrability of the approximation, researching of the parent livel their appropriate), a contraben of processes.	The information is required in a statement for Court. The information is required in a statement for Court. The statistical interpretation provides apport for the proposition has the normatide support of contribution in require in a statement for court. The commutation apposite if the information is require in a statement for court. The commutation support can be excluded as a potential contributor to the CMA potential support can be excluded as a potential contributor to the CMA potential courses of the information. The commutation of DMA factors are presenting in a statement for any association for the information. This learning and the state information in the information are according to DMA factors. The statement of the contributors. This minutes is not stated for maximally alterpretation and makes of combutors and/or the Information and the information within the DMA profile. This learning are statement for for DMA analysis. Low leads of DMA were detected in the statement on the information and the low of the statement of combutors and/or the Inform processing. This learning are statement for for DMA analysis. Low leads of DMA were detected in the statement on the inform processing. Hard's were obtained and the analysis. They were cleared analy- ments and a statement on the inform processing. Hard's were cleared and any analysis. They were cleared analy- ments and a statement on the inform processing. Hard's were cleared on the information were cleared analy- ments and the information of the inform processing. Hard's were cleared on the information were cleared analy- ments and the information of the information were cleared analy- ments and the information of the information were cleared analy- ments and the information of the information were cleared analy- ments and the information of the information were cleared analy- ments and the information of the information were cleared analy- ments and the information of the information were cleared analy- ments and the inform	PP21 - seponted protein - auto-specifie protein - auto-specifie protein - auto-specifie pP21 - reported pP21 - rep21 - reported pP21 - rep21 - reported pP21 -	Nil change recommended by RMU Change recommended lincluding task information- Thi change recommended lincluding task information- Nil change recommended by RMU Nil change recommended by RMU Nil change recommended lincluding task information- Nil change recommended by RMU Nil change recommended by RMU	SC10 SC11 CPU DPP1	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsultable for integration Complex profile unsultable for integration	Integration, A reference existence surgel aduated to exposed of the information is required in a statististic for Court. The statistical responsibility of the statistical responsibility of the statistical responsibility of the statistical responsibility of the statistical responsibility of the statistical responsibility of the statistical responsibility of the statistical responsibility of the statistical statistical statistic distances of courts and the statistical statistical distances of courts and the statistical statistical distances of courts and the to DNA profiles. This female statistical statistical statistical distances of the statistical statistical statistical statistical distances of courts and and potential lying and and potential control to the statistical statistical statistical transportation also be then as complex DNA profiles. This female statistical statistical statistical statistical transportation also be then as complex by the responsibility of the automoust and be then the complexity and the combuters and the test the complexity and the combuters and the test the contexity of statistical statistical statistical to DNA and the court and the combuters and the test the complexity and the combuters and the test the complexity and the combuters and the test the complexity of statistical statistical to DNA and the combuters and the test of the combuters and test the test the complexity of complexity the assessed for further proceeding.	sight change to suggested working Removed Insect - light change to description not discussed on discussed change in exp comment change in exp comment change in exp comment not discussed	SC10 SC11 CPU DIFP1	Superi diverk - supports non contribution Support diverk - Catabated Complete profile unsatisfield for integr complete for int	comparison is other mominated surgeds interference existence sample should be provided if this information is required in a the statistic fraction on provides support of the proposition that the provided support is not controllated be the statistic fraction on provides support for the proposition that the provided support is not controllated be for initiging programs only. A reference existence sample should be provided if not the mominate support is not controllated be the initiation of the statistical control of the existence sample should be provided if not exist. The mominate support is a satistation for cont. The mominate support is a satistation for comparison of the international and a statistical control is satisfied and a statistical from this iteritiamption profile. This thereinamption and the the the statistical for total and the the the scale statistical for the the the scale statistical for total and the the the scale statistical for total and the the the scale scale statistical for the the the scale scale scale statistical in the the the scale scale scale statistical for the the the scale scale scale scale scale and the scale scale scale scale scale scale and the scale of the their processing.	Support change Support change Refers to Paula Broots Support change Support change Refers to Paula Broots Support change Refers to Paula Broots Refers to Paula Broots
SCSNC SCANM IBPPSR ANT CMPU DIFP HENSA HENSA	Suspect check - supports non contribution Suspect check Action - No Match Persongene block der pro- discher State - No Match Persongene motor gende Alf som non tende Complex motor product aussider for aller per companion aller per companion aller per companion personanty in a located. Not suitable for analysi infair located. Not suitable for analysi aller located. Scientified er analysi pending.	for Cost.  The statistical integration provides support for the proposition that the normality asserts have not costballed to this must DMA profile. This comparison was done for intelligence proposes only. American cost of the ample should be provided in this internation is required in a statistical disport on only. Ample should be provided in this internation is required in a statistical disport on only.  This international support on the ample should be provided in this internation is required in the should be approximated in the statistical disport of the ample should be provided in the should be provided in the should be provided in the internation is the should be approximated in approximate the should be provided in the should be provided be assessed by the should be provided in the should be provided in the should be provided by th	The information is required in a statement for Court.  The information is required in a statement for Court.  The statistical interpretation provides acquort for the proposition that the normated acquerch has not contributed to this mance DAA profit. This manually acquerch has not contributed in a statement for court.  The contributed acquerch can be enabled on a spatient of contributer to the DAA profits database the lambda acquerch has acquered in a database.  This terrolutery is that data provides acquerch acquered in a database of the provides acquerch can be enabled on a spatient or contributer to the DAA profits database the lambda acquered in a spatient or contributer to the DAB profits that the courts and the statement of DAB profits that the courts and the lambda acquered in a spatient DAB profits that the courts and the lambda acquered in a spatient DAB profits that the courts and the lambda acquered in a spatient DAB profits that the lambda acquered in a set showed on DAB profits that the lambda acquered in a spatial profits and the profits and the lambda acquered in acquered in the lambda acquered in the profits acquered in the lambda acquere	PP21 - reported	Hi change recommended by RMU     Change recommended by RMU     Change recommended by RMU     Hi change recommended by RMU     Hi change recommended by RMU     Hi change recommended by RMU	SC10 SC11 CPU DEP1 DEP1	Suspect check - suspect neck Camples profile monstable for interp or comparison	Integration, A reference excision sample disculta les provided frain information in sequeral in a astamment for Court. The admition integration provides support that and a stamment for Court. The admition integration provides support has not controlled to the DNA profile. The comparison was also for the DNA profile. The comparison status does not admitted to a sup- scitation of the Instagnees provides and the astamment or court. The normality support can be excluded a a protectual control being the DNA profile. The temperature status for meaningh admitted to the temperature of the DNA profile takened for court. The temperature status for the second of annexes of information with the DNA profile takened for the temperature of the second annexes of information with the BNA profile takened for admittance and the facilitation of the temperature of the second of the second annexes of information with the DNA profile the temperature of comparison and the temperature of comparison and the temperature the memory of the associated for further DNA profiles The comparison of the second temperature of the base associated for further processing.	sight change to suggested wording. Removed traved : slight change to description not discussed ord discussed danage in each comment change in each comment rol discussed not discussed	SC10 SC11 CPU DIFP1	Support check - support check - contribution Support check - Excluded Contractions of comparison CORA resultioner for white processing Corporation	comparison is other momentation supports interpretention of the second second second second second periodical of the information is required in a the statistical interpretention periodical support of the proposation that the second second second second second second second second to interpretention second second second second ter intelligence purposes only. A reference production of the second second second second second ter intelligence purposes only. A reference production of the second second second second ter intelligence purposes on the NMA periodic ter intelligence purposes on the NMA periodic ter intelligence purposes on the NMA periodic ter intelligence and second second second second ter intelligence and second second second second ter intelligence and second second second second territorial interpretation due to be NMA periodic categories of the territory second second second territorial interpretation due to be the territorial second second second second second second territor between the territorial second second territorial interpretation due to the territorial second second second second second second territorial second second second second territorial second second second second territorial second second second second second territorial second second second second territorial second second second second territorial second second second second territorial second second second second second second territorial second second second second second second second territorial second sec	Support charge Support charge Refer to Paula Bitocto Refer to Paula Bitocto
SCSNC SCANM IBPPSR AINT CMPU DIFP HLNSA HLSRP INTER4	Suspect check - supports non contribution Suspect check Action - No Match Presumptive blood teat coss downtheal events people Promptive most people receiptive results for every or comparison CRA insufficient for further processing Hair located. Not subtable for analysis Hair located. Submitted results results professional and the subtable processing	for Cost. The advanced interpretation provides apport for the proposition that the norminate august for advanced interpretation provides apport for the proposition that the norminate august for advanced interpretation provides apport for the proposition that the norminate august for advanced interpretation provides apported advanced in the provide of the interpretation for advanced interpretation provides apported advanced in the provide of the interpretation for advanced interpretation provides approximate the for the interpretation for advanced interpretation provides approximate the for the interpretation for advanced interpretation provides approximate the for the interpretation for advanced interpretation approximate approximate the for the interpretation for the interpretation approximate approximate advanced for the interpretation approximate approximate and provides for the interpretation approximate approximate advanced for the interpretation approximate approximate advanced for the interpretation advanced interpretation advanced interpretation for advanced interpretation advanced interpretation advanced the interpretation for the interpretation advanced interpretation advanced the interpretation for the interpretation for for the VMA profile. The event advanced for the interpretation of the interpretation advanced interpretation for the interpretation of the interpretation of the interpretation of the interpretation for the interpretation of the interpretation of the interpretation of the interpretation for the interpretation of the interpretation of the interpretation of the interpretation for the interpretation of the interpretation of the interpretation for the interpretation of the interpretation of the interpretation for the interpretation of the interpretation of the interpretation for the interpretation of the interpretation of the interpretation for the interpretation of the interpretation of the interpretation for the interpretation of the interpretation of the interpretation of the interpret	The information is required in a statement for Court. The information is required in a statement for Court. The statistical information provides august for the proposition had the memory of the statement of the statement of the statement for court. The information is required in a statement for court. The information is the statement of the statement of the statement of the statement of the statement of the statement of the statement of the statement of the statement of the statement statement of the statem	IP21 - sponded     Image: sponded image:	Nil change recommended by RSNU Nil change recommended by RSNU Nil change recommended by RSNU Change recommended by RSNU Change recommended by RSNU Nil change recommended by RSNU	SC10 SC11 CPU DSP1 DECOMMESSION see P	Support non contribution Support non contribution Support Anal Complex profile comparison DNA insufficient DNA insufficient SUR	Interpretation, A reference on excision cample disculate is provided the information is a square in its automation for Gaussi the automation of the information of the the automation of the automation of the automation of the information of the automation of the automation provided of the information on equivalent and automation of the information of the automation provided of the information of the automation provided of the information of the automation automation of the information of the automation automation of the information of the automation of the information of the automation automation of the automation of the automation automation of the automation of the information automation of the automation of the automation of the automation automation of the automation of the automation of the automation automation of the automation of the automation of the automation automation of the automation of the automation of the automation automation of the automation of the automation of the automation automation of the automation of the au	slight change to suggested wording Removed Insect light change to description and dataset of descended change in exp comment change in exp comment ind discussed	SC10 SC11 CPU DJFP1	Bugent dwok -     separat non     separat non     separat dwok -     Excluded     Complex profile     comparison     Complex profile     comparison     Complex profile     comparison     compariso	comparison is other momentation supports interference evidence sample should be provided if this influence. The sample should be provided if this influence is a support of the the statistical directory and the sample should be support of the proposation that be the statistical directory and the sample should be detained for this damakange. This memory and a subserve to be DNA profiles not statistical to make the sample sample should be and statistical to make the sample sample should be and statistical to make the sample sample sample sample sample sample sample samples. The both profiles not statistical to the samples is being the directory of the samples of the samples is being the directory of the samples of the samples is being the directory of the samples of the samples is being the directory of the samples of the samples is being the directory of the samples of the samples is being the directory of the samples of the samples is being the directory of the samples of the samples is being the directory of the samples of the samples is being the directory of the samples of the samples is being the directory of the samples of the samples is being the directory of the samples of the samples is being the directory of the samples of the samples is being the directory of the samples of the samples is being the directory of the samples of the samples is being the directory of the samples of the samples is being the directory of the samples of the samples of the samples is being the samples of the samples of the samples of the samples is being the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the sample	Support change Support change Refers 19 August Biscoto Support change Refer to Paula Biscoto - slight changes Refer to Paula Biscoto - slight changes Refer to Paula Biscoto - slight changes Refer to Paula Biscoto - Slight changes
SCSNC SCANM 18PPSR AINT CMPU BEPSR HENSA	Susped check - supports non contribution Suspect check Action - No Match Protumptive block lest post All ferm once traded Complex most particle watep or comparison watep or comparison Protosal Substrate for analysis Hair located, Not suitable for analysis Protosal Substrate and protosal Substrate Research Regid	for Cost: The statistical interpretation provides apport for the propagation that the norm-lated sequent has not contributed to this mixed DM profile. This comparison was done for intelligence properses only, Alexandre exceeded as a potential coefficient to the intelligence properses only. Alexandre exceeded as a potential coefficient to the DMA profile that many the statistical sequence of the second as a potential coefficient to the DMA profile that many the second as a potential coefficient to the DMA profile that many the second as a potential coefficient to the DMA profile that many the profile profile that the second as a potential coefficient to the DMA profile that many the profile profile that the second as a potential coefficient to the DMA profile that the comparison that the profile that the the the profile of the DMA profile the temportary the temportary that the profile with multiple coefficients. The moture is not statistical for manippil integration due to where it of board (TMA) and we submitted the temportary the statistical coefficient due to the temportary and the second of the temportary that the coefficient due to the temportary and the second of the temportary temportary that the temportary and the second of the temportary temportary that the temportary and the temportary and the temportary and the second coefficient coefficient of the temportary of the parent time (where appropriate), and the second coefficient coefficient of the temportary of the parent time (where appropriate), that the collection on the temportary time to the temportary and temportary and temportary the temportary temportary temportary temportary temportary temportary the temportary temportary temportary temportary temportary temportary the temportary temp	This information is required in a statement for Court. The information is required in a statement for Court. The statistical interpretation provides apport for the proposition that the interpretation statement of the statement	PP21 - reported	Ni change recommended by RMU Ni change recommended by RMU Ni change recommended by RMU Ni change recommended by RMU Change recommended pelkAU Change recommended pelkAU Ni change recommended by RMU Ni change recommended by RMU Ni change recommended by RMU	SC10 SC11 CPU CPU DECOMMESSION use RC	Suspect check - supports non contribution Suspect check - Excluded Complex profile comparison CMA insufficient for further processing	Integration, A reference existence surgel advances of a statisticant for Court. Together line a statisticant for Court. The statistical responsibility of the statistical responsibility of the Court of Court. The statistical responsibility of the COURT of Court of the Court of Court. The statistical responsibility of the COURT of Court of the Court of C	inght change to suggested worting Removed Interest Sight change to description and discussed allowed been created change in easy comment of discussed and discussed	SC10 SC11 CPU DFP1 INTER4	Superi diverti seporte diverti seporte di esti seporte di esti	comparison is other mominated surgedial interference existence sample should be provided if this information is required in a the statistical and existence of the second support of the proposition that the the statistical and existence of the second support of the proposition that the the statistical and exist the second second the statistical and exist the second second the statistical and exist the second second the support of the proposition that the support of the proposition that the the statistical and the second second the second of the second second second the second second second second second second relation of the second second second second existence any second second second second existence and the second second second existence and the second second second relation that the second second second sector the second second second second second second second second second second second second second	Support change Support change Support change Refer to Paula Briototo Decommission - see RESUR
SCSNC SCANM 18PPSR AINT CMPU DEP FENSA FENSA FESRP INTER4	Suspect check - supports non contribution Suspect check Action - No Match Presumption block test pos- tion and and a support of the support All term none tested and term none te	Nor Cost: The adaptional Interpretation provides acquord for the proposition that the norminated acquerits have not contributed to this mixed DMA prefile. This comparison was done for intelligence proposes only. Alternative code: a sample should be provided if this internation is acquered to a submitted for code. The interpretation acquerits and the adoptional state prefile and the interpretation of the constrained states of the adoption of the provided in the interpreta- tion of the interpretation acquerits and the adoption of the interpretation of the interpretation of the interpretation of the adoption of the interpretation of the interpretation of the Provide states acquerity in the adoption of the interpretation of t	The information is required in a statement for Court. The information is required in a statement for Court. The statistical interpretation provides apport for the proposition that the normatical support has not contributed to this make DMA pdfM. This many statistical provided the information is required in a statement for court. The interpretation support can be enabled in a splitering contribution to be DMA pdfM dotted the information is required in a subtraction of the DMA pdf pdfM dotted the information is required in a splitering contribution to be DMA pdfM dotted the information is required in a splitering of the DMA pdfM dotted the information is an information. This temperature tested position to a parametritise test for blood (146) pdfM and pdfM dotted the information in appointed by pdfM dotted the DMA pdfM dotted tested in the information is an optimated by pdfM dotted the DMA energy for the information is not unable for more appointed by pdfM dotted tested the DMA energy for the information is not unable the information information in the information information is affered to expected in the information information information the information information is not unable the information information information information is not unable the information information information the information	PP21 - reported	NE change recommended by RMU NE change recommended by RMU NE change recommended by RMU Change recommended by RMU Change recommended including task information. NE change recommended by RMU NE change recommended by RMU NE change recommended by RMU	SC10 SC11 CRU DRP1 DECOMMESSION see R	Support non contribution	Integration, A inference excision sample disculta la provided first infernation in trading the statement for Cause the admitest in respectively and the statement of the admitest integration provides suspect that and control the inference provides suspect that may be admitest the statement of the cause inference of the inference provides of a provided of their inference provides of a statement of orcult.	slight change to suggested wording. Removed treat? slight change to description not discussed of discussed change in any comment not discussed not discussed	SC10 SC11 CPU DIFP1 INTER4	Sugard deck - support next - control/con- control/con- control/con- control/con- comparison - Complex prolife- monitable for prolife- dational Reverk Reverk	comparison to give momentation supports interpretention of the inter	Support change Support change Support change Refer to Paula Brocks Support change Refer to Paula Brocks Refer
BCBNC SCANM TIBPPSR ANT CMPU HENSA	Supped check - supports non contribution Suppert check Action - No Match Presumptive blood test pos. 2014 Emilion - No Match Present - State - State - State Processing Filter Incided. Substituted results Provided Statement results Filter Incided. Statement results Present Reput	for Cost:	The information is required in a statement for Court. The statement for Court is the statement for Court is the statement of the sta	PP21 - seponed	Nil change recommended by RMU Change recommended field-ding task information Nil change recommended by RMU	SC10 SC11 CFU DFP1 DECOMMESSION see IR	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsustation comparison CNA insufficient for further processing	Interpretation, A reference on extension assumption devolution is provided the interfactors assumption to partie of its additional competence provides assumption that additional competence provides assumption that additional competence provides and the provided of the interfactors are provided in a advanced to competence and the COM parties that additional competence and the provided of the interfactors are provided of an advanced to competence and the provided of the interfactors are provided of an advanced to competence and the advanced to make a complex DAM parties. The formations are provided in a advanced to make an advanced on advanced to the second second to the provided of the the the advanced to make an advanced on advanced of the the advanced on the test and the advanced of the the advanced on the test and the advanced of the the advanced on advanced of the test advanced on the advanced of the test advanced of the Advanced on advanced of the test advanced of the Advanced on advanced of the test advanced of the Advanced on advanced of the test advanced of the advanced of the	sight change to suggested working Removed Insect - light change to description and discussed change in sep comment change in sep comment ind discussed	SC10 SC11 CPU OFP1	Support Alexik - supports non - contribution - Support Alexik - Excluded - Complex profile - and - Complex profile - and - Complex profile - turber processing - - - - - - - - - - - - -	comparison is other mominated surgeds interference existence sample should be provided if this information is required in a difference existence sample should be provided if this information is required in a difference existence and the contentibuted be support of the proposition that the provided arguest in the contentibuted be for initigance purposes only. A reference existence sample should be provided if for the mominate arguest in the contentibuted be for initigance purposes only. A reference existence sample should be provided if for exist. The mominate arguest in a satematic for exist. The mominate arguest can be excluded and a detailed on the horizontal a detailed for mit beautypoints and a detailed on the horizontal patients by programs of complex DNA profile. This DNA profiles in an attailable for experision of the horizontal of a detailable of experision of the horizontal of a detailed patient by program as complex DNA analysis. Now levels of DDA were detected an in the sample and a large of the UNA analysis. Large on Alarge of the UNA analysis the DNA profile.	Support change Support change Support change Refer to Paula Briocito Support change Refer to Paula Briocito Support change Refer to Paula Briocito Refer to Paula Briocito Concentratedd
SCINC SCANI IBPSR ANY CMPU DFP RASA HLSR NTERI	Suspect check - supports non contribution Suspect check Action - No Match Percentry of the Control of the Control Advantation evaluation of the Control Advantation evaluation of the Control Advantation evaluation of the Control Advantation of the Control of the Control Match Control of Science of the Control Network Registion of the Control of the Control Network Registion of the Control of the Control Control of the Control of the Control of the Control Control of the Control of the Control of the Control Network Registion of the Control of the Control of the Control Network Registion of the Control of the Control of the Control of the Control Control of the Control of the Cont	for Cost: The statistical integration provides support for the proposition that the norm-lade support have not contributed in this muse DMA profile. This comparison was done for intelligence proposes only, American control and provided in this internation in register in a statement for work. This monotonic and the statement is a provided in this internation in the statement for more and the statement is a provided in this internation in the statement is a statement for work. This monotonic and the statement is a statement of the statement is the statement from this statement and the statement is a statement of the statement is a statement of the statement is a statement of the statement is a statement of a statement is a statement of the first international provides a statement of the statement is a statement of the statement is a statement of control days profile with multiple contributions. This is used whereas and potentially large number as atometication and to the limited amount of information within the DAA profile. This limitshaming and control days and the statement of the statement of the statement of control days and the limited and out the limited and out the statement is been as atometicate for DAA analysis. Low levels of DAA were decoded the statement is been as atometicate for the statement of the limited and out the limited and out the statement is been to the statement of the statement of the statement of the low levels of DAA were decoded in the statement of the statement of the low levels of DAA were decoded in the statement of the low levels of DAA were decoded in the statement of the statement of the statement of the low levels of DAA were decoded in the statement of the statement of the statement of the low levels of DAA were decoded in the low levels of D	The information is required in a statement for Court. The information is required in a statement for Court. The statistical interpretation provides apport for the proposition that the inner term of the proposition that the information of the proposition of the term of term of the term of t	PP21 - reported	Hi change recommended by RMU     Hi change recommended by RMU     Ni change recommended by RMU     Ni change recommended by RMU     Change recommended by RMU     Change recommended by RMU     Ni change recommended by RMU	SC10 SC11 CPU DEP1 DEP1 DECOMMESSION see P	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsultable for interp or comparison CDNA insufficient for further processing SUR	Integration, A reference excision sample disolute to provide the information is a togated in a statement for Court. The admitted integration provides support that and admitted integration provides support that and control together in the statement of the admitted integration provides support that and controllated to the DNA profile. This comparison was done for the DNA profile admitted for the ternsample. Admitted together is a complex DNA profile admitted for the ternsample. The ternsample game a complex DNA profile admitted for the ternsample. The ternsample game a complex DNA profile admitted for the ternsample. The ternsample game a complex DNA profile amount of information with the DNA profile amount of information and the information amount of information and the information and the information amount of information and the information amount of information and the information amount of information and the information and the information amount of information and the information and the information am	sight change to suggested wording Removed Intend". Slight change to description not discussed on discussed change in each content discussed not discussed	SC10 SC11 CPU DEP1 NTER4	Support Areas apports non contribution Bargard Areas Bargard Areas Bargard Areas Comparison Compari	comparison is other monitories supports interpretention is other monitories supports interpretention exclusions support for the support interpretention exclusion is a support of the support is support for the proposition that the sup- tention of the support of the support of the support is support for the proposition that the support is support of the support of the support of the support of the support of the support of the support is support of the suppor	Support charge Support charge Support charge Refer to Paula Brocto Stormmesion - see RBUR Decommesion - see RBUR
SCINC SCANA IBPPSR ANT CAPU HENSA NTERA	Suspect check - supports non contribution Suspect check Action - No Match Presumption blood ted pos- functional events and an anti- al feats non-trade All feats non-trade and performance and anti- al feats non-trade and performance and anti- al feats on trade and performance and anti- al feats on trade anti- processing feature results no profile obtained reserve Regist	for Cost:               The statistical integration provides acquort for the proposition that the normality acquort	The information is required in a statement for Court. The additional interpretation provides august for the proposition that the memory of the second statement of the statement of DNA profile. This memory is a supervise and combanded to the stress DNA profile. This memory is a statement of the interfaced as a potential combander to be CDA profile dataset to the interfaced as a potential combander to be CDA profile datasets and the interfaced as a potential combander to be CDA profile datasets and the interfaced as a potential combander to be CDA profile datasets and the interfaced as a potential combander to be CDA profile datasets and the interfaced as a potential combander to be CDA profile datasets and the interfaced as a potential combander to be CDA profile. The state is the interfaced as a potential combander to be CDA profile. The state is the interfaced as a potential profile and the state statements of the based as a potential profile and the interfaced as after the state is the interfaced as a potential profile and the comparison of the state is the interface and the interfaced as a state of the interfaced as a state is the interfaced as a potential profile and the profile in required to the interfaced as and potential profile and the profile in required to the interfaced as a potential profile and the interfaced as a profile in required to the interfaced as a potential profile and the interfaced as a profile in required to the interfaced as a potential profile and the interfaced as a profile in required to the interfaced as a potential profile interfaced as a profile in required to the interfaced as a profile come level of DNA were detected in the americand as a profile come interfaced as a profile in required to the interfaced as a profile come level of DNA were detected in the americand as a profile come interfaced as a profile in required to the interfaced as a profile come interfaced as a profile in required to the interfaced as profile come interfaced as a profile in	IPP21 - reported     Implicit       praties - such spatial     Implicit       praties - such spatial     Implicit       PP21 - reported     Implicit	NE change recommended by RMU Change recommended by RMU Change recommended by RMU NE change recommended by RMU	SC10 SC11 CPU CPU DECOMMISSION' see RC DECOMMISSION' see RC	Suspect check - supports non contribution Suspect check - Excluded Complex profile unsultable for integ or comparison Complex profile comparison Complex profile of further processing	Integration, A reference excision ample disorder to provide the information ample disorder to provide the information and trading to the additional excision provides support that additional integration provides support has not contributed to this DNA profile. This comparison was also not to infolgance provides of a provide of their information is equated as a submert for court. The remember support can be excised as a provide of their information is equated as a submert of courts. The information support can be excised as a provide of their information is equated as a submert of courts. The information support and the infoldation of their information and provide support and the information and provide support and the information and provide support and the information and the infoldation amount of information and the infoldation of the information and the infoldation amount of information and protein amount of information and protein am	slight change to suggested wording Removed travel."	SC10 SC11 SC11 CFU CFU CFU	Support divers - separation and - control scale - control scale - control scale - control scale - control scale - control control	comparison is other momentation supports interpretention of the second second second second second provided of the interpretention provides interpretention of the second second second second second for the proposation that the second second for the proposation that the second second second for intelligence paperses only. A reference interpretention of the second second second second second for intelligence paperses only. A reference interpretention of the second second second second for intelligence paperses only. A reference interpretention of the second second second second for intelligence paperses only. A reference interpretention of the second second second for intelligence paperses on the second second for intelligence paperses on the second second for intelligence and second second second second for intelligence and second second second patiential variants and second second for the maching interpretention development of the maching interpretention of the second second action for the Interpretention of the second second second second second second second in the second second second second second in the second second second second second in the second second second second second second for the interpretention second second in the second second second second second second in the second second second second second second second is the second second second second second second second is the second second second second second second second is the second	Support change Support change Support change Refer to Paula Brocks Refer to Paula Brocks Support changes Concommission - see RESUR
SCSNC BCANM IBPPSR JANT CSPU RENSA RTERG	Suspect check - supports non contribution Suspect check Action - No Match Protungete blood best pos- antipation - No Match Protungete blood best pos- al fams now traded Complex most generation water processing complex most generation water processing control - Not subtact for analysis have been and subtaction processing family control - Not subtact for analysis Reserver, Regel	for Cost:	The information is required in a statement for Court. The information is required in a statement for Court. The statistical interpretation provides apport for the proposition that the interpretation approximation as the provide in the information provides approximation as the provide in the information provides approximation as the provide in the information approximation and the provide interpretation approximation approxi	PP21 - reported	Ni change recommended by RMU Change recommended recluding task information Ni change recommended by RMU	SC10 SC11 CPU CPU DECOMMESSION see IR DECOMMESSION see IR	Suspect check - supports non - control on - Suspect check - Excluded Complex profile insulation of for comparison Complex profile comparison Complex profile comparison Complex profile comparison CONA insulficient SUR	Interpretation A reference on exceed a supple double to provide the inclusion. The address in the substantiant for Gould the provide the provide the inclusion. The address interpretation provides support that address interpretation is support. The ampropriate was address to the DNA profile. This comparison was address to the DNA profile. The normality support can be exceeded as a provide of the information is support. The normality support can be exceeded as a provide of the information in the support address to the DNA profile. The normality support can be exceeded as a provide of the information in the support address to the DNA profile. The support of the support the DNA profile. The support of the support of the support address to the support of the support of the support address to the support of the support of the support address to the support of the support of the support address to the support of the support of the support address to the support of the support of the support address to the support of the support of the support of the support address to the support of the	elight change to suggested worting Removed Interd.	SC10 SC11 CPU CPU NTER4 NTER4	Superci check -     support check -     support check -     contribution     Support check -     Contribution     Support check -     Complex profile     complex profile     complex profile     comparison     co	comparison is other monitories supports interference existence sample should be provided if this information is required in a the statistical and the sample should be the statistical and the sample should be support for the proposition that the sample is support of the proposition that the sample is support of the proposition that the sample the statistical and the sample statistical sample statistical support for the proposition that the sample is support of the proposition that the sample is support of the sample statistical sample statistical support for the proposition that the sample is support of the sample statistical sample statistical is supported and the sample statistical sample statistical is supported and the sample statistical sample statistical existing statistical sample statistical sample statistical existing statistical sample statistical sample statistical patient by pages and on patient sample statistical sample statistical sample sample statistical sample statistical patient by pages sample statistical for DNA analysis. Low leads of DDA ware desceled when the DDA patients and statistical sample statistical samples statistical sample statistical samples statistical samples statistical sample statistical samples statistical samples samples statistical samples statistical samples and statistical samples statistical samples and statistical samples statistical samples	Support charge Support charge Support charge Refer to Paula Broots Support charge Refer to Paula Broots Support charge Refer to Paula Broots Refer to Paula Broots Becommandor
SCINC SCAM IBPPSR ANT CMPU HURF RESP REPSR RESP REPSR	Suspect check - supports non contribution Suspect check Action - No Match Presemptive blood test cost Actionship - subscription All term non tested CMA medicisent for Larber processing Infair localed. Not sublish for analysi Infair localed. Subscription - Subscription Reverse Rep	Nor Cent:  The statistical interpretation provides support for the proposition that the normality support in the filter on the statistical interpretation provides support for the strength of the provide of the interpretation provides support for the strength of the provide of the interpretation provides support for the strength of the provide of the interpretation provides support for the strength of the provide of the interpretation provides support for the strength of the provide of the interpretation provides support for the strength of the provide of the interpretation provides support for the strength of the provide of the interpretation of the interpretation of the strength of the provide of the interpretation of the strength of the provide of the interpretation of the strength of the provide of the interpretation of the strength of the provide of the provide of the provide of the interpretation of the in	The information is required in a statement for Court. The statistical interpretation provides acport for the proposition that the normatical suspect has not contributed to this mano (DAA profit. This manual suspect has not contributed to this mano (DAA profit. This manual suspect has not contributed in a systemic line a statement for court. The intermediate suspect can be analysis in required in a statement for court. The intermediate suspect can be analysis in required in a statement for court. The intermediate suspect can be analysis in the intermediate of the topological and the intermediate and profits database to the same suspect of the foreign of the topological and the intermediate and profits database to profits an any suspectively with the foreign of the intermediate suspect and the interference of the non-intermediate and the limited amount of intermediate to ather the control of the analysis of the state of the intermediate and the limited amount of intermediate and the state of the analysis of the analysis of the based of the analysis in regulated the based state of the based of the based of the based intermediate and the based states and the based of the based of the based of the analysis of the analysis of the analysis of the based of the based intermediate and the based states of the based of the based of the based intermediate and the based states and the based of the based of the based of the analysis of the analysis of the analysis of the based of the based of the analysis of the analysis of the analysis of the based of the based of the analysis of the analysis of the analysis of the based of the based of the analysis of the analysis of the analysis of the based of the based of the analysis of the analysis of the theory top of the analysis of the analysis of the analysis of the theory top of the analysis of the analysis of the analysis of the theory top of the analysis of the analysis of the analysis of the theory top of the analysis of the analysis of the theory top	PP21 - regorded	NE change recommended by RMU NE change recommended by RMU NE change recommended by RMU Change recommended by RMU Change recommended by RMU NE change recommended by RMU	SC10 SC11 CPU DEP1 DECOMMESSION: see IR DECOMMESSION: see IR	Suspect check - suspect non control of the control	Integration, A inference excision sample disculate is provided the inference in a super- trapartie in a statement for Cause. The admitted integration provides support that and integration provides support and admitted integration provides support and admitted integration provides support and admitted integration of the integration provides provided of their integration provides using a statement for court. The monitorial support can be excited as a provided of their integration provides and admitted in the international integration of admitted on the international support admitted in the international support admitted in the international support integration also admitted for Manufactures and the international for the NMA profile. This international admitted for Manufactures and the international for the internation and the international for the internation of admitted admitted for Manufactures and the international for the internation of admitted integration admitted for Manufactures and the international of the internation international to be assessed for further providential controllation (2004) for admitted international to be assessed for further and the international of the internation international international international international international international international for further and the international international international international international international int	slight change to suggested wording. Removed travel : slight change to description not discussed of discussed change in any comment rel discussed not discussed	SC10 SC11 CPU CPU CPU	Bugend direkt- sepatist non- controlution biological direkt- biological direkt- biological direkt- biological direkt- comparison direkt- comparison direkt- comparison direkt- comparison direkt- biological direkt- biological direkt- direkt- biological direkt- direkt- biological direkt- direk	comparison is other monitories supports interpretention is other monitories supports interpretention evidence supports for the support interpretention evidence supports and the support is support for the proposition that the support continuous support of the support of the support is support for the support of the suppo	Support change Support change Support change Refer 19 Paula Brocks Support change Support changes Support chan
SCSNC BCANM IBPSR ANT CMPU DSFP RENSA RENSA RENSA	Suspect check - supports non     contribution     Suspect check Action - No Match     Presumptive block that poss     device Action - No Match     Presumptive block that poss     device Action - No Match     Presumptive block     result of the poss     device Action - No Match     Presumptive block     result of the poss     device Action     ONA insufficient for further     processing     Not subtle for analysis     Hart located. Not subtle for analysis     Renew Reg     Renew Reg     Renew Reg     Renew Profile collamone     Renew Reg     Renew Profile collamone	for Cost.	The information is required in a statement for Court. The information is required in a statement for Court. The statistical information provides asyport for the proposition had the memory of the statement of the statement of the provide the statement of court. The contrastic specific data is statement for court and provides asystem of the information is equired in a statement for court. The contrastic support data is statement for courts the provide statement of the information is equired in a statement for court. The contrastic support data is excluded as a potential contributor to the DMA profile statement which, Teshan as provides a statement for (MB) and associated for DMA statements and the statement of the information to allow the statement of the statement of the statement of the statement of DMA statements and the statement of the statement of the statement of DMA statements and statement of the statement of the DMA profile statement is not stateled for the means of alternative statement of DMA were statement of DMA statements and statement of the DMA were statement or possible statement of the statement of the statement of the Name to backets of this temphases that be associated of the statement and the statement or possible attement of controls. The temphases statement for the temphases the temphase temphases the statement or possible attement of controls and the statement of the temphases and temphases. The statement or possible attement of controls attemphases the temphases that the statement of the temphases and temphases. The statement or possible attemphases that have been statement of the process is obtained on the statement and the statement or additional temphases. This is not for the temphases attemphase is a statement of the process is obtained on the statement or additional temphases. The statement or possible attemphases are considial undephases the statement of the process is obtained and anaples tamphases attemphases attemphases attemphases. The statement	PP21 - sponded	Ni change recommended by RMU Ni change recommended by RMU Ni change recommended by RMU Change recommended by RMU Change recommended problem Change recommended problem Ni change recommended problem Ni change recommended by RMU	SC19 SC11 CPU CPU DECOMMESSION see IR DECOMMESSION see IR	Supert check - supports non contribution Support non Complex profile unstatibution Complex profile comparison Complex profile comparison CAL number processing SUR	Integration, A reference on exceeder a surgel advanced to a proceeder the information on tradent or in a subsembler for Gaussian the advanced integration provides support that advanced integration provides support that advanced integration provides and advanced provided of the information in expands in a subsembler of combined and the information subsembler of combined and the information subsembler of the information with the DBA profile and the information with the DBA profile and the information with the DBA profile and the information in the information in the information and the information in the information DBA profiles. Plant action in the information integrate is an extension of the information of the information with the DBA profile and the information in the information of the information of the information of the information of the information of the information of the information of t	sight change to suggested wording Removed Insect light change to description and discussed change in say comment change in say comment and discussed and discussed	SC10 SC11 CPU CPU DEP1 NTER4	Support check - separation and - eventuation     Support check - Excluded     Complex profile - unstability for	comparison is other momentation supports interpretention of the second second second second second periodical of the second second second second second second sequent for the periodical periodical second second second sequent for the periodical second second second second second to second	Support change Support change Support change Refer to Paula Brochs Support change Refer to Paula Brochs Refer to Paula Brochs Refer to Paula Brochs Commencient
SCINC SCANM IBPSR DIPPSR LANSA ALNSA RUSA RUSA RUSA RUSA RUSA	Susped check - supports non contribution Suspect check Action - No Match Percentry of the Control of the Con- Advantation results of the Control Advantation results of the Control of the Con- complex model profile accurate and profile accurate profile accurate processing CINA insufficiant for further processing CINA insufficiant for further processing CINA insufficiant for further processing CINA insufficiant for further processing CINA insufficiant for analysis CINA insufficiant for analysis	for Cost:	The information is required in a statement for Court. The information is required in a statement for Court. The statistical interpretation provides apport for the proposition that the information apport is a statement of Court of the information of the provides apport in the apport of the statement of the provides apport in the apport of the statement of the provides apport in the apport of the statement of the provides apport in the apport of the statement of the provides appendix of the provides a	PP21 - reported	Hi change recommended by RMU     Hi change recommended by RMU     Hi change recommended by RMU     Ni change recommended by RMU     Change recommended by RMU     Change recommended by RMU     Mi change recommended by RMU     Ni change recommended by RMU	SC10 SC11 CPU DEP1 DECOMMESSION see IR DECOMMESSION see IR	Suspect check - suspect needs - suspect controlution Suspect check - Excluded Complex portion comparison DMA medicates processing SUR	Integration, A reference excision sample disolution is provided the information is a together in a statement for Court. The datability integration provides support that and courter of the court of the statement of the statement integration provides support. This microarchitecte is the DNA profile. This comparison was done for the INMA profile. The comparison statement of the DNA profile statement of occurs. The the DNA profile is not be DNA profile statement of occurs. The the DNA profile is not a state is the DNA profile statement of occurs. The the INMA profile is not a state is the DNA profile statement of occurs. The the INMA profile is not a state is the DNA profile statement of occurs and the state is the state of the INMA profile. The the DNA profile is the INMA profile is not a state of the INMA profile is the INMA profile. The the INMA profile is not a state is the DNA profile is not a state of the INMA profile is the INMA profile is not a state of the INMA profile is the INMA profile is not a state of the INMA profile is the INMA profile is not a state of the INMA profile is not a state is the DNA profile is not a state of the INMA profile is not a state is the DNA profile is not a state of the INMA profile is not a state is the DNA profile is not a state of the INMA profile is not a state is the DNA profile is not a state of the INMA profile is not a state is the DNA profile is not a state of the INMA profile is not a state is the DNA profile is not a state of the INMA profile is not a state is the INMA profile is not a state of the INMA profile is not a state is the INMA profile is not a state of the INMA profile is not a state is the INMA profile is not a state of the INMA profile is not a state is the INMA profile is not a state of the INMA profile is not a state is the INMA profile is not a state is the INMA profile. Is not a state of the INMA profile is not a state is the INMA profile is not	inght change to suggested wording. Removed tread? slight change to description not discussed of discussed change in exp comment change in exp comment not discussed not discussed	SC10 SC11 CPU CPU OFP1 NTER4	Support check - supports non- construction and the support support of the support support of the support construction of the support support of the support support of the support suppor	comparison is other monitories supports interpretention is other monitories is supports interpretention exclusions support in a the statistical attraction periodical support of the proposition that the the statistical attraction periodics support for the proposition that the the statistical attraction periodics in the proposition that the support of the proposition that the support cart. The metal constraints are a statistical for DNA meaning/of interpretation due to also that the support of the limited annual of information of the support of the limited annual of information of the support of the support of the support of the support of the limited annual of information of the support of the limited annual of information of the support of the limited annual of information of the support of the support of the support of the support of the support of the support of the support of the support of the supp	Support charge Support charge Support charge Refer to Paula Broots Decommission - see RRUR Decommission - see RRUR Refer to Paula Broots Decommission - see RRUR
SCENC SCANN IBPSS IBPSS IBSS IBSS IBSS IBSS IBSS IB	Suspect check - supports non contribution Suspect check Action - No Match Presumption block that pos- functional events and a support All feats non-trained and support of comparison and support of comparison and support and support of comparison and support of comparison and support and support of comparison and	Nor Cost: The statistical integration provides apport for the proposition that the norm-state support has not contributed to the most DM profile. This comparison was done for intelligence support of a substrate of the cost of the provided the provided the the intelligence support of the substrate support can be excluded as a patiential contribution to the DMA profile. The normalized support can be excluded as a patiential contribution to the DMA profile. The normalized support can be excluded as a patiential contribution to the DMA profile. The normalized support can be excluded as a patiential contribution to the DMA profile. The normalized support can be excluded as a patiential contribution. The normalized the transmission of the support of the DMA profile. The normalized support can be excluded as a patiential contribution. The normalized to the transmission of the support of contributions and/or the binetic amount of submetter when the DMA profile. The support of contributions and/or the binetic amount of submetter when the DMA profile. The support of contributions and/or the binetic amount of advanced to the the contribution of the support of the part of the DMA profile. The termination dense supports are supported by the part of the DMA profile. The termination dense supports are supported by the part of the DMA profile. The termination dense supports are supported by the part of the DMA profile. The termination of the surge is no support to the support of the part of the DMA profile. The termination of the surge support and the support of the part of the DMA profile. The termination of the surge support and the support of the part of the DMA profile. The termination of the surge support is the surge support of the part of the phonese of DMA termination of the surge support of the submetter termination of the surge support of the surge support of the submetter termination of the s	The information is required in a statement for Court.  The additional interpretation provides apport for the proposition that the momental example. It is not contributed to this matec DNA profit. This manufacture is a statement of the provides apport for the proposition that the momental example that do contributed to this matec DNA profit. The controlled approxide of this information is equired in a distinction to be provided of this information is equired in a distinction to be provided approximation of the provided approximation of the provided approximation of the information of the provided approximation of the provided approximation of the information of the provided approximation of the provided approximation of the information of the provided approximation of the provided approximation of the information of the provided approximation of the provided approximation of the information of the provided approximation on address the information of the provided approximation of the provided approximation of the information of the provided approximation on address the information of the provided approximation of the provided approximation of the information of the provided approximation on address the information of the provided approximation of the provided approximation of the information of the provided approximation of the provided approximation of the information of the provided approximation of the provided approximation of the information of the provided approximation of	IPP21 - reported     IPP21       prater: - actor spetials     IPP21       prater: - actor spetials     IPP21       PP21 - reported     IPP21	NE change recommended by RMU Change recommended by RMU NE change recommended by RMU	SC10 SC11 CPU DEFF1 DECOMMESSION are R	Suspect check - asports non - constitution Suspect check - Excluded Complex profile unsutable for interp or comparison Co	Integration, A reference excepts analysis device to a settlement for Gaussian equate to in a settlement for Gaussian to quite the settlement of Gaussian to additional to a settlement of Gaussian to additional to a settlement of Gaussian to additional to a settlement of Gaussian to additional settlement of Gaussian additional to additional to sequel a additional settlement of Gaussian provided fibro information is equal to a additional settlement of Gaussian additional to additional to sequel a additional settlement of Gaussian additional settlement of Gaussian additional settlement of Gaussian additional to the settlement of Gaussian additional to the settlement of Gaussian additional to the settlement of Gaussian and the settlement of Gaussian and the settlement of Gaussian additional to the settlement of the Gaussian and the settlement of Gaussian and the settlement of Gaussian and the settlement of Gaussian and the settlement of the Settlement of additional to the additional to the additional to the additional to the additional to additional to addition	sight change to suggested wording Removed travel."	SC10 SC11 CPU CPU INTER4	Support diverk - separat and separat diverk - contributor Excluded Complex profile or comparison Alther profiles investigation of the second of the second meter processing charge profile charge profile	comparison is other momentation supports interpretention of the second second second second second provided of the individual second second second second second for the proposal second second second second second for the proposal second second second second second in second for the proposal second seco	Support change Support change Support change Refer to Paula Brocks Support change Refer to Paula Brocks Support change Refer to Paula Brocks Refer to Paula Brocks Refer to Paula Brocks Decommension - see RRSUR Refer to Paula Brocks Refer to P
SCING SCING IBPPSR CMPU DIPP RESERVE RTERE RTERE	Susped check - supports non contribution Suspect check Action - No Match Presumption back deet pool and here and tested of the support of comparison when per comparison per comparison when per comparison per com	For Cost: The statistical integration provides apport for the propagation that the norm-lated second has not contributed to this mixed DM profile. This comparison was done for intelligence propers only, American evidence analysis of the provided if this information is required in a statistical for out. The norm-lated subject can be excluded as a potential coefficient to the DM profile datamet for non-late interlayers the information the interlayers the information statistical subject can be excluded as a potential coefficient to the DM profile datamet for non-late interlayers the information statistical subject can be excluded as a potential coefficient to the DM profile datamet for non-late interlayers the information statistical coefficient to the DM profile datamet for the institution of the interlayers to not analogical for manipplic integrations due to short in coefficient to the DM profile difference in the institution of the interlayers in the interlayers are completed tool DM profile with multiple coefficients. The moture is not analogical for manipplic integrations due to short in coefficient of DM were described in the information while the DM profile. The profile account of the DM profile which are contradered for DMA analysis. Los incredes of DMA were described in the short analysis of the coefficient of the DMA profile. They were described in the DMA profile and and the coefficient appropriately. They the data coefficient for DMA were appropriately, and and the coefficient of the motor in the manipple of the parent time (where appropriate), the formation where the DMA profile. They were discribed relate motion or profile and and the coefficient on the interlayers. These has two team coefficient of the MA were appropriately, the coefficient on the amount of the motor approximation and the motor of the motor o	This information is required in a statement for Court. The information is required in a statement for Court. The statistical interpretation provides apport for the proposition that the interpretation statement of the court of the information processing of the information processing of the information is required in a statement of the court of the information is required in a statement of the court of the information is required in a statement of the court of the information is required in a statement of the court of the information is required in a statement of the court of the information is required in a statement of the court of the information is required in a statement of the court of the information is required in a statement of the court of the information is required in a statement of the court of the information is required in a statement of the information is required in a statement of the court of the information is required in a statement of the information is required in a statement of the court of the information is required in a statement of the court of the information is required in a statement of the court of the information is required in a statement of the information is required in a statement of the court of the information is required in the information is re	PP21 - reported     P       prefers - auto spolate     P       Automatically field on PR     P       PP21 - reported     P       PP21 - reported (sourd for PT cases)     P	Nil change recommended by RMU     Change recommended policity RMU     Change recommended policity RMU     Nil change recommended by RMU	SC10 SC11 CPU CPU DECOMMESSION see IR DECOMMESSION see IR	Suspect check - suspect needs - Complex profile Complex profile Complex profile comparison Complex profile complex profile	Integration, A reference on exceeder sample double to provide of the Vision of the Vision type of the statistical integration provides support that and the statistical integration provides support that and the Vision of the Vision of the Vision of the Vision provide of the Integration of the Vision of the Vision provide of the Integration of the Vision of the Vision provide of the Integration of the Vision of the Vision provide of the Integration of the Vision of the Vision provide of the Integration of the Vision of the Vision provide of the Integration of the Vision of the Vision provide of the Integration of the Vision of the Vision of the Integration of the Integration of the Vision of the Integration of the Integration of the Integration of the Integration of the Integra	inght change to suggested wording Removed Interest solight change to description not discussed of discussed change in easy comment of discussed of discussed not discussed not discussed not discussed not discussed	SC10 SC11 CPU CPU OFP1 NTER6 NTER6 CPU OFP1	Support check -     support check -     support check -     contribution     Support check -     Contribution     Complete profile     or comparison     Complete profile     or comparison     Complete profile     comparison     Complete profile     comparison     compari	comparison is other monitories supports interpretention is other monitories supports interpretention existence support in a the statistical article is required in a the statistical article support in a support in the statistical article support in a support of the proposition that the support in the support on the estimates card. The monitories support on the estimates card in the support of the support of the maximplication data is be understand and/or the submission data is be understand and/or the submission data is the support in the CNA profile. The submission is a support of the support of the support is a support of the support of the support and/or the submission data is a substituted for CNA analysis. Lances and Mayor Crime Line is a support of the support of the support is a support of the support of the support of the support is a support of the support of the support of the support is a support of the support of the support of the support is a support of the support of the support of the support is a support of the support of the support of the support of the support is a support of the s	Support charge Support charge Support charge Refer to Paula Brocks Support charge Refer to Paula Brocks Support charge Refer to Paula Brocks Refer to Paula Brocks Becommission - see RESUR Decommission - see RESUR Refer to Paula Brocks Decommission - see RESUR
SCINC SCANI IBPR DIFP RENSA RENSA RENSA	Suspect check - supports non contribution Suppect check Action - No Match Presemptive block test cost Actions and a support of the support Aff attem non tested check and a support of the support of attem test test cost attem of comparison attem test test cost attem test test test test test attem test test test test test test test attem test test test test test test test attem test test test test test test test	Nor Cent:  The statistical interpretation provides support for the proposition that the norminaled support has not cottabulid to this music DNA prifile. This comparison was done for intelligence propose only. A method was an experiment of the provided in the intermation is experiment on a submitted for cost.  The norminaled support case of a model support of the intermation is experiment on a submitted for cost.  The norminaled support case of a model support of the intermation is experiment on a submitted for cost.  The norminale support case of a model support of the intermation is experiment on the intermation is experiment on the intermation is the norminal support case of the experiment of the intermation is experiment on the intermation is the norminal support case of the experiment of the intermation is experiment on the intermation is the norminal support case of the experiment of the intermation is when and potentially large number of costs.  The norminal support case of the experiment of the intermation is when and potentially large number of costs.  The norminal support case of the experiment of the intermation is when and potentially large number of costs.  The norminal support case of the experiment of costs.  The norminal support case of the experiment of the intermation is when and potentially large number of costs.  The norminal support is the costs of the intermation is the intermation of the intermation of the experiment of the intermation of the interm	The information is required in a statement for Court.  The statistical interpretation provides acport for the proposition that the normatical suspect has not contributed to this mance DAA profit. This manual suspect has not contributed to this mance DAA profit. This manual suspect has not contributed in a statement for court, and the provides acport of the information is required in a statement for court, and the provides acport of the information is required in a statement for court, and profits acport of the information is required in a statement for the profits of the information is required in a statement for the profits of the information is required in a statement for the profits of the information is required in a statement of the profits of the information is required in the information is required in a statement of the profits of the information is required in the information is required in the information is required in the information in the information is required in the information in the informatin the informatin the information in the i	PP21 - reported	Ni change recommended by RMU Change recommended by RMU Ni change recommend	SC10 SC11 CPU CPU DEPT DECOMMESSION: see IR DECOMMESSION: see IR DECOMMESSION: see IR	Suspect check - suspect inner - suspect check - Suspect check - Excluded Complex profile unustable for integ or Comparison Compariso	Integration, A reference excision assigned double to provide the information in a trading in a statement for Cause. The admitest integration provides suspect that are consistent of the information of the admitest integration provides suspect and the information of the information of admitest of the information of the admitest of provided of the information of the admitest of admitest of the information of the admitest of the provided of the information of the admitest of the admitest admitest of the admitest of the admitest of the admitest of the admitest of the admitest of the admitest of the admitest of the admitest of the admitest of the admitest of the a	sight charge to suggested wording. Removed travel: Upper charge to description not discussed of discussed charge in cap comment ind discussed not discussed not discussed of discussed of discussed	SC10 SC11 CPU CPU NTER4 NTER4 NTER6	Bugend check - construction constructin construction construction construction construction construction	comparison is other monitories supports interpretention is other monitories supports interpretention evidence supports in a UNE to statistical interpretention is required in a UNE statistical interpretention is a subserved to the statistical interpretention that the uncertainty support for the proposation that the uncertainty is support for the proposation that the uncertainty is support in the proposation that the uncertainty contained by a subserved to the UNA point of the UNA profile. The UNA point is a subserved to the intelligence and support of the the uncertainty for a pointerial contribution to a subserved to the UNA pointerial contribution to a subserved to the UNA pointerial contribution due to be UNA point and/or the UNA point. The UNA point is a subserved to the interference of UNA words decision of the subserved to UNA words decision of the UNA point and/or the UNA point. The UNA words decision in the UNA point is subserved to the UNA point and/or the UNA point is subserved to the UNA pointer due to UNA point decision of UNA point decision in the UNA point of UNA words decision of UNA point (2011) (first sample are quarted to UNA word decision in the UNA point of UNA point decision of UNA point decision of UNA point decision of UNA point decision in the UNA point of UNA words decision of UNA point (2011) (first sample are quarted to be assessed for UNA point decision of una point decision of UNA point decision of UNA point decision of UNA point decision of UNA point and UNA point of UNA point decision of UNA point decision of UNA point decision of UNA point decision of UNA point decision of UNA point decision of UNA point decision of UNA point decision of UNA point decision of UNA point decision of UNA point decision of UNA point decision of UNA point decision of UNA point decision of UNA point decision of UNA point decision of UNA point decision of UNA point decision	Support change Support change Support change Refer to Paula Broats Support Suppor
SCENC SCAM IBPPSR CMPU DSP RESER RESER RESER RESER	Suspect check - supports non contribution     Suspect check - supports non contribution     Suspect check - No Match     Presumptive block teat coss development of the supports     Cost of the supports     Cost of the supports     Cost of the support     Cost of th	for Cost:               The adapted interpretation provides apport for the proposition that the nominate august             for adapted interpretation provides apport for the proposition that the nominate august             for adapted interpretation provides apport for the proposition that the nominate august             for adapted interpretation provides apport for the provides the information             for adapted interpretation provides approximate the foreignment             for adapted interpretation provides approximate             for adapted interpretation approximate             for adapted interpretation adapted contributes. The matter             for adapted interpretation and provides approximate             for adapted interpretation adapted contributes approximate             for adapted interpretation adapted contributes and the initial amount of             advances and the initial for adapted interpretation adapted in the initial advance of adapted             for adapted interpretation advances             for adapted interpretation addapted interpretation addapted             for adapted	The information is required in a statement for Court. The information is required in a statement for Court. The statement is an experison of the proposition had the memory of the provide it is an experison of the proposition had the memory of the provide of the information is required in a statement for court. The instructured analysis of the information is required in a statement for the proposition of the information is required in a statement for court. The instructured is an expected as a potential contributor to be CMA profile datasets and the instrument of the the information is a statement for CMA and the instrument of the information is a statement of CMA and the instrument of the information is a statement of CMA and the information is an appendix in the formation is a statement of CMA and the instrument of the information is a statement of CMA and the instrument of the information is a statement of CMA and the instrument of the information is a statement of CMA and the instrument of the information is a statement of CMA and the instrument of the information is a statement of CMA and the instrument of the information is a statement of CMA and the instrument of the information is a statement of CMA and the instrument of the information is a statement of CMA and the instrument of the information is a statement of CMA and the instrument of the information is a statement of CMA and the instrument of the information is a statement of CMA and the instrument of the information is a statement of CMA and the instrument of the information is a statement of CMA and the instrument of the information of the instrument of the	IPP21 - seponded     Impaired in the seponded       Impaired in the seponded     Impaired in the seponded       Impaired in the seponded     Impaired in the seponded       IPP21 - seponded     Impaired in the seponded	Ni change recommended by RMU Ni change recommended by RMU Ni change recommended by RMU Change recommended by RMU Change recommended by RMU Ni change recommended	SC10 SC11 CPU CPU CPU CPU CPU CPU CPU CPU CPU CPU	Suspect check - support neck - suspect neck - Excluded Complex profile unsubable for unsubable for unsubable for unsubable for further processing SUR	Integration, A reference on exceeder a surgely double to provide the information is an experient in a subsembler for Gaussian to quirter in a subsembler for Gaussian to additional and the information and provide of the information is majored in a double to provide the information of the provide of the information is majored in a doubler of the information and potentiary doubler of the information and potentiary instance of information within the DMA profile. This feeting and the information within the DMA profile and the subsemble and a complex DMA profile. The feeting and the subsemble is and the subsemble and a subsemble of the hyper- tical state. The feeting and the subsemble of the hyper- dited of the subsemble of the hyper- less and the subsemble of the hyper- less and the subsemble of the hyper- less and a state of the hyper- processing.	sight change to suggested wording Removed Insect Upper change to description and decoased change in exp comment change in exp comment ind decoased and decoased	SC10 SC11 CPU CPU NTER6 INTER6	Bugent divers -     separation on     separation     separati	comparison is other normanised samples methods on the other normanised samples methods of the information of the other methods of the information provides sequent for the proposition that the sequent for the proposition that the the statistical directory and the statistical directory and dataset of the statistical the statistical to appoint on this dark-target and profile of the statistical to the NMA profiles of statistical directory and the statistical to appoint and the statistical of the manufactory and the statistical to the terminangle space a complete DMA profile. The NMA profiles and statistical to the terminangle space a complete DMA profile. The NMA profiles and statistical to the terminangle space a complete DMA profile. The NMA profiles and statistical to the DMA statistical directory of the terminangle space and the terminangle space a complete DMA profile. The NMA profiles and statistical to the DMA statistical directory of the DMA statis	Support change Support change Support change Refer to Paula Brochs Support change Refer to Paula Brochs Refer to Paula Brochs Refer to Paula Brochs Decommission - see RRSUR Refer to Paula Brochs Decommission - see RRSUR Refer to Paula Brochs Refer to Paula Brochs
SCIANG SCANAI IBPPSR AXAT CXRU DIPPST RENSA RESS RESS RESS RESS RESS RESS RESS RE	Susped check - supports non contribution Suspect check Action - No Match Percentry of the Control of the Con- Advantation results of the Control Advantation results of the Control Advantation results of the Control of the Con- ency of Control of Control of Con- ency of Control of Control of Con- processing Participant Control of Control of Control Research Reg of Control of Control Control results - no politic collaboration and Control of Control of Control of Control Research Reg of Control of Control of Control Research Research Control of Control of Control Research Research Control of Control of Control Research Control of Control of Control of Control Research Research Control of Control of Control of Control Research Control of Cont	Nor Cost:	The information is required in a statement for Court. The information is required in a statement for Court. The statistical interpretation provides apport for the proposition that the information apport is a statement of Court of the information of the provides apport in the provides appendix in the provides ap	PP21 - reported	Hi change recommended by RMU     Change recommended by RMU     Change recommended by RMU     Hi change recommended by RMU	SC10 SC11 CPU DEP1 DECOMMESSION see R DECOMMESSION see R	Suspect check - suspects non - contribution Biographic check - Excluded Complete profile comparison Comparison DAA suspect check - comparison DAA suspect check - processing processing SUR SUR	Integration, A reference excision sample disculate is provided the information is supplied in a statistication provides support to admited in expendent of the information is the admited integration provides support has not controlled to the INM profile. This comparison was done for the INM profile. The comparison was done to the INM profile admited on the ternampte. The ternampted support can be excised as a profile admited to the INM profile. The ternampted support can be excised as a comparison was done to the INM profile admited on the ternampte. The ternampted support can be excised as a comparison was done to the INM profile amount of information with the INM profile. The ternampted support can be excised for table the INM profile in the comparison of the INM profile amount of information with the IDM profile. The ternampted support can be not done to the new support. Comparison can be the INM profile amount of information with the IDM profile. The ternampted support can be not address the INM profile address of the INM profile. The ternampted support can be not address the INM profile address of the INM profile. The ternampted support can be not address the INM profile. The ternampted support can be not address the INM profile address of the INM profile.	inght change to suggested wording. Removed Interest alight change to description not discussed on discussed change in exp comment change in exp comment of discussed of discussed of discussed of discussed of discussed of discussed of discussed of discussed of discussed of discussed	SC10	Support check - support check - contribution     Support check - contribution     Support check - Comparison     Comparison	comparison is other normatical supports interpretention is other normatical supports interpretention exclusions many factorial biological provided if this information is required in a the statistical attraction provides support for the proposition that the the statistical attraction provides support for the proposition that the the statistical attraction provides in the statistical attraction of the result of the statistical attraction of the statistical dataset of the third attraction of the state is not attraction of the statistical of the the mean of plantage state at attraction of the result of the statistical attraction of the result of the state of the state of the state of the mean of the limited attraction of the state attraction when the DNA profiles. The state of the state of the result of the limited attraction of the state of the result of the limited attraction of the state of the result of the limited attraction of the state of the result of the limited attraction of the state of the result of the limited attraction of the state of the result of the limited attraction of the state of the result of the limited attraction of the state of the limited attraction of the state of the limited attraction of the state of the limited attraction of the state of the limited attraction of the state of the limited attraction of the state of the limited attraction of the limited attraction of the state of the limited attraction of the result of the limited attraction of the limited attraction of the result of the limited attraction of the limited attraction of the result of the limited attraction of the limited attraction of the result of the limited attraction of the limited attraction of the result of the limited attraction of	Support charge Support charge Support charge Refer to Paula Broats Refer to Paula Broats Refer to Paula Broats Refer to Paula Broats Stafe to Paula Broats Decommession - see REUR Stafe to Paula Broats Decommession - see REUR Stafe to Paula Broats
BCONC BCANN IBPPSR ANY CAPU DSPP RATER INTERI INTERI INTERI INTERI	Suspect check - supports non contribution Suspect check Action - No Match Presumption block due pos- All ferm none testic All ferm none testic and the substantiation of the sub- reger of comparison and the substantiation of the sub- port located. Not substantiate of analysis Hard located. Substantiation exclusion factors Report and substantiation Reserver. Report	Nor Cent:  The statistical integration provides asport for the proposition that the norm-side aspect has not contributed to this music DM profile. This comparison was done for intelligence provides aspected to could. In a statistical integration provides aspect for the provided files internation a sequence to could. In a statistical support can be excluded as a patiential contributed to the DMA profile. The norm-side aspect can be excluded as a patiential contributed to the DMA profile. The comparison of the provides aspecting asp	The information is required in a statement for Court. The statistical interpretation provides acport for the proposition that the manual example has not contributed to this make DNA profile. This manual example has not contributed to this make DNA profile. This manual example has the contributed is a profile of a statement for court. The controlled segment of the information is required in a statement for court. The control is appendix on the analysis of the profile control of the DNA profile dataset backs of the information is required in a statement for court. The control is support of the information is required in a statement for the control is appendix on the analysis of the profile control of the DNA profile dataset is the state of the statement of the the DNA profile and another the DNA backs. The MNA is appendix in the DNA is the DNA profile dataset is a state the information of the DNA profile and another the DNA backs. The MNA is appendix in the DNA is appendix the information is not state for meaning of interpretation on a state is the initial appendix in the state for lateset. The back of DNA profile dataset is a state in the DNA family Line head of DNA appendix processing and desired constate for DNA stategets. They want advactured and processing. Result are profile to the DNA family Line head of DNA stategets interpret of the DNA family the DNA family Line head of DNA stategets and appendix the DNA family the DNA family Line head of DNA stategets interpret of the DNA family the state and stategets and appendix the stateget and the stateget the DNA stateget interpret of DNA family the stateget stateget and processing. Result are profile. The profile the DNA family and appendix the stateget and the profile the DNA family and appendix the data appendix the profile the could be the DNA family result and appendix the profile the could be appendix and appendix the DNA family the profile the could be appendix and appendix the data appendix the profile the could be appendix an	IPP21 - reported     Implies       prater - acta spelate     Implies       prater - acta spelate     Implies       Automatically field on FP     Implies       PP21 - reported     Implies	Ni change recommended by RMU Change recommended including task information. Ni change recommended by RMU Ni change recommended by RM	SC10 SC11 CPU DEP1 DECOMMESSION are R DECOMMESSION are R	Suspect check - suspect index - suspect index - contribution Suspect check - Excluded Complex profile unusulable for interp of comparison Compa	Integration, A reference encloses sample discultar is provided the information is an equate in a settement for Cault. The additional information is support to additional information is support. The information is support of the information provided for information is equated as advanted from information in equated as advanted from information in equated as advanted from information in equated as advanted from the territory of the DNA profile. The memory advanted support can be excluded as a provided of the information in equated as advanted from the territory of the DNA profile. The territory of the DNA profile information in the territory of the information and the information and the information and the information and the information and the information and the information and the information in the information and the information and the information and the information and the information and the information and the information and the information and the information and the information and the information and the information and the information and the information	sight change to suggested working Removed travel."	SC10 SC11 CPU CPU MTER4 MTER6	Support divers - support divers - support divers - controlscon Excluded Complex profile or comparison Complex profile or comparison Complex profile or comparison Complex profile or comparison or comparison of the comparison compari	comparison is other monitories suspects interference evidence sample should be provided if the industrial interference evidence sample should be provided if the industrial interference evidence sample should be the statistical integration provides suspect for the proposation that the the statistical integration provides integration of the proposation that the the statistical integration provides integration of the proposation that the the statistical integration of the statistical for intelligence purposes only. A reference interference with the statistical the contrast on the statistical the statistical the contrast on the statistical the statistical the contrast on the statistical the statistical the contrast of the proposation due to the the manufacture of the statistical the the statistical interference statistical statistical the the statistical protectial contrastical statistical the transmittical interference statistical statistical the transmittical statistical statistical statistical the transmittical interference statistical statistical the transmittical statistical statistical statistical the transmittical interference statistical statistical the transmittical statistical statistical statistical the transmittical statistical statistical statistical the transmittical statistical statistical statistical the transmittical statistical statistical statistical statistical the transmittical statistical statistical statistical statistical the transmittical statistical statistical statistical statistical statistical the statistical statis	Support change Support change Support change Refer to Paula Brocks Support change Refer to Paula Brocks Refer to Paula Brocks Refer to Paula Brocks Concommession - see (RSUR Concommessio

MNS	Micro pea for sperm	Spermatozoa were not detected on this item/sample by microscony	Spermatozoa were not detected on this item/sample by microscony	orelim , auto undate	Nil change recommended by RMU				pot discussed				Refer to Paula Brisotto
NDNAD	No DNA detected	This item/sample was submitted for DNA analysis; however no DNA was detected above the	This item/sample was submitted for DNA analysis; however no DNA was	PP21 - reported	Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
		limit of detection at the quantitation stage. No further processing was conducted on this	detected above the limit of detection at the quantitation stage. No further										
NDPPTP	No DNA profile – possible sub- threshold peaks	A DNA profile saw not distained from this ternshample, however the possible presence of distributed DNA was observed. This possible DNA was not present at a distributed from the base assed for comparison, purposes, at it was believ DNFSS standard reporting thresholds. This is used to disk due to the not finished to poor quality of the DNA, insufficient quantity of DNA, or inhibition of the DNA.	A DNA profile wait oct obtained from this terrolampic however the possible presence of a sufficient level to solve over. This possible DNA was not present at a sufficient level to be used for comparison purposes, at was below CMPSS subscript reporting thereads. This could be due at was below CMPSS subscript hypothyperheads. This could be due to the DNA, evaluation of the DNA, evaluation query 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 lemisample, however the possible presence or additional DNA was observed. This possible DNA for not present as a sufficient level bole DHA for not present as a sufficient level bole DHFPS standard reporting intervioled. This could be due to, but not limited to poor quality of the DNA, nor hibition of the DNA.	no change	NDPPTP	No DNA profile – possible sub- threshold peaks	A DNA profile was not obtained from this ternisample, however the possible presence of additional DNA was observed. This provide bolk and the possible and a subtained to the provide bolk of the present at a subtained to the provide the provided the provided at the table of VHFSS standard reporting thresholds. This could be due to, but not imited to poor gailing of the DNA, multiplicate 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	This item/sample was tested for the possible presence of biological material. All testing has have accepted for this item.	QPS request slight change to wording	NFEC	No further examinations	This item/sample was tested for the possible presence of biological material. All testing has been appropriated for this item.	Further discussion to be had to have this line in conjunction with Item has
NOPROF	No DNA profile	A DNA profile was not obtained from this item/sample, due to, but not limited to: no 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	new expanded comment.	NOPRO	No DNA profile	A DNA profile was not obtained from this tars learned.	Support change
NWQPS	No further work required as per	QPS have provided advice that no further work is required for this item/sample. Testing has	QPS have provided advice that no further work is required for this	Result automatically filed on FR	Nil change recommended by RMU	NWQPS	No further work	QPS have provided advice that no further work	no change	NWQPS	No further work	QPS have provided advice that no further	QPS agree
NHODED	advice from QPS	been ceased and the sample stored.	item/sample. Testing has been ceased and the sample stored.	NPM secondard	Warding has seen to share and far ONL subjets	hannen	required as per advice from QPS	is required for this item/sample. Testing has i been ceased and the sample stored.		NHODED.	required as per advice from QPS	work is required for this item/sample. Testing has been ceased and the sample stored.	000
WIGPAR	Cer S and the Annual Mark Annual Mark Annual Mark Annual Annua	that the functionargin has undergoed DMA stelling and results are available. However these have not been herepresent at its stage, DPS can an ulmit a request to QHFSB for an interpretation of the DMA results if required.	Imministrative Please note that the terministrative has undergoes DMA processing and results are available. There excited an use of a cumulation results above, or DMA poller results that have not been integreted at this stage, CPG can above a cuparts to CPF SB between works which may results above. The stage of the terministration of the terministration CMA poller results that have not been integreted at this stage. OPF can integrete a cupart of the DMA results if required.	(**** - «Врайба		NULF SK	further work required - results available	a required for this itemiciangule. Preservoire that this terinary has undergoore DNA processing and results are available. These unuslin may be Carifordiation results alone, or integrated at this stage. OPS can submit respect to QHFSS for further work which may reduce the interpretation of the DNA results alongering, results alone, or DNA profile results agained, results alone, or DNA profile results agained, results alone, or DNA profile results applied to QHFSS for UMPP work which may include the interpretation of the DNA results if required.	na change	NINGPOR	further work required - results available	been in regulated for this time/stample. Phose to the that this time/stample has undergone DNA processing and results are available these results may be Quantification results these interpreted at this stage, CPE can about a request to DHFSS for thethe work which may include the interpretation of the DAA results if request to DHFSS for thethe work which may include the interpretation of the DAA results if requests for the work, which may include the interpretation of the DNA results if requests for further work, which may include the interpretation of the DNA results if respectively.	ur s 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	This item/sample tested positive to a presumptive test for Prostate Specific Antigen (PSA) which is a component of seminal fluid. This item was	prelim - auto update	Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
PBNSC	Presumptive blood test neg.	are pending. This item/sample tested negative to a presumptive test for blood (TMB). This item was	submitted for DNA testing. Results are pending. 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
PRTN	Submitted for cells Presumptive blood test peg	submitted for general cell DNA testing. This item/sample tested penaltive 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)	prelim , auto update	Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
PPSRP	Presump. AP test positive, submitted	This item/sample tested positive to a presumptive test for seminal fluid (AP). This item was submitted for DNA testing. Besults 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 tensioample gave a partial DNA profile which was insufficient for comparison purposes or mean-inglit interpretation due to be inimide amount in information whith 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 termisample 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 recomminded	DECOMMISSION: see C	PU			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	00100			not discussed	00000			Refer to Paula Brisotto
PRINCIP	DNA profile removed from NCIDD	The UNA profile obtained from this item/sample has been removed from KULUI totowing advice from QPS, a change in the NCIDD category, or a profile with more information has been obtained.	The UNA prome docamed from this itemisample 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 - reponed	Nii change recommended by KMU	PRINCIP	removed from NCIDD	Ine UNA prote 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.		PRINCILD	removed from NCIDD	The UNA profile obtained from this tem/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.	UPS 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 politic detained from the fam: This possible dNA was not present at a district refer to be used for comparison partners, as it not solved of the Standard reporting thereadds. This sub-threaded the solution of the standard reporting thereadds BNA components in the DNA profile addated from this term.	The presence of possible additional DNA was observed within the DNA predire obtained from the from The possible DNA was not present at a predirect of the DNA and DNA was observed at a predirect of the DNA and DNA and DNA and DNA CMPSB standard reporting herabicity. The possible dna and was addressed to the predirect of the DNA and 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 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 information did not interfere with the interpretation of the reportable CNA 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 interpetation of the reportable DNA components in the DNA profile obtained from this item.	GPS 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	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. OHESS recommends OPS to commence further examination on items relation to	Spermatozoa were not observed and/or seminal fluid was not detected on the item/sample tested. OHESS recommends OPS to commence further	PP21 - reported	Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
SOHAA	Sample on hold, awaiting advice	this case if applicable. 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 on items relating to this case if applicable. n/a	Exhibit movement only - not reported to QPRIME	Nil change recommended by RMU				not discussed				Refer to Paula Brisotto
SPERU	Sample processed and final results	examination priority, screening requirements. This item/sample was processed under the barcode sent with this exhibit report. The final		PP21 - not reported to QPRIME	Nil change recommended by RMU	-			not discussed				Refer to Paula Brisotto
600	under	results will be reported under that barcode.		0004 and reported to 000011	Nil shares commended by DMU				ant discussed				Defecto Devic Drivello
app	compre poored and processed under	this exhibit report. The final results will be reported under the barcode.	104	PP21 - not reported to UPRIME	Nii chaige recommended by KMU				not uncussed				Nella lo 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	NII change recommended by RMU				not discussed				Reter 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.	nia	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 be 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 oblained 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 Lint (2011)	Changed expanded wording
SUFWC	Sample undergone further work - conditioned	This litenisample gave a mixed DNA profile that indicated the preserve of DNA from two or three contributors. Based on information provided to the laboratory, this mixed DNA profile has now been conditioned.	This terretample gave a mixed DNA profile that indicated the presence of DNA from two remore contributions. 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 more conthibutors. Based on information provided to the laboratory, this mixed DNA profile has now been conditioned.	no change	SUFWC	Sample undergone further work - conditioned	This itembargle 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/isample 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 nov required for this item/sample. Testing has been restarted.	no change	TRQ	Testing restarted or	n QPS have provided advice that testing is now required for this item/sample. Testing has been restarted.	QPS agree
Query Mns	er Hair located - not examined at this time	During the examination of this exhibit one or more hairs were located. Based or case information availation tention; measured, this has no these submitted at this time, however has been retained for potential future analysis if requested.								22	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	DNA COLD LINK - This item/sample gave a full DNA profile		DNA COLD LINK - This item/sample gave a full DNA profile	Full single source DNA profile	Nil changes
	(PP21)	which matches the DNA profile obtained from Barcode Number		which matches the DNA profile obtained from Barcode		recommended by
		********* a DNA sample obtained from SURNAME, GIVEN		Number ******** a DNA sample obtained from SURNAME,		RMU
		NAMES DOB **/**/**** CNI No. ******** DNA Profile Number		GIVEN NAMES DOB **/**/**** CNI No. ******** DNA Profile		
		LKR0000***.		Number LKR0000***.		
	Exhibit # QP****** S Partial DNA profile	DNA COLD LINK - This item/sample gave a partial DNA profile		DNA COLD LINK - This item/sample gave a partial DNA	Partial single source DNA profile	Nil changes
	(PP21) -	which matches the DNA profile obtained from Barcode Number		profile which matches the DNA profile obtained from Barcode		recommended by
		********* a DNA sample obtained from SURNAME, GIVEN		Number ******** a DNA sample obtained from SURNAME,		RMU
		NAMES DOB **/**/**** CNI No. ********* DNA Profile Number		GIVEN NAMES DOB **/**/**** CNI No. ******** DNA Profile		
		LKR0000***.		Number LKR0000***.		
	<ol> <li>Exhibit # QP****** S 2 person mixed</li> </ol>	DNA COLD LINK - This item/sample gave a DNA profile that		DNA COLD LINK - This item/sample gave a DNA profile that	1 Full profile	RECOMMEND
	DNA profile	indicated the presence of DNA from more than one contributor.		indicated the presence of DNA from more than one	2. Partial profile	CHANGE -when
	<ol><li>Exhibit # QP***** I INTEL (2 person mix)</li></ol>	Represented within the mixed DNA profile are some or all of the		contributor. Represented within the mixed DNA profile are	3. Full profile	RMU are creating
	<ol><li>Exhibit # QP****** S 3 person mixed</li></ol>	components of the DNA profile obtained from Barcode Number		some or all of the components of the DNA profile obtained	<ol> <li>Partial profile</li> </ol>	the cold link result,
	DNA profile	******** a DNA sample obtained from SURNAME, GIVEN		from Barcode Number ******** a DNA sample obtained from		they will be able to
	<ol><li>Exhibit # QP******* I INTEL (3 person</li></ol>	NAMES DOB **/**/**** CNI No. ********* DNA Profile Number		SURNAME, GIVEN NAMES DOB **/**/**** CNI No. *********	Suggested changed:	refer to the Exhibit
	mix)	LKR00*****.		DNA Profile Number LKR00*****.	If required - RMU staff can confirm from NCIDD	register and FSS
					if it is a full or partial DNA profile.	DNA Analaysis
	Change to:					table to determine in
	Exhibit # QP****** S mixed DNA profile					caveat wording
						needs to be added.

EXH line

Expanded Comment

# WIT.0020.0008.0071

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	no change suggested	Profiler plus result
		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.		
CMPULN	Complex mixed DNA profile. Unable to load to NCIDD	This item/sample gave a full or partial mixed DNA profile which indicated the	no change suggested	Profiler plus result
		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	<b>x</b>	
		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.		
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	n/a	Profiler plus result
		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 QHFS	S	
		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.		
DPPTP	9 loci DNA profile - possible sub-threshold peaks	This item/sample gave a full 9 loci DNA profile which matches the DNA profile	n/a	Profiler plus result
		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 QHFS	\$	
		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.		
FUPNPN	9 loci DNA profile. Uploaded to NCIDD	This item/sample gave a full 9 loci DNA profile which matches the DNA profile	n/a	Profiler plus result
		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.		
FUPROF	9 loci DNA profile	This item/sample gave a full 9 loci DNA profile which matches the DNA profile	n/a	Profiler plus result
		obtained from the barcode sent with this exhibit report.		

# WIT.0020.0008.0072

INTER7	Interim result- Mixed major comp NCIDD. Rework Reqd	This is not a final result, sample/s are currently undergoing rework. Rework car 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 profil for the barcode sent with this exhibit report. Final results are pending.	e	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 ca 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 threshold 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 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 car 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 coul 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 d	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	n/a	Profiler plus result
--------	---	--	-----	----------------------
		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 DN	A	
		profile will be searched against any DNA profiles already held on NCIDD (as pe	r	
		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.		
MIPDNA	Mixed DNA profile conditioned on – NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of	n/a	Profiler plus result
		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.		
MIPMAC	Mixed DNA profile. Major component	This item/sample gave a mixed DNA profile which indicated the presence of	n/a	Profiler plus result
		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.		
MIPMIC	Mixed DNA profile. Minor Component	This item/sample gave a mixed DNA profile which indicated the presence of	n/a	Profiler plus result
		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.		
MIPMUN	Mixed DNA profile. Major component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of	n/a	Profiler plus result
		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	pr	
		loading to NCIDD. The full major DNA profile matches the DNA profile obtained	ŧ	
		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.		
MIPPRO	Mixed profile. Remaining profile after conditioning – NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of	n/a	Profiler plus result
		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.		

MIDIN	Mixture Interp read Intel profile leaded to NCIDD	This item/seemple gave a mixed DNA profile that has been interpreted for	nla	Drofilor plue regult
WIRIN	Mixture interpreda - interprofile loaded to NCIDD	intelligence numeroes only. This interpretetion move not be able to be used for	n/a	Profiler plus result
		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 b	e	
		different. The Intelligence DNA profile loaded to NCIDD will be searched agains	t	
		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.		
MPCMU	Mixed profile- complex minor unsuit for interp or compar.	This item/sample gave a mixed DNA profile which indicated the presence of	n/a	Profiler plus result
		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.		
MPCO	Mixed DNA profile conditioned on	This item/sample gave a mixed DNA profile which indicated the presence of	n/a	Profiler plus result
		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"		
MPMAIN	Mixed profile, major component insuff for NCIDD matching	This item/sample gave a mixed DNA profile which indicated the presence of	n/a	Profiler plus result
	······································	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 QHESS 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)		
		corresponding components of the DNA profile obtained from the barcode sent with this exhibit report (if applicable).		

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 or contributor to this partial DNA profile, where information was obtained, the partiminor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a e al	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 or contributor to this partial DNA profile, where information was obtained, the partitiminor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a e al	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 or contributor to this partial DNA profile, where information was obtained, the partiminor DNA profile matches the DNA profile obtained from the barcode sent with this exhibit report (if applicable).	n/a e al	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
		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.	1// a	
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 exclude as being a possible contributor of DNA to this mixed DNA profile.	n/a ed	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 absent of reference samples, no further interpretation can be conducted; or compariso with additional reference samples may be possible if forthcoming.	n/a n	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	n/a	Profiler plus result
		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 DN	A	
		profile match the corresponding components of the DNA profile obtained from		
		the barcode sent with this exhibit report.		
MPPMIN	Mixed DNA profile, partial minor component uploaded to NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of	n/a	Profiler plus result
		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 obtaine	d,	
		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.		
MPRO	Mixed profile, complex mixed minor component	This item/sample gave a mixed DNA profile which indicated the presence of	n/a	Profiler plus result
		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 sample	es	
		may be possible if forthcoming.		
MPRP	Mixed DNA profile. Remaining profile after conditioning	This item/sample gave a mixed DNA profile which indicated the presence of	n/a	Profiler plus result
		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		
MPRPAC	Mixed profile, Remain profile after cond – insuff NCIDD	This item/sample gave a mixed DNA profile which indicated the presence of	n/a	Profiler plus result
		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		
1		reporting a match on NCIDD, and therefore has not been loaded to NCIDD. Th	6	
1		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)		
		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. Th 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).	6	

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 ver limited information, however in some cases it may provide enough information for 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 profil obtained from the barcode sent with this exhibit report (if applicable).	n/a / o	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 ver 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 / o	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 ver limited information, however in some cases it may provide enough information for 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 profil obtained from the barcode sent with this exhibit report (if applicable).	n/a V e	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 al	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 agains 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 h	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 pet 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 r	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 threshold. 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 t 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 D	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 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 of	Profiler plus result

SCMAJM	Suspect check - major profile match 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 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. 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 this information and subsequent statistical calculations are required in a statement for court.	n/a n/a d	Profiler plus result 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 n	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 NCIDE 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 pr	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 r	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 of 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 no 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 n e e	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 environmenta 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 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 a 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 II	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 pe 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.	ın/a r	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 car 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	n/a	Lab clean
		profile obtained against the QHFSS DNA Analysis staff DNA database and the QPS staff		not
		DNA database. If the profile obtained cannot be matched to a QHFSS DNA Analysis staf		reported
		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 onl	Y Contraction of the second seco	
		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	rt.	
ENCMDP	ENVM - Complex mixed DNA profile	This environmental sample gave a mixed DNA profile which indicated the presence of DN	<b>♠</b> /a	Lab clean
		from at least two contributors. This mixed DNA profile could not be separated into distinct		not
		DNA contributions (e.g. major and minor DNA profiles), and as such no further		reported
		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.		
ENCMPU	ENVM- Complex mixture unsuitable for interp or comparison	This environmental sample gave a complex mixed DNA profile which contained an unkno	n/a	Lab clean
		number of contributors or a limited amount of information. This mixture is not suitable for		not
		meaningful interpretation due to either its complexity relating to the unknown and potentia	lly	reported
		large number of contributors and/or the limited amount of information within the profile. It	5	-
		standard procedure to analyse environmental samples below QHFSS standard reporting		
		thresholds for quality purposes, therefore results for this sample have been interpreted ar	d	
		reported based on these lowered thresholds.		
ENFDP	ENVM - Full DNA profile	This environmental sample gave a full DNA profile. It is standard procedure to analyse	n/a	Lab clean
		environmental samples below QHFSS standard reporting thresholds for quality purposes,		not
		therefore results for this sample have been interpreted and reported based on these		reported
		lowered thresholds. Part of the Quality Assurance process for all environmental samples	S	
		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 t		
		DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this		
		instance, no matches were obtained		
ENNDP	ENVM - No DNA profile	No DNA profile was obtained from this environmental sample. It is standard procedure to	n/a	Lab clean
		analyse environmental samples below QHFSS standard reporting thresholds for quality		not
		purposes, therefore results for this sample have been interpreted and reported based on		reported
		these lowered thresholds.		
ENPDP	ENVM -Partial DNA profile	This environmental sample gave a partial DNA. It is standard procedure to analyse	n/a	Lab clean
		environmental samples below QHFSS standard reporting thresholds for quality purposes,		not
		therefore results for this sample have been interpreted and reported based on these		reported
		lowered thresholds. Part of the Quality Assurance process for all environmental samples	6	
		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 t		
		DNA Analysis Managing Scientist and the Quality & Projects Senior Scientist. In this		
		Instance, no matches were obtained		

ENPDPU	ENVM - Partial profile unsuitable for comparison purposes	This environmental sample gave a partial DNA profile which was insufficient for comparison/a	Lab clean
		purposes or meaningful interpretation due to the limited amount of information obtained. If	not
		standard procedure to analyse environmental samples below QHFSS standard reporting	reported
		thresholds for quality purposes, therefore results for this sample have been interpreted and	
		reported based on these lowered thresholds.	
QCF	Quality control failure – results not reportable	During the processing of this item/sample, a failure in one of the quality control processes no change suggested	QHFSS
		was identified. Investigations into this occurrence were undertaken: however any results for	quality
		this sample are not reportable.	control
			failure
QCFRQ	Quality control failure, refer to QPS	During the processing of this item/sample, QHFSS quality control processes identified the no change suggested	QPS
		integrity of this sample is compromised. Results for this sample are not reportable.	quality
			issue
QFIH	Quality flag identified, on hold awaiting advice from QPS	During the processing of this item/sample, QHFSS quality control processes indentified theo change suggested	QHFSS
		integrity of this sample may be compromised. Advice is required from QPS to determine	quality
		whether any results for this sample are reportable.	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 r	Information sent via Examination request notification by QHFSS to SOC / SCI officer
MIES	Sample required manual intervention - excess substra	This item/sample provided in a tube required manual intervention prior to processing through QHFSS extractior 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 OHESS extraction	n/a	Information sent via Examination
		methods as the swab stick was too long and required		/ SCI officer
		shortening to enable downstream processing. This		
		necessitated additional resources to perform manipulation		
		on the item/sample examined by OPS to ensure it was		
		appropriate for the DNA extraction process. The ideal stic		
		length should be no more than 21mm total length (swab		
		stick nlus swab head)		
MITRI	Sample regd manual intervention- tlift rolled incorrectly	This item/sample provided in a tube required manual	n/a	Information sent via Examination
		intervention prior to processing through QHFSS extraction		request notification by QHFSS to SOC
		methods as the tapelift was rolled incorrectly, impeding		/ SCI officer
		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.		
NBOS	No barcode on sample	The item/sample provided in a tube was not labelled with	an/a	Information sent via Examination
		barcode. A barcode is required for the processing of the		request notification by QHFSS to SOC
		item and for continuity purposes. A barcode the same as		/ SCI officer
		that attached to the packaging has been affixed to the		
		item.		
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	n/a	Information sent via Examination
		submission to determine what type of analysis is required		request notification by QHFSS to SOC
		for this item/sample eg, saliva, semen. This sample is to		/ SCI officer- not used since 2015
		be placed on hold until further information on the testing		
		requirements for this sample is provided.		
SRMI	Sample required manual intervention prior to extraction	This item/sample provided in a tube required manual		Information sent via Examination
		intervention prior to processing through QHFSS extraction	1	request notification by QHFSS to SOC
		methods. This necessitated additional resources to		/ SCI officer - not used since 2011
		perform manipulation on the item/sample examined by		
		QPS to ensure it was appropriate for the extraction		
		process.		

EXHIBIT 191

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

## OFFICIAL

Ο	F	F١	C	A	L
~	•		-		-

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

200 Roma Street, Brisbane



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

**EXHIBIT 192** 

From:Harris.LibbyA[ESC]Sent:Wednesday, 7 September 2022 09:30To:Neville.DavidH[OSC]Subject:FW: Minutes from meetingAttachments:Minutes\_21072021.docx

## OFFICIAL

OFFICIAL

From: Justin Howes <</td>

Sent: Thursday, 22 July 2021 09:36

To: Foxover.StephanP[OSC] <</td>

Harris.LibbyA[OSC]

McIntyre.OliviaM[OSC] <</td>

Cc: Allison Lloyd <</td>

Adrian Pippia <</td>

**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,

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 a 39 Kessels Road, Coopers Plains, QLD 4108 e w www.health.gld.gov.au/fss

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

CLEAN HANDS Was Not Save Lives

Wash your hands regularly to stop the spread of germs.

Disclaimer: This email and any attachments may contain legally privileged or confidential information and may be protected by copyright. You must not use or disclose them other than for the purposes for which they were supplied. The privilege or confidentiality attached to this message and attachments is not waived by reason of mistaken delivery to you. If you are not the intended recipient, you must not use, disclose, retain, forward or reproduce this message or any attachments. If you receive this message in error, please notify the sender by return email or telephone and destroy and delete all copies. Unless stated otherwise, this email represents only the views of the sender and not the views of the Queensland Government.

Queensland Health carries out monitoring, scanning and blocking of emails and attachments sent from or to addresses within Queensland Health for the purposes of operating, protecting, maintaining and ensuring appropriate use of its computer network.

# 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	
Participant	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 H	arris	LH	QPS	Y	
Olivia McInt	yre	ОМ	QPS	Y	
Item Topic					
1	Review of spre	adsheet			
** General discussion – points be JAH: Meeting was a 'Part A' relat Parts B and C (Presumptive and contact point to work through. The enhancements have been placed discussion. Not anticipated that the LH: bdna likely to come to QPS is progressing these revisions prior Discussion on use of SS1 and N information in the associated bar single source profile uploads. If the and barcode, then this could wor this. QPS mentioned that they do not they wait for the cold link and rep ceasing DNA Intel sample search programming amendments be con due to potential quality issues references.			elated to result lines only, after DNA profile in and Quality/Environmental) are with Paula Bri . This could be handled by phone or email. Ma ced into AZURE thus far, so will need to be e at this will be a lengthy discussion point. PS in the next few weeks, so trying to prepare rior to the bdna meeting. d NUP lines – could seek an enhancement to barcode field so that NUP could be used for r If the expanded comment for NUP could acc work. ACTION: edit wording for NUP slightly t not act upon the result sent with the DNA Inte report after receiving this link. FSS advised the arches, it is FSS's preference that the approp e completed prior to stopping DNA Intel samp a regarding donor designation for large cases; yed by FSS to amend an DNA Intel Sample m	terpretation. sotto as any extracted for for that by duplicate the nixtures and ount for UK to facilitate I barcodes; nat with riate le reporting eg, where natch 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.

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

EXHIBIT 193

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

OFFICIAL

OFFICIAL

From: McIntyre.OliviaM[OSC] <
Sent: Thursday, 9 September 2021 14:00
To: Allison Lloyd <
Cc: Harris.LibbyA[OSC] <
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: \_\_\_\_\_ Mobile

200 Roma Street, Brisbane

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		To be used as an overaching line for		New line with no barcodes
	<b>°</b>	presence of one contributor.		single source results.		needed in associated
		F		g		barcode field
SS1	Single source DNA profile - Intel	The DNA profile obtained from this item/sample indicated the		To be used for all single source unknown	Reporting	No comment
	g	presence of one contributor. If an unknown designation is sent		and intelligence link results that are		
		with this exhibit report, any reference samples associated to this		validated. To be incorrammed in the		
		case have been excluded as donors of this DNA and this DNA		same way as 1SS currently is to split the		
		case have been excluded as donors of this DIVA and this DIVA		same way as 100 currently is to split the		
		prome has been designated as an unknown. Alternatively, if a		using working depending in it is an		
		barcode is sent with this exhibit report, where information was		unknown or intel barcode linked. QHFSS		
		obtained, this DNA profile matched the corresponding information		to have the ability to add either an		
		in the DNA profile from the associated barcode. This DNA profile		unknown / intel barcode in linked field.		
		has not been statistically evaluated however a likelihood ratio can				
1SSNCD	NCIDD upload single source	A single source DNA profile was obtained from the item/sample				
ICONOD	DNA profile	This DNA profile has been selected for loading to NCIDD, and it				
	DIA pione	will be searched against any DNA profiles hold on NCIDD, and it				
		the NODD restation rules). Further advise will be previded in the				
		the NCIDD matching rules). Further advice will be provided in the				
NUP	Mix - NCIDD Upload	This item/sample vielded a DNA profile that matches the			Reporting	No comment
	inix iteles opieda	associated barcode, or has been designated as an Unknown			roporting	
		profile. This DNA contribution has been uploaded to NCIDD for				
		searching. If an Unknown profile was unloaded to NCIDD, further				
		advice will be provided in the event a match is received				
MIX	Mixed DNA profile	This item/sample provided a DNA profile that indicated the			Reporting	No comment
		presence of DNA from at least two contributors.				
LR1	Support for contribution: LR	This DNA profile is greater than 100 billion times more likely to			Reporting	No comment
	>100 billion	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	This DNA profile is between 1 billion and 100 billion times more			Reporting	No comment
	billion to 100 billion	likely to have occurred if the barcode sent with this exhibit report				
		has contributed to the DNA profile, rather than has not				
		contributed			<b>D</b>	
LR3	Support for contribution: LR 1	This DNA profile is between 1 million and 1 billion times more			Reporting	No comment
	million to 1 billion	likely to have occurred if the barcode sent with this exhibit report				
		has contributed to the DNA profile, rather than has not				
	Support for contributions LD 100	contributed.			Departing	No commont
LR4	Support for contribution. LR 100	This DNA prome is between 100 000 and 1 million times more			Reporting	No comment
		likely to have occurred if the barcode sent with this exhibit report				
		has contributed to the DNA profile, rather than has not				
I R5	Support for contribution: 10,000	CONTRIBUTED. This DNA profile is between 10,000 and 100,000 times more			Reporting	Agree with change
LIKU	to 100 000	likely to have occurred if the barcode sent with this exhibit report			reporting	Agree with change
	10 100 000	has contributed to the DNA profile, rether than has not				
		contributed				
LR6	Support for contribution: 1000	This DNA profile is between 1000 and 10 000 times more likely to			Reporting	Agree with change
	to 10 000	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: 100 to	This DNA profile is between 100 and 1000 times more likely to			Reporting	Agree with change
	1000	have occurred if the barcode sent with this exhibit report has				
		contributed to the DNA profile, rather than has not contributed.				
LR8	Support for contribution: 2 to	This DNA profile is between 2 and 100 times more likely to have			Reporting	Agree with change
	100	occurred if the barcode sent with this exhibit report has				
		contributed to the DNA profile, rather than has not contributed.				
LR9	Inconclusive	The statistical interpretation in relation to the associated barcode			Reporting	No comment
		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				

LR10	Supports non contribution	The statistical interpretation provides support for the proposition		Reporting	No comment
		that the associated barcode has not contributed to this mixed			
		DNA profile.			
AC	Assumed Contributor	Based on information provided to the laboratory, it has been		Reporting	No comment
		assumed that the associated barcode has contributed to this			
		interpretation has been performed			
ACINT	Assumed contributor - Intel	For Intelligence purposes, it has been assumed that the		Reporting	No comment
		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			
REMINT	Contribution for NCIDD - Intel	The DNA profile from the designated unknown sent with this		Reporting	No comment
	purposes	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			
		strength of the support for contribution will your			
CCUNK	Remaining contribution	Based on this assumption, a remaining DNA profile has been		Reporting	No comment
	consistent with unknown	separated. This is consistent with the unknown designation			
		(previously identified within this case and loaded to NCIDD) sent			
EVEX	Single evidence sample	The statistical interpretation shows that the associated barcode		Reporting	No comment
	excluded	sent with this exhibit report has been compared, and can be		1 5	
		excluded as having contributed to this mixed DNA profile.			
1.1.7.4				<b>D</b>	
INT1	Interim result - Intel NCIDD.	A DNA contribution has been uploaded to NCIDD for intelligence		Reporting	No comment
IRRFI	Intel report required for further	The results for this item/sample require further explanation which		Reporting	No comment
	information	will follow in an intelligence report.			
CWBC	Consistent with being child of	The DNA profile obtained from this exhibit was consistent with		Reporting	No comment
		being the biological child of the barcode sent with this exhibit			
	Not consistent with being shild	report		Benerting	No commont
NCWBC	of	being the biological child of the barcode sent with this exhibit		Reporting	No comment
	01	report			
SC1	Suspect check - support for	The DNA profile is between 2 and 100 times more likely to have		Reporting	No comment
	contribution: LR 2 to 100	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			
SC2	Suspect check - support for	This DNA profile is between 100 and 1000 times more likely to		Reporting	No comment
	contribution: LR 100 to 1000	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			
SC3	Suspect check - support for	This DNA profile is between 1000 and 10 000 times more likely to		Reporting	No comment
	contribution: LR 1000 to 10 000	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	This DNA profile is between 10 000 and 100 000 times more		Reporting	No comment
	contribution: LR 10 000 to 100	likely to have occurred if the nominated suspect sent with this			
	000	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	This DNA profile is between 100 000 and 1 million times more		Reporting	No comment
	contribution: LR 100 000 - 1	likely to have occurred if the nominated suspect sent with this			
	million	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	This DNA profile is between 1 million and 1 billion times more		Reporting	No comment
	contribution: LR 1 million - 1	likely to have occurred if the nominated suspect sent with this			
	billion	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			
0.07		if this information is required in a statement for court		Descritere	NI.
507	Suspect check- support for	This DNA profile is between T billion and TOU billion times more		Reporting	No comment
	Contribution:LR 1 billion- 100	likely to have occurred if the nominated suspect sent with this			
	Dillion	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			
SC8	Suspect check - support for	It this information is required in a statement for court. This DNA profile is greater than 100 hillion times more likely to		Reporting	No comment
000	contribution: $L R > 100$ hillion	have occurred if the nominated suspect sent with this exhibit		rteporting	
	Contribution. EIC > 100 billion	report has contributed to the DNA profile, rather than has not			
		contributed. This comparison was done for intelligence purposes			
		contributed. This comparison was done for intelligence purposes			
		information is required in a statement for court			
SC9	Suspect check inconclusive	The interpretation in relation to the nominated suspect is		Reporting	No comment
		inconclusive. As this interpretation relates only to the associated		1 0	
		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			
SC10	Suspect check - supports non	The statistical interpretation provides support for the proposition		Reporting	No comment
	contribution	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			
SC11	Suspect check - Excluded	The nominated suspect can be excluded as a potential		Reporting	No comment
0.011		contributor to the DNA profile obtained from this item/sample.		Demention	NI
CPU	Complex profile unsultable for	This item/sample gave a complex DNA profile. This DNA profile		Reporting	No comment
	interp or comparison	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.			
IRSUR	Interim Result Sample	This is not a final result and sample/s are currently undergoing		Reporting	No comment
	undergoing rework	rework. Rework can mean that part of the process to obtain a		rteporting	
		DNA profile is repeated or additional testing to improve the DNA			
		profile is being undertaken. Final results are pending			
NDPPTP	No DNA profile – possible sub-	A DNA profile was not obtained from this item/sample, however	Removed last sentence from expanded	Reporting	Agree - removal of last line
	threshold peaks	the possible presence of additional DNA was observed. This	wording		is acceptable.
		possible DNA was not present at a sufficient level to be used for	5		'
		comparison purposes, as it was below QHESS standard reporting			
		thresholds			
NOPRO	No DNA profile	A DNA profile was not obtained from this item/sample.		Reporting	No comment

NWQPSR	QPS advised no further work	QPS have provided advice that no further work is required for this			Reporting	No comment
	required - results available	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. OPS can submit a request to				
		OHESS for further work which may include the interpretation of				
		the DNA results if required, results alone, or DNA profile results				
		the block results in required. Tesuits alone, or DNA prome results				
		request to OHESS for further work which may include the				
		request to QHFSS for further work which may include the				
		interpretation of the DNA results if required.				
PRNCID	DNA profile removed from	The DNA profile obtained from this item/sample has been			Reporting	No comment
	NCIDD	removed from NCIDD following advice from QPS, a change in the				
		NCIDD category, or a profile with more information has been				
		obtained.				
PSTI	Possible sub-threshold	The presence of possible additional DNA was observed within the			Reporting	No comment
	information	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				
SPFRU	Sample processed and final	This item/sample was processed under the barcode sent with this			Reporting	No comment
	results under	exhibit report. The final results will be reported under that				
000	0	barcode.			D finan	N1
SPP	Sample pooled and processed	This item/sample was pooled and submitted for DINA testing			Reporting	No comment
	under	under the barcode sent with this exhibit report. The final results				
	This seconds has undersone	will be reported under the barcode.			Denertier	Nia a anna an t
SUFP	This sample has undergone	This item/sample has undergone further processing and an			Reporting	No comment
NSID	No statistical interpretation	In the absence of a reference sample/s for comparison, a	To nominate a person of interest for comparison to		Peparting	No comment
NOI	norformed	statistical interpretation has not been performed	the mixed DNA Brefile obtained from this exhibit		reporting	No comment
	performed	statistical interpretation has not been performed.	alesse send a task to the DNA Lisison and Major			
TRO	Testing restarted on advice from	QPS have provided advice that testing is now required for this			Reporting	No comment
	OPS	item/sample. Testing has been restarted			i topot i i ig	
SRP	Submitted-results pending	This item/sample was submitted for DNA testing. Results are		Change from exhibit movement to Auto	Evidence Recovery	Evidence Recovery
		pending.		filed examination result line.	,	,
	Describle heir leasted not	Describle beir/e were leasted on this item/semple. These have not			Evidence Recovery	Evidence Recovery
PHNFA	evening of further	Possible flair/s were located on this item/sample. These have hold				
	examined iurther	been examined further and have been retained with the exhibit.				
	Possible bair located Not	Possible hair/s were located on this item/sample. These have not			Evidence Recovery	Evidence Recovery
PHNSA	suitable for analysis	been submitted for DNA testing and have been retained with the				
		exhibit.				
PHSRP	Possible hair located. Submitted	Possible hair/s were located on this item/sample. These have			Evidence Recovery	Evidence Recovery
111014	for analysis	been submitted for DNA testing. Results are pending.				
MPS	Micro positive for sperm	Spermatozoa were detected on this item/sample by microscopy.			Evidence Recovery	Evidence Recovery
	A 11 12					<b>F F</b>
AINT	All items now tested	All items for this exhibit have now been examined			Evidence Recovery	Evidence Recovery
DIFP		This item/sample was submitted for DINA analysis. Low levels of	Please serio a task to the DNA Liaison and Major		Anaiyucal	Analylical
	processing	DIVA were detected in this sample and it was not submitted for	crime Unit (3211) if this sample is required to be			
	Items Prioritised Not examined	Turiner UNA profiling.	assessed for further processing.		Evidence Recovery	Evidence Recovery
	at this time	provided by OPS. Examinations may be conducted in the fitture			Lindence Recovery	Lvidence Recovery
		provided by QFS. Examinations may be conducted in the future.				
IPNST	Items prioritised not submitted	This item/sample has been prioritised and as such samples			Evidence Recovery	Evidence Recovery
	at this time	taken from this exhibit have not been submitted at this time				
MNS	Micro neg for sperm	Spermatozoa were not detected on this item/sample by			Evidence Recovery	Evidence Recovery
		microscopy				

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 anolicable			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 OPRIME	Evidence Recovery	Evidence Recovery
ENAQS	ENVM additional quality search o	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		Lab clean - not reported - new	Environmental	
		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 OHESS DNA Analysis staff DNA				
		database the OPS 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				
		Quality Scientists. In this instance, no matches were obtained.				
New	ENVM - Mixed DNA profile	This environmental sample provided a DNA profile that indicated		Lab clean - not reported - new	Environmental	
		the presence of DNA from at least two contributors. An attempt				
		was made to resolve the contributors of this mixed DNA profile for	1			
		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.				
ENNDP	ENVM - No DNA profile	No DNA profile was obtained from this environmental sample. It	n/a	Lab clean - not reported	Environmental	
		is standard procedure to analyse environmental samples below				
		QHFSS standard reporting thresholds for guality purposes,				
		therefore results for this sample have been interpreted and				
		reported based on these lowered thresholds				
QCF	Quality control failure – results r	During the processing of this item/sample, a failure in one of the	no change suggested	QHFSS quality control failure	Quality failure result	
		quality control processes was identified. Investigations into this				
		occurrence were undertaken; however any results for this sample				
		are not reportable				
QCFRQ	Quality control failure, refer to C	During the processing of this item/sample, QHFSS quality control	no change suggested	QPS quality issue	Quality failure result	
		processes identified the integrity of this sample is compromised.				
		Results for this sample are not reportable.	na abanana ayana ata d		Ouglitu failung nagutt	
QFIH	Quality flag identified, on hold a	During the processing of this item/sample, QHFSS quality control	no change suggested	QHESS quality control failure	Quality failure result	
		processes indentified the integrity of this sample may be				
		compromised. Advice is required from QPS to determine whether				
		lany results for this sample are reportable				

Result type	Mnemonic	Cold link line	Review by DRMU	
Powerplex21 /	FULLCL	Full DNA profile	DNA COLD LINK - This item/sample gave a full DNA profile	New cold link line
Verifiler Plus			which matches the DNA profile obtained from Barcode	
			Number ******* a DNA sample obtained from SURNAME,	
			Number LKR0000***	
Powerplex21 /	PARTCL	Partial DNA profile	DNA COLD LINK - This item/sample gave a partial DNA	New cold link line
Verifiler Plus			profile which matches the DNA profile obtained from Barcode	
			Number ******** a DNA sample obtained from SURNAME,	
			GIVEN NAMES DOB **/**/**** CNI No. ********* DNA Profile	
Devue melev 21	MIXI		Number LKR0000***.	New cold link line
Powerplex21		Mixed DNA profile	indicated the presence of DNA from more than one	New cold link line
			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. ********	
	INTOT		DNA Profile Number LKR00*****.	
Powerplex21		Interstate DNA profile		Retain
Profiler Plus		9 loci DNA profile		Retain for legacy purposes
Profiler Plus	FUPROF	9 loci DNA profile		Retain for legacy purposes
Profiler Plus		9 loci DINA Profile – possible sub-threshold peaks		Retain for legacy purposes
Profiler Plus	PDNA	Partial DNA Profile		Retain for legacy purposes
Profiler Plus		Partial DNA Profile – possible sub-threshold peaks		Retain for legacy purposes
Profiler Plus		Mixed DNA profile, 9 Loci Major Component		Retain for legacy purposes
Profiler Plus	МРРМА	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	мррмі	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 necessari
Powerplex21	MIXCON	Mixed DNA profile – conditioned contribution		Decommission - not necessari
Powerplex21	INT2M1	INTEL – 2 person mix LR < 100		Decommission - not necessari
Powerplex21	2MIXT	2 person mixed DNA profile		Decommission - not necessari
Powerplex21	3MIXT	3 person mixed DNA profile		Decommission - not necessari
Powerplex21	INT2MX	INTEL – (2 person mix)		Decommission - not necessari
Powerplex21	INT3MX	INTEL – (3 person mix)		Decommission - not necessari
Powerplex21	INTRE	INTEL – remaining contribution		Decommission - not necessari
Powerplex21	INTREP	See INTEL report		Decommission - not necessari
Powerplex21	FULL21	Full DNA Profile (PP21)		Decommission - not necessari
Powerplex21	PART21	Partial DNA profile (PP21)		Decommission - not necessari

Recommndations
y deleted - required for legacy purposes
y deleted - required for legacy purposes
y deleted - required for legacy purposes
y deleted - required for legacy purposes
y deleted - required for legacy purposes
y deleted - required for legacy purposes
y deleted - required for legacy purposes
y deleted - required for legacy purposes
y deleted - required for legacy purposes
y deleted - required for legacy purposes
v 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	Thinking: could 1SS just have the	Thinking: could 1SS just have the expanded comment	Discussed
		presence of one contributor. If an unknown designation is sent with	expanded comment changed as	changed as per SS1?	with
		this exhibit report, any reference samples associated to this case have	per SS1?		Justin,
		been excluded as donors of this DNA and this DNA profile has been			agreed to
		designated as an unknown. Alternatively, if a barcode is sent with this			move to
		exhibit report, where information was obtained, this DNA profile			
		matched the corresponding information in the DNA profile from the			551
		associated barcode. This DNA profile has not been statistically			
		evaluated however a likelihood ratio can be provided if required.			
1SS20L	Single source 20 loci DNA profile LR > 100	This item/sample provided a DNA profile that indicated the presence	Agreed	FR code to operate for LR1	
	billion	of one contributor. It obtained all of the DNA information potentially	5		
		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.			
1S9L10	SS DNA profile 9 loci and above LR > 100 billion	This item/sample provided a DNA profile that indicated the presence	Agreed	FR code to operate for LR1	
		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.			
1SS9L9	SS DNA profile 9 loci and above LR 1 billion-	This item/sample provided a DNA profile that indicated the presence	Agreed	FR code to operate for LR2	
	100 billion	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			
1SS9L8	SS DNA profile 9 loci and above LR 1 million - 1	This item/sample provided a DNA profile that indicated the presence	Agreed	FR code to operate for LR3	1
	billion	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			
1SS9L7	SS DNA profile less than 9 loci LR > 100 billion	This item/sample provided a DNA profile that indicated the presence	Agreed	FR code to operate for LR1	1
-	,	of one contributor. It consisted of less than 9 DNA loci and therefore	0		
		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			J

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
змх	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 <u>not</u> 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	Agreed	ER code to operate for EVEX
	g	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 evaluated as having contributed		
		to this mixed DNA profile		
	Interim result_ mixed profile - Intel NCIDD	This is not a final result, sample/s are currently undergoing rework	Agrood	No codo: monuel line
	Rework Road	Powerk con mean that part of the presses to obtain a DNA profile in	Agreeu	No code. manual line
	Rework Requ	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 DINA 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		
		interpretation assumptions. I mai results are pending.		
INTSSR	Interim Result- incomplete single source.	The interim result obtained from this sample/item was an incomplete	Agreed	No code: manual line
	Rework reqd	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.		
CWBM	Consistent with being biological mother	The DNA profile obtained from this exhibit is consistent with being a	Agreed	No code: manual line
		biological child of the barcode sent with this exhibit report.	-	
EXBF	Excluded as biological father	The DNA profile obtained from the barcode sent with this exhibit report	Agreed	No code: manual line
		is excluded as being a biological father of the DNA profile obtained		
		from the exhibit.		
NCWBM	Not consistent with being biological mother	The DNA profile obtained from the barcode is not consistent with	Agreed	No code: manual line
		being a biological mother of the DNA profile obtained from the exhibit.	-	
NEXBF	Not excluded as biological father	The DNA profile obtained from the barcode sent with this exhibit report	Agreed	No code: manual line
	-	is not excluded as being a biological father of the DNA profile obtained	-	
		from the exhibit.		
SCLOW	Suspect check - low support for contribution	The DNA profile provides low support for the proposition that the	Agreed	No code: manual line
		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		
SCSC1	Suspect check - support for contribution 100 to	This DNA profile is between 100 and 1000 times more likely to have	Agreed	No code: manual line
	1000	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		
SCSC2	Suspect check - support for contribution 1000 to	This DNA profile is between 1000 and 10 000 times more likely to	Agreed	No code: manual line
00002		have occurred if the nominated suspect sent with this exhibit report	ABICCU	
		has contributed to this DNA profile, rather than an unknown, unrelated		
1		individual/a. This comparison was done for intelligence recorded and		
1		individual/s. This comparison was done for intelligence purposes only.		
1		A reference evidence sample should be provided if this information is		
1	1	required in a statement for court	1	

SCSC3	Suspect check- support for contribution 10 000	This DNA profile is between 10 000 and 100 000 times more likely to	Agreed	No code: manual line	
	to 100 000	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.			-
SCSC4	Suspect check - support for contrib 100 000 - 1	This DNA profile is between 100 000 and 1 million times more likely to	Agreed	No code: manual line	
	million	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			
SCSC5	Cuspect sheet, support for contribut million 1	required in a statement for court.	Americal	No. and a second line	-
50505	Suspect check- support for contribility million - 1	This DNA profile is between T million and T billion times more likely to	Agreed	No code: manual line	
	Dillion	have occurred in 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			
SCSC6	Suspect check- support for contrib 1 billion- 100	This DNA profile is between 1 billion and 100 billion times more likely	Agreed	No code: manual line	-
00000	billion	to have occurred if the nominated suspect sent with this exhibit report	Agreed	No code. mandal line	
	Simon	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			
SCSC7	Suspect check - support for contribution > 100	This DNA profile is greater than 100 billion times more likely to have	Agreed	No code: manual line	
	billion	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.			
SCINMX	Suspect check inconclusive - mixed DNA profile	The statistical interpretation in relation to the nominated suspect is	Agreed	No code: manual line	
		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.			
SCSNC	Suspect check - supports non contribution	The statistical interpretation provides support for the proposition that	Agreed	No code: manual line	
		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.			
SCANM	Suspect check Action - No Match	The nominated suspect can be excluded as a potential contributor to	Agreed	No code: manual line	
CMDU	Complex mixed profile unquitable for internet	The DINA profile obtained from this item/sample.	A area ad	CD and a to an areta for CDU	-
CMPU	Complex mixed profile unsuitable for interp or	This item/sample gave a complex Mixed DNA profile with multiple	Agreed	FR code to operate for CPU	
	companson	contributors. This mixture is not suitable for meaningful interpretation			
		due to either its complexity relating to the limited encount of information			
		large number of contributors and/or the limited amount of information			
		within the DNA profile.			
DIFP	DNA insufficient for further processing	This item/sample was submitted for DNA analysis. Low levels of DNA	Thinking: could DIEP just have the	Thinking: could DIFP just have the expanded comment	Discussed
	Provinsumoion for further processing	were detected in this sample and it was not submitted for further DNA	avaanded comment shares die	changed as nor DICP1, or makes as difference shore	with
		nrofiling Please contact the DNA Management Section if this sample	expanded comment changed as	changed as per DIFP1, or makes no difference given	with
		is requested to be assessed for further processing. Further processing	per DIFP1, or makes no difference	already in the FR?	Justin,
		could include concentration of the low levels of DNA obtained processing	given already in the FR?		agreed to
		with other samples (where appropriate) resampling of the parent item			move to
		(where appropriate) or a combination of processes			SS1
INTER4	Interim result- mixed profile obtained. Rework	The interim DNA profile obtained from this sample/item indicated the	Agreed	No code: manual line	
--------	--	---	-------------	--------------------------------------	
	Reqd	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.			
INTER6	Interim result- no profile obtained- undergoing	This is not a final result and sample/s are currently undergoing rework.	Agreed	No code: manual line	
	rework	Rework can mean that part of the process to obtain a DNA profile is	0		
		repeated or additional testing to improve the DNA profile is being			
		undertaken. The interim result is no DNA profile. Final results are			
		pending.			
NOPROF	No DNA profile	A DNA profile was not obtained from this item/sample, due to, but not		FR code to operate for NOPRO	
		limited to: no DNA present, poor quality of the DNA, insufficient			
		quantity of DNA, or inhibition of the DNA.			
PAPPRP	Presump. PSA test positive, submitted - results	This item/sample tested positive to a presumptive test for Prostate	NOT TO DECO	OMMISSION until new lines available.	
	pending	Specific Antigen (PSA) which is a component of seminal fluid. This			
		item was submitted for DNA testing. Results are pending.			
PBNSC	Presumptive blood test neg. Submitted for cells	This item/sample tested negative to a presumptive test for blood	Agreed		
		(TMB). This item was submitted for general cell DNA testing.			
PPUCP	Partial DNA profile unsuitable for comparison	This item/sample gave a partial DNA profile which was insufficient for	Agreed	FR code for CPU	
	purposes	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.			
PSNSC	Presump saliva negative. Submitted for cells	This item/sample tested negative to a presumptive test for saliva	Agreed		
		(Phadebas). This item/sample was submitted for general cell DNA			
		testing.			
SOFWC	Sample undergone further work - conditioned	This item/sample gave a mixed DNA profile that indicated the	Agreed	No code: manual line	
		presence of DNA from two or more contributors. Based on information			
		provided to the laboratory, this mixed DNA profile has now been			
		conditioned.			
SUFNS	Sample undergone reprocessing - new software	This item/sample has undergone further processing and/or	Agreed	No code: manual line	
		assessment with new software available to the laboratory. An updated			
	I lais la sata d. Ostanitta dina sulta nan dia n	DNA profile interpretation has been provided.			
HLSRP	Hair located. Submitted results pending	Hair/s were located on this item/sample. These hairs have been	NOT TO DECO	OMMISSION until new lines available.	
	Mission a stilling for an army Outbraithed as sufficient	submitted for DNA testing. Results are pending.			
SPPDNA	Micro positive for sperm. Submitted-results	Spermatozoa were detected on this item/sample by microscopy. This	NOT TO DECC	JMMISSION until new lines available.	
	penaing	item/sample was submitted for DNA testing. Results are pending.			
EMDP	Excluded from mixed DNA profile	This item/sample provided a mixed DNA profile that indicated the	Agrood		
LIVIDE	Excluded from mixed DNA profile	proscence of DNA from two or three contributors. All of the reference	Agreed		
		DNA profiles associated with this asso have been compared with this			
		DNA profile apparetaly. The statistical interpretation shows that some			
		DNA prome separately. The statistical interpretation shows that some			
		or all of the donors of the reference DNA profiles associated with this			
1		case are excluded as having contributed to this mixed DNA profile.			
MINAI	Multiple items - not all tested	This exhibit consisted of multiple items packaged together under one	Agreed		
		exhibit barcode of which not all were selected for examination. If more	, Breed		
1		or all of the remaining items are required to be examined, this can be			
1		completed upon request			

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 profile sassociated 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 linterpretation 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	
ISSIND	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	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	Agreed	
2.110 (1112)		order to resolve any DNA profiles suitable for loading to NCIDD. In this	NBI CCU	
		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.		
	O no service descent for a settile stice	This item /s see is a second start a DNIA was file that is discussed the second second	•	
ZINIXLOW	2 person mix - low support for contribution	I his item/sample provided a DNA profile that indicated the presence	Agreed	
		of DNA from two contributors. The DNA profile provides low support		
		tor the proposition that the associated barcode is a contributor of DNA		
		to this mixed DNA profile. Please contact DNA Analysis if further		
2MXNC	2 person mix - supports non contribution	This item/sample provided a DNA profile that indicated the presence	Agrood	
210170110	2 person mix - supports non contribution	of two contributors. The statistical interpretation provides support for	Agreeu	
		the proposition that the associated barcode has not contributed to this		
		mixed DNA profile		
2MXNCD	NCIDD upload - mixed DNA profile	The mixed DNA profile result for this sample has been deconvoluted in	Agreed	
-		order to resolve any DNA profiles suitable for loading to NCIDD. In this	, B. CCC	
		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		
1		ratio. Depending on the nature of the mixed DNA profile, the strength		
1		of the support for contribution will vary.		
1				
1				

2MXNIR	Mixture contribution loaded to NCIDD - see Intel	The mixed DNA profile result for this sample has been deconvoluted in	Agreed	
	report	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		
2MXR1	2 person mix remaining - support for contrib 100	This item/sample provided a DNA profile that indicated the presence	Agreed	
	to 1000	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		
2MXR2	2 person mix remaining- support for contrib	This item/sample provided a DNA profile that indicated the presence	Agreed	
	1000 to 10000	of two contributors. When conditioning on the assumed known	0	
		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		
2MXR3	2 person mix rem - support for contrib 10 000 to	This item/sample provided a DNA profile that indicated the presence	Agreed	
	100 000	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		
2MXR4	2 person mix rem- support for contrib 100000 to	This item/sample provided a DNA profile that indicated the presence	Agreed	
2.000	1 million	of two contributors. When conditioning on the assumed known	, Bicca	
		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		

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 individuel	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	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	
ЗМХЗ	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. 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	This item/sample provided a DNA profile that indicated the presence	Agreed	
0	to 1000	of three contributors. When conditioning on the assumed known	, greed	
	10 1000	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 accumed known		
		antributer this DNA profile is between 400 and 4000 times more		
		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,		
3MXR2	3 person mix remaining, support for contrib	This item/sample provided a DNA profile that indicated the presence	Agrood	
01117(172	1000 to 10000	of three contributors. When conditioning on the assumed known	Agreeu	
	1000 10 10000	contributor, some or all of the components of the DNA profile from the		
		contributor, some of all of the components of the DNA profile from the		
		associated balcode sent with this exhibit report are represented within the remaining DNA profile. When conditioning on the provinced known		
		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,		
3MXR3	3 person mix rem - support for contrib 10 000 to	This item/sample provided a DNA profile that indicated the presence	Agreed	
01174140		of three contributors. When conditioning on the assumed known	Agreed	
	100 000	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		
		contributor, this DNA prome 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,		
3MXR4	3 person mix rem- support for contrib 100000 to	This item/sample provided a DNA profile that indicated the presence	Agreed	
	1 million	of three contributors. When conditioning on the assumed known	, greed	
		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		
		contributor, this DNA prome is between 100 000 and 1 minion times		
		hore likely to have occurred if the barcode sent with this exhibit report		
		has also contributed to this DNA profile, rather than two unknown,		
2MXCND	NCIDD upload - conditioned contribution	The mixed DNA profile result for this sample has been deconvoluted in	Agreed	
2.0.70112		order to resolve any DNA profiles suitable for loading to NCIDD. For	, greed	
		ease of differentiation between the resolved contributions, the		
		designations 'conditioned' and 'remaining' have been applied. The		
		conditioned contribution described by the associated barcode bas		
		been selected for leading to NCIDD. This DNA profile will be searched		
		against any DNA profiles already hold on NCIDD. (as nor the NCIDD		
		against any DNA promes aready new on NCIDD (as per the NCIDD)		
		matching rules). Any subsequent profiles that are loaded to NCIDD will		
		be searched against this DNA profile.		
3MXR5	3 person rem - support for contrib 1 million to 1	This item/sample provided a DNA profile that indicated the presence	Agreed	
	billion	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 hillion times		
		more likely to have occurred if the barcode sent with this exhibit report		
		has also contributed to this DNA profile, rather than two upknown		
		unrelated individuals		

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	

	2 menone assisted anofile assistance associations	This item/seconds are vided a DNA arefile that indicated the averages	A mus and	
3MXRND	3 person mixed profile, mixture remaining	I his item/sample provided a DNA profile that indicated the presence	Agreed	
	NCIDD	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		
3MXRUN	3 Person Mix Rem DNA contrib unsuitable for	The mixed DNA profile result for this sample indicates three	Agreed	
	NCIDD	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.		
MXREMI	Remaining contribution - inconclusive	This item/sample provided a DNA profile that indicated the presence	Agreed	
	· · · · · · · · · · · · · · · · · · ·	of two or three contributors. When conditioning on the assumed	, gi ceu	
		known contributor, the statistical interpretation in relation to the		
		associated barcode is inconclusive		
2MXUNM	Mix Remaining DNA contribution indicates male	The remaining contribution separated after conditioning the mixed	Agreed	
	origin	DNA profile indicates male origin	0	
2MXUNS	Mix Rem DNA contrib unsuitable for NCIDD	The mixed DNA profile result for this sample indicates two	Agreed	
	searching	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.		

SCLNSC	Suspect check - low support or non contrib	One or more of the contributors to this DNA profile has limited	Agreed	
		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		
1SS9L3	Single source DNA profile < 9 loci LR 10 000 -	This item/sample provided a DNA profile that indicated the presence	Agreed	
	100 000	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		
1SS9L2	Single source DNA profile < 9 loci LR 1000 - 10	This item/sample provided a DNA profile that indicated the presence	Agreed	
	000	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		
1SS9L1	Single source DNA profile < 9 loci LR 100 -	This item/sample provided a DNA profile that indicated the presence	Agreed	
	1000	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		
1SSLND	Single source DNA profile < NCIDD matching	The incomplete DNA profile obtained from this item/sample indicated	Agreed	
	stringency	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 OHSS 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		
		a intellitood ratio can be provided il required.		
NHLNE	No hair located. No further examination conducted	The item/sample was examined for the presence of hair and none was	NOT TO DECON	MMISSION until new lines available.
		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.		
		Č		
OHPFW	On hold, pending further work	These results are currently subject to quarantine pending the	Agreed	
		completion of further quality checks. The outcome of these quality		
		checks will be reported once complete.		
PPSANS	Presump. PSA test positive, no sperm found	This item/sample tested positive to a presumptive test for Prostate	Agreed	
		Specific Antigen (PSA) which is a component of seminal fluid. No		
		spermatozoa were detected by microscopy. This item was submitted		
1		for DNA testing. Results are pending.		

PSPSRP	Presump saliva positive. Submitted-results pend	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	Decommission	Lab clean - not reported
		insufficient for comparison purposes or meaningful interpretation due		
		to the limited amount of information obtained. It is standard procedure		
		to analyse environmental samples below QHFSS standard reporting		
		thresholds for quality purposes, therefore results for this sample have		
		been interpreted and reported based on these lowered thresholds.		

Mnemonic	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	no change suggested	Profiler plus result	Retain as required
		presence of DNA from at least two contributors. This mixed DNA profile could			for old cases
		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.			
CMPULN	Complex mixed DNA profile. Unable to load to NCIDD	This item/sample gave a full or partial mixed DNA profile which indicated the	no change suggested	Profiler plus result	
		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 il forthcoming.			
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	n/a	Profiler plus result	
		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.			
DPPTP	9 loci DNA profile - possible sub-threshold peaks	This item/sample gave a full 9 loci DNA profile which matches the DNA profile	n/a	Profiler plus result	
		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.			
FUPNPN	9 loci DNA profile. Uploaded to NCIDD	This item/sample gave a full 9 loci DNA profile which matches the DNA profile	n/a	Profiler plus result	
		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			
	A loci DNA profile	UNA profile. This item/sample gave a full Q loci DNA profile which matches the DNA profile.	n/a	Profiler plus recult	
FUFRUF	S IOCI DIAR PIOIIIE	abtained from the bareade cont with this exhibit report	11/4	Fromer 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	n/a	Profiler plus result	
		DNA profile contained insufficient information for NCIDD matching as it was		in the place resource	
		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			

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. This result should always be used in SDNA profile has been selected for loading to NCIDD. This DNA profile will be searched against any DNA profile 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 that are uploaded to NCIDD will be searched against the 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 evidential statement of the interpreted against this intelligence to NA profile. It will be outlined in the Intelligence report that this mixed DNA profile may be reported differently in an evidential 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 which indicated the presence of DNA regulation of DNA profile.	n/a	Profiler plus result
MPCO		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"	iva	
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 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 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	
		DNA from two contributors. This mixed DNA profile winth indicated the presence of 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.	liva		
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 orthocoming.	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 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 obtained from the barcode sent with this exhibit report (if explicitly).	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 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 equition.	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 profile loaded to 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 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	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 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	no change suggested	Information sent via Examination	Retain for
		hanging in and out of the tube. It is unclear if this hair was		request notification by QHFSS to SOC	discussion with
		part of the collected item or incorrectly transferred during		/ SCI officer	QPS in the future
		collection. This hair/hair portion has been stored and will			
		only be analysed if a request is provided			
ISCB	Incorrect submission of cigarette butt	This cigarette butt was received in a tube. Items provided	n/a	Information sent via Examination	Retain for
		in a tube are intended to be submitted directly for DNA		request notification by QHFSS to SOC	discussion with
		processing with minimal manual intervention. This sample		/ SCI officer	QPS in the future
		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			
LDIS	Labelling discrepancy	There is a labelling discrepancy (Occurrence number or	n/a	Information sent via Examination	Retain for
		sample description) between the exhibit packaging and the		request notification by QHFSS to SOC	discussion with
		AUSLAB/Forensic Register interface records. This sample		/ SCI officer	QPS in the future
		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			
MIES	Sample required manual intervention - excess substrat	This item/sample provided in a tube required manual	n/a	Information sent via Examination	Retain for
		intervention prior to processing through QHESS extraction		request notification by QHESS to SOC	discussion with
		methods as excess substrate was contained within the		/ SCI officer	QPS in the future
		tube. This necessitated additional resources to perform			
		manipulation on the item/sample examined by OPS to			
		ensure it was appropriate for the DNA extraction process			
MIISB	Multiple items incorrectly submitted under single barco	Multiple items, or multiple AP positive areas have been	n/a	Information sent via Examination	Retain for
		submitted under a single barcode identifier. Each item		request notification by QHFSS to SOC	discussion with
		requires its own unique barcode, as the barcode is used		/ SCI officer	QPS in the future
		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			
MISSIL	Sample required manual intervention - swab stick too lo	I his item/sample provided in a tube required manual	n/a	Information sent via Examination	Retain for
		intervention prior to processing through QHFSS extraction		request notification by QHFSS to SOC	discussion with
		methods as the swab stick was too long and required		/ SCI officer	QPS in the future
		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).			
1	1		l		

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
ОНІІ	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** 

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

## OFFICIAL

## OFFICIAL

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

McIntyre.OliviaM[OSC] < Adrian Pippia <

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		
<b>DNA Analysis</b> Prevention Division, Queensland Health		
p 07 e w <u>www.hea</u>	lth.qld.gov.au/fss	
Queensland Health acknowledges the Traditional Owners	s of the land, and pays respect to Elders past, present and emerging.	
From: Justin Howes <		
Sent: Wednesday, 8 September 2021 3:10	PM	
To: McIntyre.OliviaM[OSC] <		
<b>Cc:</b> Harris.LibbyA[OSC] <	Allison Lloyd <	Adrian
Pippia <		
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



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



Wash your hands regularly to stop the spread of germs.

From: Justin Howes		
Sent: Wednesday, 8 September 2021 2:28	PM	
To: McIntyre.OliviaM[OSC] <		
Cc: Harris.LibbyA[OSC] <	Allison Lloyd <	Adrian
Pippia <		
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 <u>we</u> <u>do not want</u> 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



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



# Wash your hands regularly to stop the spread of germs.

From: McIntyre.OliviaM[OSC] <
Sent: Wednesday, 8 September 2021 1:44 PM
To: Justin Howes <
Cc: Harris.LibbyA[OSC] <</pre>

McIntyre.OliviaM[OSC]

Subject: Result wording for discussion

<

155	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: Mobile

200 Roma Street, Brisbane



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

CONFIDENTIALITY: The information contained in this electronic mail message and any electronic files attached to it may be confidential information, and may also be the subject of legal professional privilege and/or public interest immunity. If you are not the intended recipient you are required to delete it. Any use, disclosure or copying of this message and any attachments is unauthorised. If you have received this electronic message in error, please inform the sender or contact <u>1300ITPSBA@psba.qld.gov.au</u>. This footnote also confirms that this email message has been checked for the presence of computer viruses.

# 

Disclaimer: This email and any attachments may contain legally privileged or confidential information and may be protected by copyright. You must not use or disclose them other than for the purposes for which they were supplied. The privilege or confidentiality attached to this message and attachments is not waived by reason of mistaken delivery to you. If you are not the intended recipient, you must not use, disclose, retain, forward or reproduce this message or any attachments. If you receive this message in error, please notify the sender by return email or telephone and destroy and delete all copies. Unless stated otherwise, this email represents only the views of the sender and not the views of the Queensland Government.

Queensland Health carries out monitoring, scanning and blocking of emails and attachments sent from or to addresses within Queensland Health for the purposes of operating, protecting, maintaining and ensuring appropriate use of its computer network.

EXHIBIT 195

From:	Harris.LibbyA[ESC]
Sent:	Tuesday, 13 February 2018 07:25
То:	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 3:02 PM		
To: Taylor.EwenN[OSC] <			
Cc: Collopen.RubenB[OSC] <		Gee Kee.KenN[OSC]	
<	>; Harris.LibbyA[OSC] <		
Subject: RE: FSS results identified	d 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:
 | fax:

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

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 ph: \_\_\_\_\_\_ fax:

EXHIBIT 196

### De Marco.JennaL[LD]

From: Sent:	McIntyre.OliviaM[OSC] Friday, 2 March 2018 07:32
То:	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

 GPO Box 1440 | Brisbane QLD 4001 | Australia

 Level 4, Police Headquarters | 200 Roma Street | Brisbane QLD 4000 | Australia

 ph:
 | fax:

EXHIBIT 197

From:	Cathie Allen
Sent:	Tuesday, 20 November 2018 08:48
То:	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



From: Simpfendorfer.Gerard			
Sent: Monday, 19 November 201	8 3:34 PM		
To: Cathie Allen			
Cc: Neville.David	McNab	Collopen	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

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



We have more than 12,000 crimes with DNA evidence. We just need the offender. Always check/take offender's DNA.

CONFIDENTIALITY: The information contained in this electronic mail message and any electronic files attached to it may be confidential information, and may also be the subject of legal professional privilege and/or public interest immunity. If you are not the intended recipient you are required to delete it. Any use, disclosure or copying of this message and any attachments is unauthorised. If you have received this electronic message in error, please inform the sender or contact 1300ITPSBA@psba.qld.gov.au. This footnote also confirms that this email message has been checked for the presence of computer viruses.

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

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

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

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

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

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

EXHIBIT 198

From:	Cathie Allen
Sent:	Thursday, 6 December 2018 11:42
То:	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

 p
 m

a 39 Kessels Road, Coopers Plains, QLD 4108

e

w www.health.qld.gov.au/healthsupport

Integrity Customers and patients first Accountability Respect Engagement

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

From: Simpfendorfer.GerardM[OSC] [mailto:
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

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



We have more than 12,000 crimes with DNA evidence. We just need the offender. Always check/take offender's DNA.



From: Cathie Allen < Sent: Thursday, 6 December 2018 9:07 AM To: Simpfendorfer.GerardM[OSC] < Cc: Craig Russell < McNab.BruceJ[OSC] < < Har

Neville.DavidH[OSC] < Collopen.RubenB[OSC]

Harris.LibbyA[OSC] <

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

 p
 m

a 39 Kessels Road, Coopers Plains, QLD 4108

e

w www.health.qld.gov.au/healthsupport



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

From: Simpfendorfer.GerardM[OSC] [mailto:
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

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

> We have more than 12,000 crimes with DNA evidence. We just need the offender. Always check/take offender's DNA.



From: Cathie Allen <
Sent: Wednesday, 5 December 2018 5:51 PM
To: Simpfendorfer.GerardM[OSC] <
Cc: Craig Russell < Neville.
McNab.BruceJ[OSC] < Col
Harris.LibbyA[OSC] <

Neville.DavidH[OSC] <

Collopen.RubenB[OSC]

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

 p
 m

 a 39 Kessels Road, Coopers Plains, QLD 4108

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



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

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

 p
 m

 a 39 Kessels Road, Coopers Plains, QLD 4108

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



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

From: Simpfendorfer.GerardM[OSC] [mailto:
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. 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

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

> We have more than 12,000 crimes with DNA evidence. We just need the offender.

Always check/take offender's DNA



From: Simpfendorfer.GerardM[OSC] Sent: Thursday, 22 November 2018 3:54 PM To: Cathie Allen < Neville.DavidH[OSC] < Cc: Craig Russell < McNab.BruceJ[OSC] < Collopen.RubenB[OSC] Harris.LibbyA[OSC] <

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





From: Cathie Allen < Sent: Wednesday, 21 November 2018 12:14 PM To: Simpfendorfer.GerardM[OSC] < Cc: Craig Russell < McNab.BruceJ[OSC] <

Neville.DavidH[OSC] < Collopen.RubenB[OSC]

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	Trace DN	A Kit 🗗	08/11/2018		40
6D: TRACE QHSS POS QHSS POS QHSS POS	DNA TAPEL	IFT COLLECTED FROM FND Scientific Sec DNA INSUFFICIENT FO THIS SAMPLE HAS UN COMPLEX MIXED PRO	CENTRAL BODY O tion - Exam Suite OR FURTHER PROC DERGONE FURTHE FILE UNSUITABLE	OF STICK COLL 2 CESSING ER PROCESSIN FOR INTERP C	ECTED FROM S
Cheers Cathie					
$\prec$					
Cathie Allen Managing Scientis	t				
Police Services S Health Support Qu	<b>itream, Forens</b> leensland, Que	ic & Scientific Services ensland Health			
p m a 39 Kessels Road e	l, Coopers Plai	ns, QLD 4108 <mark>w</mark> <u>www.health.qld.gov.au/healt</u>	<u>hsupport</u>		
Integrity	Custome	ers and patients first	Accountability	Respect	Engagement
Queensland Health ad	knowledges the T	raditional Owners of the land, and pay	s respect to Elders past, prese	ent and future.	

From: Simpfendorfer.GerardM[OSC] [mailto: 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 Internal PHQ Extension: Fax: +61 7 Email: Address: Level 4 Police Headquarters, 200 Roma St, Brisbane, Qld, 4000 Postal: GPO Box 1440, Brisbane, Queensland 4001, Australia

> We have more than 12,000 crimes with DNA evidence. We just need the offender. Always check/take offender's DNA.

 From: Cathie Allen 

 Sent: Friday, 16 November 2018 4:01 PM

 To: Simpfendorfer.GerardM[OSC] <</td>

 Cc: Craig Russell 

 McNab.BruceJ[OSC] <</td>

 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



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

 p
 m

 a 39 Kessels Road, Coopers Plains, QLD 4108

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



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

From: Simpfendorfer.GerardM[OSC] [mailto:
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

Phone: +61 7 3364 6916 Internal PHQ Extension: 66916 Fax: +61 7 Email: Address: Level 4 Police Headquarters, 200 Roma St, Brisbane, Qld, 4000 Postal: GPO Box 1440, Brisbane, Queensland 4001, Australia

From: Cathie Allen <		
Sent: Thursday, 15 November 2018 9:	20 AM	
To: Simpfendorfer.GerardM[OSC] <		McNab.BruceJ[OSC]
<		_
Cc: Craig Russell <	Neville.DavidH[OSC] <	
Subject: FW: Removal of the microcon	n 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:

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 1<sup>st</sup> 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 12<sup>th</sup> 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 12<sup>th</sup> 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

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



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

From: Neville.DavidH[OSC] [mailto:
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 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:



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 <	>; O'Malley.TroyS[OSC] <
Cc: Paul Csoban <	
Subject: RE: Options Paper for considera	ation
Hi Cathie and Paul,	
Thank you for your time this afternoon a	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 'ai
- Option 2. "Cease the 'auto-microcon' process for Priority 2 casework...." Would appear to be a
- · 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 updated
- DNA staff can request this additional processing if/when a request is received from the invest

I trust this is of assistance.

Kind regards,

Dale.

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

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 Email Address

s GPO Box 1440 Brisbane 4001

CONFIDENTIALITY: The information contained in this electronic mail message and any electronic files attached to it may be confidential information, and may also be the subject of legal professional privilege and/or public interest immunity. If you are not the intended recipient you are required to delete it. Any use, disclosure or copying of this message and any attachments is unauthorised. If you have received this electronic message in error, please inform the sender or contact <u>1300ITPSBA@psba.qld.gov.au</u>. This footnote also confirms that this email message has been checked for the presence of computer viruses.

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

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

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

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

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

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

\*

CONFIDENTIALITY: The information contained in this electronic mail message and any electronic files attached to it may be confidential information, and may also be the subject of legal professional privilege and/or public interest immunity. If you are not the intended recipient you are required to delete it. Any use, disclosure or copying of this message and any attachments is unauthorised. If you have received this electronic message in error, please inform the sender or contact <u>1300ITPSBA@psba.qld.gov.au</u>. This footnote also confirms that this email message has been checked for the presence of computer viruses.

CONFIDENTIALITY: The information contained in this electronic mail message and any electronic files attached to it may be confidential information, and may also be the subject of legal professional privilege and/or public interest immunity. If you are not the intended recipient you are required to delete it. Any use, disclosure or copying of this message and any attachments is unauthorised. If you have received this electronic message in error, please inform the sender or contact <u>1300ITPSBA@psba.qld.gov.au</u>. This footnote also confirms that this email message has been checked for the presence of computer viruses.

CONFIDENTIALITY: The information contained in this electronic mail message and any electronic files attached to it may be confidential information, and may also be the subject of legal professional privilege and/or public interest immunity. If you are not the intended recipient you are required to delete it. Any use, disclosure or copying of this message and any attachments is unauthorised. If you have received this electronic message in error, please inform the sender or contact <u>1300ITPSBA@psba.qld.gov.au</u>. This footnote also confirms that this email message has been checked for the presence of computer viruses.

CONFIDENTIALITY: The information contained in this

electronic mail message and any electronic files attached to it may be confidential information, and may also be the subject of legal professional privilege and/or public interest immunity. If you are not the intended recipient you are required to delete it. Any use, disclosure or copying of this message and any attachments is unauthorised. If you have received this electronic message in error, please inform the sender or contact <u>1300ITPSBA@psba.qld.gov.au</u>. This footnote also confirms that this email message has been checked for the presence of computer viruses.

CONFIDENTIALITY: The information contained in this electronic mail message and any electronic files attached to it may be confidential information, and may also be the subject of legal professional privilege and/or public interest immunity. If you are not the intended recipient you are required to delete it. Any use, disclosure or copying of this message and any attachments is unauthorised. If you have received this electronic message in error, please inform the sender or contact 1300ITPSBA@psba.qld.gov.au. This footnote also confirms that this email message has been checked for the presence of computer viruses.

**EXHIBIT 199** 

From:	McLaren.ScottA[PCAP]
Sent:	Thursday, 3 January 2013 12:42
То:	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

EXHIBIT 200

From:McNab.BruceJ[OSC]Sent:Wednesday, 22 June 2022 16:44To: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

Police HQ 200 Roma Street Brisbane QLD 4000



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

From: Neville.DavidH[OSC] < Sent: Wednesday, 22 June 2022 09:18 To: McNab.BruceJ[OSC] < 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] <
Sent: Wednesday, 22 June 2022 08:34
To: Neville.DavidH[OSC] <
Subject: FW: FSS advice regarding DNA reporting</pre>

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



Bruce McNab BM Superintendent 7417 Forensic Services Group OPERATIONS SUPPORT COMMAND

Police HQ 200 Roma Street Brisbane QLD 4000



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

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

**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 Bruce

On Monday, 6<sup>th</sup> 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 6<sup>th</sup> 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



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

Disclaimer: This email and any attachments may contain legally privileged or confidential information and may be protected by copyright. You must not use or disclose them other than for the purposes for which they were supplied. The privilege or confidentiality attached to this message and attachments is not waived by reason of mistaken delivery to you. If you are not the intended recipient, you must not use, disclose, retain, forward or reproduce this message or any attachments. If you receive this message in error, please notify the sender by return email or telephone and destroy and delete all copies. Unless stated otherwise, this email represents only the views of the sender and not the views of the Queensland Government.

Queensland Health carries out monitoring, scanning and blocking of emails and attachments sent from or to addresses within Queensland Health for the purposes of operating, protecting, maintaining and ensuring appropriate use of its computer network.

EXHIBIT 201

From:	Matthew Rigby <
Sent:	Wednesday, 17 August 2022 19:09
То:	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

**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 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



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

м	
Е	
w	health.qld.gov.au

A Level 14, 33 Charlotte Street, Brisbane QLD 4000

Disclaimer: This email and any attachments may contain legally privileged or confidential information and may be protected by copyright. You must not use or disclose them other than for the purposes for which they were supplied. The privilege or confidentiality attached to this message and attachments is not waived by reason of mistaken delivery to you. If you are not the intended recipient, you must not use, disclose, retain, forward or reproduce this message or any attachments. If you receive this message in error, please notify the sender by return email or telephone and destroy and delete all copies. Unless stated otherwise, this email represents only the views of the sender and not the views of the Queensland Government.

Queensland Health carries out monitoring, scanning and blocking of emails and attachments sent from or to addresses within Queensland Health for the purposes of operating, protecting, maintaining and ensuring appropriate use of its computer network.

\*

## WIT.0020.0008.0169

Procedure for Case Management

#### **19.4 Quantification workflow**









# **MEMORANDUM**

То:	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 Prio	rity 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

From:	Neville.DavidH[OSC]	
Sent:	Friday, 19 August 2022 09:22	
То:	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: Mob: From: Matthew Rigby < Sent: Wednesday, August 17, 2022 7:10 pm To: Neville.DavidH[OSC] < Cc: David Rosengren < Subject: FSS SOP draft memo

**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 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

d

lotte Street, Brisbane QLD 4000
-

Disclaimer: This email and any attachments may contain legally privileged or confidential information and may be protected by copyright. You must not use or disclose them other than for the purposes for which they were supplied. The privilege or confidentiality attached to this message and attachments is not waived by reason of mistaken delivery to you. If you are not the intended recipient, you must not use, disclose, retain, forward or reproduce this message or any attachments. If you receive this message in error, please notify the sender by return email or telephone and destroy and delete all copies. Unless stated otherwise, this email represents only the views of the sender and not the views of the Queensland Government.

Queensland Health carries out monitoring, scanning and blocking of emails and attachments sent from or to addresses within Queensland Health for the purposes of operating, protecting, maintaining and ensuring appropriate use of its computer network.

\*\*\*\*\*

## WIT.0020.0008.0175

Procedure for Case Management

#### **19.4 Quantification workflow**









# MEMORANDUM

То:	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 Prio	rity 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

EXHIBIT 203

From:	Helen Gregg <	
Sent:	Friday, 19 August 2022 15:42	
То:	Neville.DavidH[OSC]	
Cc:	Foxover.StephanP[OSC]; McCarthy.DuncanJ[OSC]	
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.

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



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

From: Neville.DavidH[OSC] <	
Sent: Wednesday, 17 August 2022 8:19 AM	
<b>To:</b> Helen Gregg <	
Cc: Foxover.StephanP[OSC] <	McCarthy.DuncanJ[OSC]
<	

Subject: FW: 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.

#### 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: Mob:

 From: Pobar.DarrenJ[OSC] 

 Sent: Wednesday, 17 August 2022 07:14

 To: Neville.DavidH[OSC] 

 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

I 200 Roma Street Brisbane



From: Helen Gregg

Sent: Wednesday, 20 July 2022 12:36
## To: Pobar.DarrenJ[OSC] <

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] <
Sent: Wednesday, 20 July 2022 9:51 AM
To: Helen Gregg <
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

I 200 Roma Street Brisbane



From: Pobar.DarrenJ[OSC] Sent: Friday, 15 July 2022 12:00 To: 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



CONFIDENTIALITY: The information contained in this electronic mail message and any electronic files attached to it may be confidential information, and may also be the subject of legal professional privilege and/or public interest immunity. If you are not the intended recipient you are required to delete it. Any use, disclosure or copying of this message and any attachments is unauthorised. If you have received this electronic message in error, please inform the sender or contact <u>1300.psaict@police.qld.gov.au</u>. This footnote also confirms that this email message has been checked for the presence of computer viruses.

Disclaimer: This email and any attachments may contain legally privileged or confidential information and may be protected by copyright. You must not use or disclose them other than for the purposes for which they were supplied. The privilege or confidentiality attached to this message and attachments is not waived by reason of mistaken delivery to you. If you are not the intended recipient, you must not use, disclose, retain, forward or reproduce this message or any attachments. If you receive this message in error, please notify the sender by return email or telephone and destroy and delete all copies. Unless stated otherwise, this email represents only the views of the sender and not the views of the Queensland Government.

Queensland Health carries out monitoring, scanning and blocking of emails and attachments sent from or to addresses within Queensland Health for the purposes of operating, protecting, maintaining and ensuring appropriate use of its computer network.

CONFIDENTIALITY: The information contained in this electronic mail message and any electronic files attached to it may be confidential information, and may also be the subject of legal professional privilege and/or public interest immunity. If you are not the intended recipient you are required to delete it. Any use, disclosure or copying of this message and any attachments is unauthorised. If you have received this electronic message in error, please inform the sender or contact <u>1300.psaict@police.qld.gov.au</u>. This footnote also confirms that this email message has been checked for the presence of computer viruses.

EXHIBIT 204

From:	Matthew Rigby <
Sent:	Friday, 19 August 2022 16:29
То:	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

**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 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



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

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 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: Mob:

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

**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 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



Matt Rigby Executive Director

Office of the Director-General Queensland Health

of the sender and not the views of the Queensland Government.

М	
Е	
w	health.qld.gov.au
_	

A Level 14, 33 Charlotte Street, Brisbane QLD 4000

Disclaimer: This email and any attachments may contain legally privileged or confidential information and may be protected by copyright. You must not use or disclose them other than for the purposes for which they were supplied. The privilege or confidentiality attached to this message and attachments is not waived by reason of mistaken delivery to you. If you are not the intended recipient, you must not use, disclose, retain, forward or reproduce this message or any attachments. If you receive this message in error, please notify the sender by return email or telephone and destroy and delete all copies. Unless stated otherwise, this email represents only the views

Queensland Health carries out monitoring, scanning and blocking of emails and attachments sent from or to addresses within Queensland Health for the purposes of operating, protecting, maintaining and ensuring appropriate use of its computer network.

CONFIDENTIALITY: The information contained in this electronic mail message and any electronic files attached to it may be confidential information, and may also be the subject of legal professional privilege and/or public interest immunity. If you are not the intended recipient you are required to delete it. Any use, disclosure or copying of this message and any attachments is unauthorised. If you have received this electronic message in error, please inform the sender or contact <u>1300.psaict@police.qld.gov.au</u>. This footnote also confirms that this email message has been checked for the presence of computer viruses.



# MEMORANDUM

То:	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
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

<

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

## WIT.0020.0008.0189

Procedure for Case Management

## **19.4 Quantification workflow**







EXHIBIT 205







































From:	Neville.DavidH[OSC]
Sent:	Thursday, 8 September 2022 08:58
То:	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: Mob:

From: Matthew Rigby < Sent: Friday, 19 August 2022 16:29 To: Neville.DavidH[OSC] < Cc: McCarthy.DuncanJ[OSC] <

David Rosengren

Subject: RE: FSS SOP draft memo

**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 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



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

М	
Е	
w	<u>health.qld.gov.au</u>

A Level 14, 33 Charlotte Street, Brisbane QLD 4000

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

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

**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 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



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

Μ	
Е	
w	health.qld.gov.au
Α	Level 14, 33 Charlotte Street, Brisbane QLD 4000

Disclaimer: This email and any attachments may contain legally privileged or confidential information and may be protected by copyright. You must not use or disclose them other than for the purposes for which they were supplied. The privilege or confidentiality attached to this message and attachments is not waived by reason of mistaken delivery to you. If you are not the intended recipient, you must not use, disclose, retain, forward or reproduce this message or any attachments. If you receive this message in error, please notify the sender by return email or telephone and destroy and delete all copies. Unless stated otherwise, this email represents only the views of the sender and not the views of the Queensland Government.

Queensland Health carries out monitoring, scanning and blocking of emails and attachments sent from or to addresses within Queensland Health for the purposes of operating, protecting, maintaining and ensuring appropriate use of its computer network.

CONFIDENTIALITY: The information contained in this electronic mail message and any electronic files attached to it may be confidential information, and may also be the subject of legal professional privilege and/or public interest immunity. If you are not the intended recipient you are required to delete it. Any use, disclosure or copying of this message and any attachments is unauthorised. If you have received this electronic message in error, please inform the sender or contact <u>1300.psaict@police.qld.gov.au</u>. This footnote also confirms that this email message has been checked for the presence of computer viruses.



# MEMORANDUM

То:	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
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

<

Dr David Rosengren Acting Director-General 19/08/2022
## WIT.0020.0008.0217

Procedure for Case Management

## **19.4 Quantification workflow**



