STATEMENT OF ALICIA QUARTERMAIN

I **Alicia Quartermain** of Queensland Health Forensic and Scientific Services, 39 Kessels Road, Coopers Plains, state as follows:

Background

1. I have a Bachelor of Health Science from Griffith University.
2. I was awarded a Master of Science (Forensic Service) from Griffith University.
3. I am a member of the Australian and New Zealand Forensic Service Society.
4. I am currently employed by Queensland Health Forensic and Scientific Services (**QHFSS**) as a scientist in Reporting team 1 of the Forensic DNA Analysis Unit.
5. I have held the position of Reporting Scientist since 2008.
6. The duties of my role are to interpret DNA profiles, write Statements of Witness detailing DNA profile interpretations, and to give evidence in Court as an expert witness.
7. I commenced employment at QHFSS in 2005.

2022 Decisions

Changes to process – 6 June decision

8. There have been two decisions made about the processing of samples this year.
9. From 6 June 2022 until 19 August 2022, QHFSS process required all samples with initial quantitation values between 0.001 and 0.0088 nanograms per microlitre, irrespective of their sample type, to be amplified following extraction without any initial assessment or Microcon concentration occurring (**Auto-Amp Process**).
10. Prior to the Auto-Amp Process, samples with quantitation values between 0.001 and 0.0088 nanograms per microlitre were reported as '*DNA insufficient for further processing*' and were not automatically tested by FSS beyond quantitation.

[redacted] ..... [redacted]

Alicia Quartermain

Discussion with Ms Allen about Auto-Amp Process

Premier's decision

11. In June 2022, after the Auto-Amp Process commenced, Ms Cathie Allen, Managing Scientist, walked around the desks of the reporting scientists in the DNA Analysis laboratory.

12. I understand from discussions with Ms Allen during her walk around the Reporting team area that the Auto-Amp Process was decided by the Premier and Cabinet (**Premier's Decision**).

13. At this time, I said to Ms Allen words to the effect of "*Why have they* [Premier and Cabinet] *decided to amplify samples without making any assessment of the case type, sample type, etc. Didn't we recommend Microconning high priority samples before amplifying because it would be the best chance of getting a useable profile*?"

14. Ms Allen responded words to the effect of "*I did put that point forward, but they* [Premier and Cabinet] *decided to go with automatic amplification at 15 microlitres".*

15. I responded to Ms Allen, words to the effect of "*why would we* [FSS] *not tell them* [Premier and Cabinet] *that's not the best option? Historically, we would make an assessment based on the sample, quantitation value and case type about whether to Microcon the sample*".

16. Ms Allen responded, words to the effect of "*We gave them* [Premier and Cabinet] *the options and that's* [automatic amplification] *what they went for*".

17. During the conversation, I recall Ms Allen stated, in words to this effect, that she did not believe the Auto-Amp Process would have a large impact, and that microconning samples 'may' improve our [FSS] chances of obtaining an interpretable DNA profile.

18. I consider that the Auto-Amp Process was unlikely to produce good results, given DNA samples with lower quantitation values have lower amplification success rates and

should be Microcon concentrated *before* any amplification to increase the chances of obtaining a DNA profile.

19. Ms Allen also stated to me, during that conversation, words to the effect that she '*would not want to make a recommendation to the Premier and Cabinet to subject multiple hundreds of samples to Microcon concentration because of the extra work that would need to be completed by the analytical scientists, and that the extra work would 'break' the people carrying out that process'.*

20. In my view as a forensic scientist, the Premier's Decision did not have sound scientific basis. I do not consider that it was the best way forward.

Ms Allen's conceptualisation of Microcon concentration

21. During the above conversation with Ms Allen, following the commencement of the Auto-Amp Process in June 2022, Ms Allen compared Microcon concentration with baking a cake. Ms Allen stated to me, words to the effect of:

> "*Microconning to me is like baking a cake. You can bake two cakes with the same ingredients and processes and get completely different results. It isn't a perfect process. We can have two samples that go through the same process and get different results.*"

22. In my experience at FSS, I have observed laboratory staff to get accurate and effective results in the Microcon concentration process. I am confident in the QHFSS Microcon concentration process.

23. During the same conversation within the Reporting team area, I heard Ms Allen tell another reporting scientist that she had not lost a "*wink of sleep over this*". It is my understanding that Ms Allen was referring to the fact that Forensic DNA Analysis was likely to have to undergo an External Review.

Concerns about the Auto-Amp Process

24. I have concerns about the Auto-Amp Process.

25. I outline my concerns below.

Limited scientific basis

26. In my opinion, there is limited scientific basis for the Auto-Amp Process.

27. It is my view that the Auto-Amp Process was not the most effective process FSS could, or should, have undertaken for lower quantitation value samples.

28. Further, I am of the view that amplifying lower quantitation value samples at 15 microlitres is unlikely to produce good results. This is because there is, essentially, not enough DNA in the sample to produce effective amplification. This is particularly in comparison to the results that would be produced if the lower quantitation value samples had undergone Microcon concentration first.

Wasting sample liquid and potential DNA that should be Microcon concentrated first

29. Ordinarily, after extraction and quantitation a sample contains approximately 90 microlitres of liquid. Under the Auto-Amp Process, 15 microlitres of each sample was automatically amplified regardless of its quantitation value or sample type (providing the quantitation value fell within the 0.001 to 0.0088 nanograms per microlitre).

30. My concern is that amplifying samples with low quantitation values (i.e. samples under 0.0088 nanograms per microlitre) before Microcon concentration was undertaken wasted 15 microlitres of potentially DNA-containing sample. My view is that samples with a lower quantitation value, and depending on the sample type (in particular, priority 2 samples), should have gone straight to Microcon concentration (or at the very least be assessed by a reporting scientist as to the best way forward) before amplification. This is because the amount of DNA produced at amplification will be increased if a sample has undergone Microcon concentration, compared to if it has not, and so that Forensic DNA Analysis was not wasting 15 microlitres of sample automatically.

31. In my expert opinion, the 15 microlitres potentially wasted during the Auto-Amp Process could have been the difference between interpretable and uninterpretable results later in the DNA analysis process. This is because if 15 microlitres was not used in the automatic amplification, it could have been used in Microcon concentration. If 15 microlitres was already being used in the Auto-Amp Process, this means there was less sample available for use in any later Microcon concentration process. As a matter of scientific logic, a lesser volume of sample, means a lesser amount of DNA present in the sample. Therefore, there is a greater chance of finding a usable DNA profile from a larger sample that undergoes Microcon concentration first, and then amplification.

Impact of Auto-Amp Process

32. Every day the Auto-Amp Process was in effect, QHFSS potentially wasted 15 microlitres of each low quantitation value sample by automatically amplifying it without making any assessment regarding the initial quantitation value and sample type.

33. Hundreds of samples each week are processed by QHFSS and may have been affected by the Auto-Amp Process, depending on their initial quantitation value.

Rationale behind removal of Microcon concentration process

34. In my view as an employee at QHFSS, the main drivers for removing the Microcon concentration process were financial and budget considerations and laboratory turnaround times. The 'Options Paper' provided to QPS in 2018 states that 'time and cost' were elements to be considered.

35. I understand from my experience in the FSS laboratory that Microcon concentration is a costly process. I have formed this view over the years, after discussions with my colleagues concerning costs of sample processing.

36. I also understand from my experience in the FSS laboratory that turnaround time is an indication of laboratory efficiency. My experience working at FSS has been that Ms Allen is concerned about turnaround time. We (Forensic DNA Analysis) have been sent emails from Ms Allen, Mr Howes, Ms Rika and Ms Johnstone outlining outstanding samples awaiting interpretation and our turnaround times **[annexed and marked Exhibit AQ-01]**.

37. I agree that turnaround times are important. I disagree that turnaround times are more important that outputting high quality results.

19 August 2022 decision

38. The DG directive dated 19 August 2022 describes the following:

> *'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.'*

39. I was not consulted about this decision.

40. I do not believe that this decision was the best way forward. Samples should be assessed on a 'sample by sample' basis to determine the best reworking strategy. I do not believe that microcon concentrating all samples to 35 microlitres regardless of the quantitation value (between 0.001 and 0.0088 nanograms per microlitre) and sample type was the best way to treat these samples.

Obtaining results on samples initially reported as 'No DNA detected' or 'DNA insufficient for further processing' ('DIFP')

41. I am concerned by the process, which was in place between early 2018 and 6 June 2022, of reporting samples with quantitation values between 0.001 and 0.0088 nanograms per microlitre as 'DIFP'. Similarly, I am concerned by the FSS process of

reporting samples with quantitation values of less than 0.001 nanograms per microlitre as 'No DNA detected'.

42. This concern is in circumstances where I believe, based on experience, that DNA profiles can be obtained on many of those samples with further testing (namely, Microcon concentration and amplification).

43. As a result of my concern I began to record samples initially reported as DIFP or 'no DNA detected' that I, as the reporting scientist, had elected to process further and subsequently obtained alleles and a single-source or mixed DNA profile.

44. I have provided some recent samples in an excel spreadsheet which provided their barcode and case priority/type, initial quantitation value, quantitation value after Microcon concentration and the DNA profile results and interpretation.

45. All the samples referred to in the excel spreadsheet are samples from cases I have either managed or reviewed. I note that this spreadsheet has not been formally reviewed by other scientists.

46. A copy of the excel spreadsheet that records the results of the DIFP and 'no DNA detected' I processed further is **annexed and marked Exhibit AQ-02** to this statement. A bundle of the corresponding electropherograms obtained from the further processed samples is **annexed and marked Exhibit AQ-03** to this statement.

47. In the excel spreadsheet, I have recorded 14 'No DNA detected' samples from my casework which, after further processing, resulted in 7 single-source profiles and 7 mixed DNA profiles.

48. I also recorded 5 DIFP samples from my casework which, after further processing, resulted in 4 two-person mixed profiles and 1 three-person mixed profile.

'DIFP' samples

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

Alicia Quartermain Witne

49. Between 6 June 2022 and 19 August 2022, while the 'auto-amplification' process was in effect, every 'DIFP' sample that I interpreted or reviewed produced an interpretable DNA profile(s). These profiles may have been 'complex mixed' or 'complex unsuitable', however, there were still DNA profiles that were obtained.

50. Notwithstanding DNA is being detected when 'DIFP' or 'No DNA detected' samples are sent straight to amplification, my view remains that these 'DIFP' or 'No DNA detected' samples should be Microcon concentrated *first* before amplification occurs, in order to maximise the effectiveness of the amplification.

51. In my expert opinion and based on my experience in the QHFSS laboratory, I consider the statement '*DNA insufficient for further processing'* to be untrue. In my experience, the 'DIFP' samples that I have resubmitted for further testing have *all* yielded DNA profiles capable of interpretation. The wording of '*DNA insufficient for further processing'* has been used by me in some of my Statements of Witness. At the time of issuing these statements, I believed this statement to be true. I became concerned about the reporting of these samples over time.

52. I have reworked many samples further that were originally reported as '*DNA insufficient for further processing'* after a statement had been requested. I obtained interpretable DNA profiles from many of these, which changed my approach on how I treated these samples. For approximately the past 18 months, I have routinely reworked 'DIFP' samples that I have come across during case management and reporting, especially if those samples were SAIK (sexual assault investigation kit) swabs or swabs that were presumptive positive for blood (as indicated by QPS).

53. I have full confidence in the reliability of the results of further testing (i.e. Microcon concentration and amplification) on samples initially reported as 'DIFP'. I have full confidence in interpreting such results.

54. In particular, I have even greater confidence in the ability to obtain usable results and the reliability of such results since the commencement of the 3500 Genetic Analyzer in February 2021. I consider the results produced by this instrument to be reliable.

55. I am also concerned with the level of understanding of Queensland Police Service (**QPS**) officers who receive results that report 'DIFP' or 'No DNA detected' samples. I understand that QPS officers are able to request further testing of 'DIFP' samples, however, I query to what extent they understand this.

Case example of value in Microcon concentration

56. In approximately November 2021, I reviewed the samples tested and interpreted for a sexual assault case (QPS Reference: [redacted] for the purposes of preparing a Statement of Witness (Report No. [redacted]) (**Initial Statement**).

57. In preparing the statement, I reviewed five internal swab samples that were reported as spermatozoa-positive and '*DNA insufficient for further processing'*. They were as follows:

(a) Sample 1: Low vagina swab 1 – Spermatozoa fraction

(b) Sample 2: Low vagina swab 2 – Spermatozoa fraction

(c) Sample 3: Posterior fornix swab 1 – Spermatozoa fraction

(d) Sample 4: Posterior fornix swab 2 – Spermatozoa fraction

(e) Sample 5: Labia minora swab 2 - Spermatozoa fraction

58. As the 5 samples were internal swabs where spermatozoa had been detected by microscopy, I formed the view that further testing should be conducted. It was my belief that, given the presence of spermatozoa, it may be possible to obtain an interpretable profile. It is also my view that there is low risk of obtaining complex mixed profiles, given the swab was internal.

59. The classification of such a sample as '*DNA insufficient for further processing'* is, in my view, unacceptable from a scientific perspective.

60. I submitted the five samples stated above for rework, to undergo Microcon concentration and amplification. As I am a reporting scientist, and given that reporting '*DNA insufficient for further processing'* is technically an interim classification, I do not require permission to request further testing. However, I have to proactively request it be conducted.

61. In my Initial Statement, I stated, at page 9, "*the swabs listed above* [being the five samples stated above] *are currently undergoing DNA Analysis, the results of which will be reported in an addendum statement".*

62. A copy of relevant extracts of my Initial Statement is **annexed and marked Exhibit AQ-04** to this statement.

63. Two of the samples (Samples 3 and 4) returned from further testing with clear, two-person mixed DNA profiles. These DNA profiles are what I would expect to see if both the complainant and the defendant contributed DNA.

64. The DNA profiles obtained from Samples 3 and 4 were reported as: It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if the defendant had contributed DNA along with the complainant, rather than if he had not.

65. These samples were the first and only DNA profiles in the case that identified foreign male DNA obtained from internal swabs taken from the complainant (results described above in point 57). I understand from the investigating officer that these results were of assistance in establishing the offence of rape. There were other results reported in my first statement, namely samples from the complainant's neck and the defendant's SAIK which were reported as follows:

66. Complainant's neck:

> A mixed DNA profile was obtained from this sample indicating the presence of DNA from three contributors. Given this sample is said to have been taken from the complainant, the finding of DNA that could have originated from her would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from three contributors, one of whom is the complainant.

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with the complainant.

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if the defendant had contributed DNA rather than if he had not.

67. Defendant's SAIK (Glans penis (wet) swab)

A mixed DNA profile was obtained from this sample indicating the presence of DNA from three contributors. Given this sample is said to have been taken from the defendant, the finding of DNA that could have originated from him would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from three contributors, one of whom is the defendant.

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with the defendant.

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if the complainant had contributed DNA rather than if she had not.

68. I believe this case also demonstrates the danger of not fully processing samples of this type. If the defendant had not been located in sufficient time for a SAIK to be carried out, the only DNA evidence linking him to the complainant's body would have been the DNA profile obtained from the sample taken from her neck.

69. I wrote a replacement statement dated 22 April 2022 stating the results of the further testing at pages 10 and 11 (**Replacement Statement**).

70. A copy of my Replacement Statement is **annexed and marked Exhibit AQ-05** to this statement.

Lack of understanding by QPS officers

71. I had a recent case ([redacted] for which I was writing a Statement of Witness. Two out of the three samples had been reported back to QPS as 'DNA insufficient for further processing'. I contacted the Investigating Officer, PCSC Tayla Smith, to discuss my recommendation to process these two DIFP samples. PCSC Smith told me words to the effect of 'Please process these samples however you like. DNA is not my area of expertise, please just do whatever you need to do'. I am concerned that a large proportion of Investigating officers with the QPS do not know that they can request samples reported back as 'DIFP' and 'No DNA Detected' to be worked further.

'No DNA detected' samples

72. Presently, if a sample returns a quantitation value of less than 0.001 nanograms per microlitre, it is reported by the analytical team as 'No DNA detected'. This is not technically incorrect, because the Quant Trio (being the kit used by QHFSS for quantitation) cannot reliably detect DNA under that threshold. However, quantitation is just an estimate and can be unreliable.

73. For example, a sample could produce a quantitation value of 0.001 nanograms per microlitre on the first quantitation. It could then be quantified again and produce a different, higher value.

74. In my view, based on my experience, all low range quantitation samples should be quantified twice, because of the unreliability of quantitation.

75. I am concerned with the current QHFSS laboratory process whereby samples that are initially reported as 'No DNA detected' may never be reviewed by a reporting scientist, unless a statement request is subsequently submitted by the QPS.

76. I have processed samples originally reported as 'No DNA detected' further (through Microcon concentration and amplification) and obtained usable DNA profiles. An example of this is barcode [redacted] from a priority 2 rape case. The initial quantitation value of this sample was 0.00038 nanograms per microlitre (less than 0.001 therefore reported as 'No DNA Detected'). The sample was microconned, resulting in a single source DNA profile containing 23 out of a possible 40 alleles matching to the suspect. The Likelihood ratio for this result was '>100 billion favouring the defendant'.

77. Historically, as a reporting scientist, I would not have resubmitted samples reported as 'No DNA detected' for further testing as I would have trusted management and their findings, and because of the low quantitation value. However, now that I have witnessed DNA profiles being obtained from further testing of samples initially reported as 'No DNA detected', I do not rely on the management team/analytical team's reporting of 'No DNA detected' samples. I consider the sample type (e.g. in particular, internal swabs and blood swabs) and know that further testing can obtain usable profiles in some circumstances.

78. In my view, QHFSS should educate and inform QPS more thoroughly about further testing through comments in the Forensic Register.

Sexual assault swabs and blood swabs reported as 'No DNA detected' or 'DIFP'

79. With respect to intimate sexual assault swabs or blood swabs, scientists can reasonably expect to detect only one or two DNA contributors. Ordinarily, it is not expected that complex mixed profiles with multiple contributors will be obtained.

Therefore, even with very low DNA profiles, it is still possible to interpret the results with a level of accuracy because there are only one or two contributors.

80. I am concerned by intimate sexual assault samples that are initially reported as 'No DNA detected' or 'DIFP' and therefore not tested further through Microcon concentration and amplification.

81. In my experience, samples of this kind (internal swabs and blood swabs) can be expected to yield DNA profiles.

82. While it is not technically impossible that a DNA profile cannot be established on an intimate sample (even after Microcon concentration and amplification), it is uncommon.

83. As a matter of practice, I would not report an intimate sexual assault swab as 'No DNA detected' or 'DIFP' without further testing. In my expert opinion, samples of this kind should always be Microcon concentrated and amplified, given the likelihood that the sample will contain at least one DNA profile.

Samples with spermatozoa identified in microscopy being reported as 'No DNA detected'

84. In my role as a reporting scientist, I have seen samples that have had spermatozoa identified via microscopy, go on to be reported as 'DIFP' or 'No DNA detected'. I am concerned by this process, given the presence of spermatozoa is a strong indication that a usable DNA profile can be obtained with further testing.

'DIFP' and 'No DNA detected' decisions made by analytical team not reporting scientists

85. In previous processes, based on the initial quantitation of a sample, the analytical team would report a sample as 'DIFP' or 'No DNA detected' if it falls within the following quantitation values :

(a) No DNA detected - less than 0.001 nanograms per microlitre; and

(b) DNA insufficient for further processing - between 0.001 and 0.0088 nanograms per microlitre.

86. The decision is made by the analytical team based only on the numerical value of one quantitation run of the sample and its comparison to these thresholds.

87. The analytical team is also responsible for reviewing the 'DIFP' and 'No DNA detected' reporting lines. I understand Luke Ryan undertakes this task.

88. Standard Operating Procedure '*Procedure for Case Management'* states, at section 8:

> '*Peer review of 'No DNA detected' and 'DNA insufficient for further processing' is usually performed by a competent Analytical Section staff member'.*

89. Once a member of the analytical team has reviewed the 'DIFP' and 'No DNA detected' reporting lines (which I understand is just a review to check whether the quantitation value falls within the threshold), the sample is finalised and reporting scientists do not get an opportunity to assess or interpret the sample. The 'DIFP' or 'No DNA detected' sample is only seen and considered by a reporting scientist *if* a statement is requested by the QPS for the case that the sample is in.

90. I understand from my experience working at QHFSS that reporting scientists will often accept the analytical team's finding that a sample has 'No DNA detected' or 'DIFP' and include this in their report, without considering further processing. In doing so they are adopting the analytical team's findings (which were based on an automatic threshold) as their own expert opinion without having interpreted the sample themselves.

91. As I have resubmitted 'No DNA detected' and 'DIFP' samples for rework, including Microcon concentration and amplification, and obtained interpretable samples, I do not now accept the analytical team's reporting of 'No DNA detected' and 'DIFP'.

92. In preparing a witness statement, I will resubmit any 'No DNA detected' or 'DIFP' samples for rework irrespective of the sample type. I understand this process is not commonly used by reporting scientists. Prior to becoming aware that I could obtain

usable profiles from further testing of 'No DNA detected' or 'DIFP' samples, it was not my practice to resubmit samples of this type.

93. In my view, the reporting scientists should have been reviewing any initial 'DIFP' and should be presently reviewing 'No DNA detected', reporting lines and determining, based on all the circumstances, whether further testing should have been / should be undertaken. This should occur well before the report writing stage.

Emails sent to Justin Howes over concern with the 'DIFP' process

94. I have expressed my concerns about the 'DIFP' process on at least two occasions to Justin Howes, being in April 2020 and April 2021.

95. I recall that the email I sent to Justin Howes in April 2020 details the same concerns that the email I sent in 2021. I am unable to locate a copy of the email sent in April 2020.

96. On 29 April 2021, I sent an email to Mr Howes with the subject line 'DNA Insuff. For further processing'. In that email, I stated, amongst other things:

> '*In the past I had noticed some samples which had originally been called DIFP, were subsequently processed on the 3130, resulting in some decent profiles. Even if these profiles were low level, if the number of contributors was only one or two, then they were still interpretable. For example, light combur-pos stains or SAIK samples.*
>
> *With the introduction of the 3500, I am seeing the same thing happening, except the peaks are much higher due to the sensitivity of the instrument.* ***I feel that reporting these samples as DIFP is technically incorrect. I strongly feel that we should be processing a lot of these samples these days, especially ones that may have a quant value close to the cut-off range.'*** (emphasis added)

97. In my email dated 29 April 2021, I also proposed sending combur-pos or SAIK samples with any quant value through the full analytical testing process for a set period of time to assess the results. I volunteered myself to take on that work.

98. On the basis of my experience with these types of samples, I considered that this would reveal that DNA profiles are able to be obtained despite their previous reporting as 'DIFP'.

99. On 30 April 2021, Justin Howes responded by email. The response did not make any substantive comments but invited me to speak with Justin Howes in person.

100. A copy of my email and Mr Howes' response is **annexed and marked Exhibit AQ-06** to this statement.

On or around 30 April 2021, I spoke with Mr Howes about the concerns raised in my email of 29 April 2021. During that conversation, Mr Howes said words to the effect of, based on data mining he had completed previously, he did not see the benefit of undertaking my proposal contained in the email dated 29 April 2021 "*just to see what happens*".

Reworking samples at insufficient DNA stage and final reporting stages

101. The '*Procedure for Case Management* 17117V21' states, at section 6.5.4 – Samples with undetermined quantitation values or insufficient DNA:

> *'It is understood by QPS that samples reported post-quant as 'No DNA Detected' or 'DNA Insufficient for further processing' can be requested for processing at any time.*
>
> *...*
>
> *Similarly, case managers may at their discretion order a rework in cases where the only results are low quant samples'.*

102. However, a reporting scientist as a case manager must proactively submit the sample to analytical for rework. Until recently, there were no samples that went through to rework automatically.

103. In my experience in the QHFSS laboratory, not all reporting scientists will resubmit 'DIFP' or 'No DNA detected' samples for rework even if, on analysis of the case, the sample appears to be crucial or has the potential to yield a DNA profile.

Final stage – authority required

104. Final reporting lines are where the final result / status (e.g. DNA profile type) has been identified and reported against the relevant sample barcode.

105. If, at the time of statement writing, a reporting scientist wishes for a rework to be undertaken for a sample that has been finalised, they must get approval from Ms Allen by completing and submitting an 'MS teams form'.

106. The '*Procedure for Case Management* v17117V21' states, at section 6.3.6 – Rework DNA extract if necessary:

> '*As of 30 June 2019, any rework on a previously reported Major Crime (Priority 2) result is not to be ordered without Managing Scientist or Executive Director authorisation. A MS Form* **[annexed and marked Exhibit AQ-07]** *can be used to provide information to the Managing Scientist of* [sic] *Executive Director to assess the reasons for the rework, and the potential risks associated with proceeding (or not proceeding) with a requested rework.*
>
> *… After submission, the form then goes to the Team Leader for consideration and endorsement prior to the Managing Scientist (or Executive Director) for final consideration."*

107. Kylie once mentioned in a reporting Team 2 meeting (when I was still in Kylie's team) that she had once commented in a Management Team meeting that the MS Teams form may act as a deterrent to Reporting scientists to rework samples at Statement

stage if they think it is appropriate. I recall her saying that Cathie Allen acknowledged this to be the case.

108. In my experience, Ms Allen does not turn around MS Teams requests for rework authority promptly and can take up to one week.

109. I make this solemn declaration conscientiously believing the same to be true by and virtue of the provisions of the *Oaths Act 1867*.

TAKEN AND DECLARED before me at Brisbane in the State of Queensland this 21st day of September 2022.

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

Alicia Quartermain

Schedule of Exhibits

AQ-01	E-mails exchanged between Alicia Quartermain and Cathie Allen
AQ-02	Spreadsheet summarising results of "DIFP" and No DNA samples further tested by Alicia Quartermain
AQ-03	Electropherograms for results contained within spreadsheet of "DIFP" and No DNA samples further tested by Alicia Quartermain
AQ-04	Extracts from Initial Statement Report, No. [redacted], relating to [redacted]
AQ-05	Replacement Statement relating to [redacted]
AQ-06	Email chain (2 emails) between Justin Howes and Alicia Quartermain on 29 April 2021 and 30 April 2021 titled "DNA Insuff. For further processing"
AQ-07	Email from Alicia Quartermain containing DNA Rework Authorisations Form