



REPORT CONCERNING USE
BY QUEENSLAND HEALTH
FORENSIC AND SCIENTIFIC
SERVICES OF CERTAIN
EVIDENTIARY STATEMENTS

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REPORT CONCERNING USE BY QUEENSLAND HEALTH FORENSIC AND SCIENTIFIC SERVICES OF CERTAIN EVIDENTIARY STATEMENTS

EXECUTIVE SUMMARY

1. Immediately before early 2018, Queensland Health Forensic and Scientific Services ("FSS") would process samples submitted for Major Crime Casework¹ that returned a quantitation value between 0.001 ng/μL and 0.0088 ng/μL by submitting them automatically to concentration using Microcon filters (referred to within FSS as "auto-microcon"), amplification, capillary electrophoresis and profiling.²
2. In early 2018, FSS began to process such samples in accordance with "option 2" referred to in paragraph 8 on page 9 of '*A review of the automatic concentration of DNA extracts using Microcon® Centrifugal Filter Devices: Options for QPS consideration*' dated January 2018 and submitted under the names of Mr A³ and Ms B, both FSS officers.
3. Option 2 provided as follows:

Cease the 'auto-microcon' process for Priority 2 (Major Crime) casework and report the exhibit result of 'DNA insufficient for further processing' based on Quantification result.⁴
4. The result of the adoption of this process by agreement between FSS and the Queensland Police Service ("QPS") was that samples for Priority 2 (Major Crime) Casework that returned a quantitation value in the range between 0.001 ng/μL and 0.0088 ng/μL:
 - a. would not be processed further (unless expressly requested by QPS or unless a scientist within FSS did so)⁵ and,

¹ "Major Crime" includes the most serious offences, such as sexual assaults and homicide. It excludes property offences.

² Queensland Health Forensic and Scientific Services, *Procedure for Case Management* (Doc No. 17117V19), pages 18-19.

³ I have used pseudonyms in this report because I am not presently concerned with questions of responsibility.

⁴ Queensland Health Forensic and Scientific Services, *A review of the automatic concentration of DNA extracts using Microcon® Centrifugal Filter Devices: Options for QPS consideration*, page 9.

⁵ Queensland Health Forensic and Scientific Services, *Procedure for Case Management* (Doc No. 17117V21), pages 11-12, 19.

- b. would be reported in the Forensic Register as containing “DNA insufficient for further processing” or words to similar effect (hereafter referred to as “the DIFP Statement”⁶) and accompanied by the words:

This item/sample was submitted for DNA analysis; however the amount of DNA detected at the quantitation stage indicated the sample was insufficient for further processing (due to the limitations of current analytical and interpretational techniques). No further processing was conducted on this item. Please contact Forensic DNA Analysis if further information is required.⁷

- c. would be reported in Queensland Police Records and Information Management Exchange (“QPRIME”) as containing the DIFP Statement and accompanied by the words:

This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further 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.

5. In instances in which a witness statement was required for criminal proceedings, samples with quantitation within the range 0.001 ng/μL and 0.0088 ng/μL would be reported as having “Insufficient DNA for analysis” or words to similar effect.⁸
6. In fact, the possibility of obtaining a profile from these samples cannot be excluded because, although it might be that the samples contained insufficient DNA to develop a DNA profile, it might also be that the samples contained:
 - a. sufficient DNA to obtain a partial DNA profile, or,
 - b. sufficient DNA to obtain a full DNA profile.
7. It follows that the DIFP Statement as used in witness statements was untrue.

⁶ Within FSS it became common to refer to this as “DIFP” and I will adopt that convenient label.

⁷ Queensland Health Forensic and Scientific Services, Explanation of Exhibit Results for Forensic Register (Doc No. 34229V3), page 39.

⁸ Queensland Health Forensic and Scientific Services, *Procedure for the Release of Results using the Forensic Register* (Doc No. 34006V3), page 118.

8. When a quantitation result is below 0.001 ng/μL, FSS reports the result on the Forensic Register as “No DNA detected”. When a witness statement is prepared for criminal proceedings, the result is reported in the same way.
9. In fact, such a quantitation result signifies that technical equipment did not have the capacity to determine either the presence or absence of DNA with reliability.
10. Samples with quantitation results below 0.001 ng/μL are capable of generating useable profiles although the likelihood is low.
11. As a consequence, the description “No DNA detected” as used in witness statements is misleading.
12. The following are my reasons for reaching these conclusions. At the end of this report I have made recommendations for action.

DNA

13. DNA is a very long molecule that is found in the nucleus of almost every cell in the human body. DNA is itself made of smaller molecules. DNA is so long that, to fit into a human cell, it is wrapped around, and wrapped with, protein molecules.⁹ Each of these wrapped DNA molecules is called a chromosome.
14. There are 46 chromosomes in each of these cells.¹⁰ The DNA in each chromosome contains chemical (also known as genetic) characteristics. For practical forensic purposes, the characteristics, or genetic markers, of the entire set of 46 chromosomes in one cell are identical to the characteristics of every other set of chromosomes *in the cells of that particular individual*. Excluding identical twins, the genetic characteristics between and among individuals differ.
15. This set of 46 chromosomes is actually two sets of 23 chromosomes - one set inherited from a mother and one set inherited from a father. Thus, there are 23 pairs of chromosomes. Because there are two sets of chromosomes any genetic marker will be represented by two copies.
16. There are various classes of genetic markers contained within the DNA between and among individuals. One class of genetic markers is comprised of repetitive patterns. These patterns are called Short Tandem Repeats, or STRs. There are thousands of STRs dispersed along the human DNA housed on the set of chromosomes. However, only 20-30 STRs are used for forensic DNA typing. This subset of STRs were selected because they are highly informative

⁹ If the DNA molecules in a single cell were laid end to end, they would span almost 2 metres.

¹⁰ Although there are exceptional cases.

for genetically distinguishing between individuals. The number of repetitive sequences varies between and among individuals and this variation is at the heart of DNA profiling.

17. The complete set of forensically-relevant STRs is different in every individual,¹¹ excluding identical twins, and it is the existence of these differences which means that DNA can be used:
 - a. to compare the potential suspect's DNA profile (ie. a reference sample) to a DNA profile generated from a sample taken from a crime scene;
 - b. to compare the potential donor of forensic biology evidence by comparing a sample DNA profile to DNA profiles of known offenders maintained in a DNA database; and
 - c. to exclude a person as having possibly contributed DNA found at a crime scene.
18. The ability of scientists to analyse STRs depends upon the amount of DNA and the quality of that DNA in a sample. Skin cells left by a person who has touched an object will be few in number, perhaps very few. Blood and saliva samples are known generally to furnish many cells and, therefore, a lot of DNA. DNA can be damaged in many ways, such as by long exposure to the elements or by contact with substances or microorganisms that tend to degrade DNA molecules.
19. The less DNA present and the poorer its quality, the less probable is the prospect of obtaining useable data from an analysis.
20. While it is unnecessary for present purposes to spell out in fine detail the technology employed at FSS, in order to understand what has led me to write this report, it is necessary to have some understanding of the processes used. The processes described below are used by FSS. Laboratories in other jurisdictions use similar processes. These processes are:
 - a. Collection: during which a sample is obtained from a crime scene or the body of a person.
 - b. Extraction: during which DNA is separated from all other materials in the sample so that it can be analysed.

¹¹ Actually, it is mathematically possible, for reasons that need not be examined, that there might be two individuals with identical DNA. That mathematical possibility means that DNA comparison of two samples is expressed by stating the probability that the same person has contributed the DNA in each sample, usually expressed as a probability of billions to one. For practical purposes, decisions are actually made on the footing that no two people will ever have the same DNA.

- c. Quantitation: during which the sample is analysed to determine whether it contains any DNA at all and, if it does, how much DNA is present.
- d. Amplification: during which the molecules of DNA present in the sample are reproduced until a large enough number of molecules is available for study.
- e. Genetic Analyzer: during which the available DNA is analysed to identify the presence of STRs.
- f. Interpretation: during which a scientist interprets the graphic profile generated by the software used by the Genetic Analyzer and compares it to a reference sample to arrive at an opinion about identity.

The collection phase

- 21. A police officer or, in sexual assault cases, a medical practitioner will collect a sample that might yield DNA for analysis and QPS will submit it to FSS for testing.

The extraction phase

- 22. The first relevant phase of the analytical process leading to a possible comparison of two samples of DNA takes place. It involves the extraction of DNA molecules from any cells in the sample and the isolation of that DNA from the rest of the sample, which is of no further use. The resulting liquid (or extract) may or may not contain DNA.

The quantitation phase

- 23. The sample must now be tested to determine whether it contains any detectable DNA and, if there is, how much DNA is contained within the extract. This process is called "quantitation" and is central to the issues addressed in this report.
- 24. Quantitation involves applying a synthesized chemical consisting of molecules that are designed to attach to a specified DNA target in human DNA. The more DNA molecules that are present in an extract, the more targets are available to which the synthesized molecules can attach. The synthesized molecule has a special property: it contains another molecule that will fluoresce when laser light is applied to it – but the fluorescence will not occur unless the synthesized molecule found its target on a molecule of DNA; that is, only if the sample extract contains DNA. The more DNA there is the more fluorescence there will be.

25. The laboratory at FSS uses an instrument that automatically performs this task. It contains a laser to cause the fluorescence to occur and then measures the degree of that fluorescence. Software supplied by the manufacturer of the equipment then converts the degree of fluorescence into an estimate of the concentration of the DNA molecules present. The concentration is expressed in nanograms per microlitre of liquid, ng/ μ L, and this is usually referred to by scientists in shorthand as a "quant".
26. It must be borne in mind that this instrument does not really "weigh" the DNA. It merely detects the intensity of fluorescence and, using a formula within its software, it derives an estimated concentration. Quants are only estimates because of the potential variability that is inherent in the process. At times samples, particularly low concentration samples, are quantified twice so that an average can be used to inform later decisions.
27. For this reason, once a quant has been obtained, a decision can be made by FSS scientists whether there is enough DNA to produce a result that can be analysed and, if the process is to continue, how it is to continue.
28. Although a very small quant is less likely to produce a useful result than a larger quant, it is possible to obtain useable results from very small quants.

The amplification phase

29. Within the human body cells must replicate themselves so that the body can continue to function. For example, new skin cells appear because existing skin cells divide again and again. In order to create a new functioning human skin cell the DNA within the cell must first replicate itself. By a complicated process, the 46 individual chromosomes duplicate themselves so that, when the cell finally divides, each new cell has a complete and identical set of 46 chromosomes.
30. This natural process can be artificially fabricated in the lab using a procedure called Polymerase Chain Reaction (PCR). However, rather than making a single copy of a DNA molecule, the PCR method repeats the doubling process again and again, typically about 28 to 32 times, producing under ideal conditions a billion or more copies of the parts of the molecule that contain the desired genetic markers, in this case STRs.
31. At this stage of the analytical process the sample consists of about 95 millilitres of liquid extract in a tube. A sub-sample must be removed for amplification, typically 15 millilitres. The less DNA there is in the sample, the less is the chance that this sub-sample will contain very much DNA or, perhaps, any DNA. If one thinks of a 100-litre water tank containing 100 balls suspended randomly in the liquid, the prospect of dipping a 10-litre bucket

into the tank and removing a few balls is high. However, if the 100-litre tank only contains only 10 balls, then the prospect of taking out 10 litres of liquid that contain many, or any, balls is much reduced. In the same way, a standard sized tube might contain very few (invisible) DNA molecules. The removal of the sub-sample may not involve getting much DNA at all for amplification.

The concentration phase

32. A solution to this problem of too little DNA in a sub-sample of an extract is to condense the liquid (known as concentration) in which the DNA is suspended. A sample can be concentrated to increase the prospect of capturing a greater amount of DNA for the amplification phase. At FSS, typically if the sample is to be concentrated, the solution is condensed to one third of its former volume, although sometimes it is condensed to a much greater extent. The FSS laboratory uses Microcon Centrifugal Filter Devices to carry out concentration and the phase is often referred to as the "microcon".

The "Genetic Analyzer"

33. Once the DNA has been replicated in the amplification phase, a sub-sample of the amplified product (which may or may not contain sufficient replicated molecules for subsequent typing) is placed into a machine called the "Genetic Analyzer". This machine analyses the amplified DNA in the sample in order to produce useable data about STRs.
34. The technology used in DNA profiling involves the use of materials and equipment that isolates 20 particular locations¹² where STRs reside in human DNA and generates a graphic pattern that displays the genetic variants for human identification purposes.
35. The Genetic Analyzer employs software to produce data in graphic form. This is a diagram called an electropherogram or, more commonly, a profile. It is a pictorial representation of the repetitive patterns, the STRs, at the 20 markers (or loci) used for DNA profiling – or as many markers as can be induced to produce data. Each of these markers has a unique identifying number (ie. an address) that refers to the particular genetic marker that is being analysed and the place in human DNA where the particular STR marker can be found.¹³

¹² Each location at which STRs are examined is a "locus", the plural of which is "loci" which, given the American influence in this field, is pronounced "Low Sigh".

¹³ For example, on the diagram that the software finally produces, a pair of peaks will be attributed to a locus identified as "D16S539". "D" signifies that the analysis relates to DNA. "16" signifies that the alleles are found on chromosome pair 16. "S" signifies that the analysis concerns STRs. "539" identifies the 539th locus on chromosome 16. Each allele pair will have an identifying code of this kind. Other codes are also used but they are immaterial here.

36. An example of an electropherogram or, more commonly, a “profile” is in Figure 1 below.
37. It is vital to understand that the electropherogram is not a picture of the molecule or even a picture of the patterns of interest in the molecule. The profile generated by the genetic analyser is comprised of a set of numbers that the software writers represented as a series of peaks on a graph. These peaks are a metaphor that represents:

a. The number of alleles

Each peak on the profile represents a portion of a molecule exhibiting STRs – called an “allele”. In a sample contributed by a single individual, there should be two alleles at each locus, representing the data from each of two DNA molecules for a particular STR residing on an analogous locus on a pair of chromosomes. If the DNA is of poor quality or there is too little of it, or both, one or both targeted molecules might have failed to generate any or sufficient data to generate these peaks, or alleles.

b. The amount and quality of DNA available for analysis that exhibits the particular locus

The amount of DNA in a sample is directly related to the height of the peak(s) shown in the profile. It is represented by a number related to the intensity of fluorescence of each allele.

c. The number of repeats in each STR

The number of repeats represent genetic variants at a single STR that may be similar or different among individuals. The operationally-defined number of repeats are displayed by the number in the box below the peak. There will be a separate number for each allele per locus. At most loci two alleles will be observed. When two alleles are observed, the profile at that locus is called a heterozygote. At times the two alleles that were inherited from each parent contain the same number of repeats and thus will display only one peak which is called a homozygote.

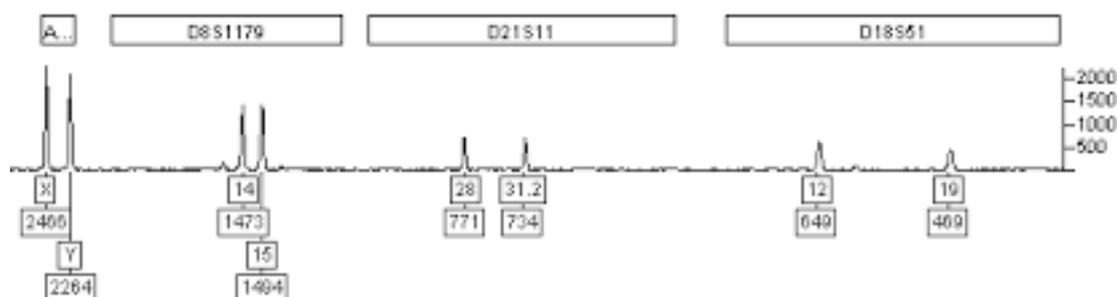


Figure 1.

38. In an ideal or pristine sample that has been contributed by a single individual, the profile will show 20 pairs of peaks each with its own particular number of STRs. The twenty first will show the gender of the contributor.

The interpretation phase and subjectivity

39. The processes involved in reaching this point have been improved substantially by technology manufacturers over the last 25 years and, although they continue to improve, they are imperfect.
40. Although, as I have said, a single source sample will ideally produce a pair of alleles for each locus, it may not be possible to obtain a full profile. For example, the extraction phase might fail to yield any or too little DNA because other chemical contaminants in the sample have obstructed the extraction. Depending on the quality of the DNA, the replication step may only be able to replicate shorter molecular strand targets generating a partial profile; a partial profile contains less information and is, therefore, less informative for human identification purposes.
41. During the amplification phase an artifact occurs which scientists call "stutter". Typically, but not always, these artifacts emerge from the data as a relatively small peak just before the peak (or allele) of interest, as if the small peak was a stutter before the intended statement of real data. Sometimes a stutter appears after the substantive peak. These stutter artifacts can generally be identified because they have a recognisable height proportion compared to the real allele. However, these stutter peaks complicate interpretation of mixtures particularly when there is a minor contributor¹⁴ to the mixture. An example of stutter is in Figure 2.

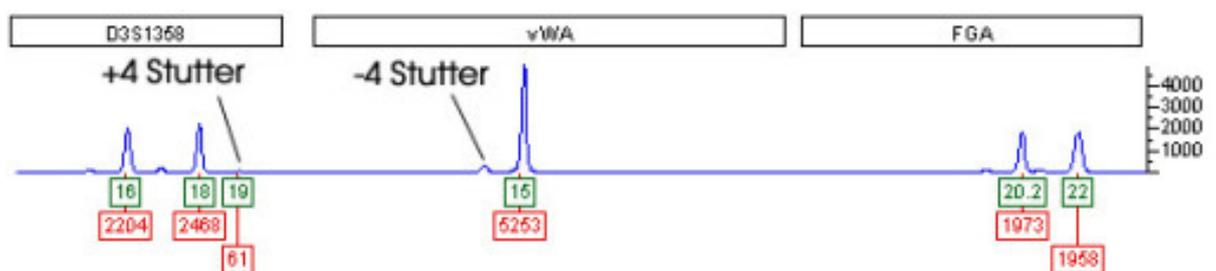


Figure 2.

42. Sometimes, some alleles of the donor of the sample do not appear on the profile. These missing peaks are called "drop-outs". Sometimes apparently healthy peaks appear but are not attributable to the donor and are called "drop-ins". All of these false indications are equivalent to static or "noise".

¹⁴ A "minor contributor" is a secondary contributor of DNA whose DNA profile is weak because of a low quantity or quality.

Techniques have been evolved to determine a baseline for these and other “stochastic artifacts”¹⁵ so that they can be eliminated from consideration.

43. If the quant was low and the quality of DNA was also poor, the peaks that represent actual alleles will have a low height. They may be close to the height where stochastic effects are exacerbated and hard to tell apart so that artifacts might be confused with alleles.
44. Sometimes, because of the poor quality of the sample, only one of the two alleles appears at a locus (ie. drop out of one of the alleles). Such a single allele may be accompanied by stutter. Because of increased stochastic effects, at times, with low level DNA, it can be challenging to discern if the stutter is truly stutter or an actual allele or combination thereof. A judgment has to be made.
45. If a sample contains DNA from two individuals, ideally the profile should show four alleles at each locus. An allele or two can be shared between individuals, if the number of repetitive STRs is the same. This is known as masking. Also, depending on the quantity and quality of the DNA, one allele might have dropped out leaving three or fewer alleles for analysis. Or two might have dropped out. The alleles that dropped out are unknown (because they are not visible in the DNA profile) and so add uncertainty to interpretation of the DNA profile. For example, do the missing alleles both belong to the same individual or is there one allele missing from the contribution made by each individual, or is there yet another explanation? If the deficiently represented alleles are low in height, and if some are missing from the locus, and there is stutter, the interpretation of the DNA profile becomes more challenging because it is necessary to decide what are true DNA alleles and what was contributed by each donor of the mixture. For example, if the profile at a locus contains three alleles it could represent a pair of alleles from one individual and a single allele from another individual, or a pair of alleles and stutter, or three single alleles from three contributors. There are many other possible explanations.
46. These kinds of factors introduce subjectivity in the interpretation of DNA profiles because the profiler must consider the significance of ambiguous data in the profile and make a judgment. An example of a complicated and ambiguous profile is in Figure 3.

¹⁵ “Stochastic”: having a random probability distribution; “artifacts”: meaningless signals with no origin in DNA.

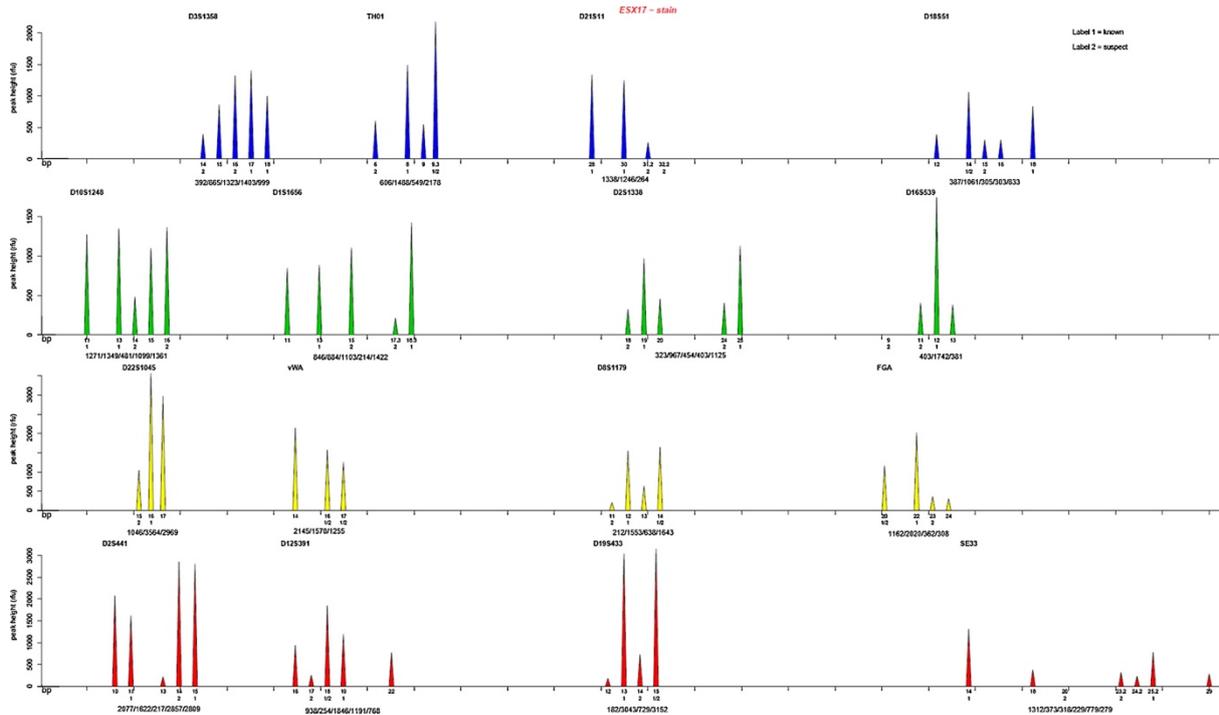


Figure 3.

47. Scientists are assisted by a software program called STRmix. It can take such variables into account in a way that is difficult to do manually. The resulting profile is assessed and "deconvoluted" by STRmix, for example, by placing different weights (or probabilities) regarding whether a peak is an allele or stutter or a combination of an allele and stutter. However, even this software depends upon parameters that are set by the scientists in the particular laboratory that uses it. Different laboratories may use different parameters to assess the data and accommodate stochastic effects.
48. Consequently, even with the aid of software of that kind, a profiler must still apply judgment based upon scholarship, skill and experience. The result of this kind of analysis is not evidence of an objective fact: it is opinion evidence.

THE OPTIONS PAPER

49. FSS and QPS place offences into two categories. "Volume Crime" comprises mostly property offences. "Major Crime" includes serious offences such as sexual assaults and homicide.
50. Immediately before early 2018 it was the practice of FSS to process fully all samples in Major Crime cases unless they returned a quant under 0.001 ng/μL. In addition, samples with quants between 0.001 ng/μL and 0.0088 ng/μL

automatically underwent concentration before further processing¹⁶ in order to maximise the prospect of getting a useable profile.

51. In late January 2018, FSS presented QPS with a document titled *A review of the automatic concentration of DNA extracts using Microcon Centrifugal Filter Devices: Options for QPS Consideration* (see Annexure 1 to this report). This document suggested that processing of Major Crime samples with quants between 0.001 ng/μL and 0.0088 ng/μL was not an efficient use of resources. It was pointed out that there were advantages to abandoning such testing:

The ability to potentially reallocate staff time currently allocated to processing, interpreting and reporting 'auto-microcon' samples, to samples with higher DNA yield, thus improving the turnaround time for results on these samples.¹⁷

52. The paper proposed two options. First, to leave processes as they are. Second, to cease processing samples with quants between 0.001 ng/μL and 0.0088 ng/μL unless QPS made a specific request (or unless a scientist within FSS decided to do so¹⁸).

53. Representatives of FSS and QPS met in early 2018 to discuss the content of the Options Paper. A few days later, QPS agreed that these samples were no longer to be processed unless QPS asked for that to be done. The new process was undertaken after January 2018 for all samples within the range 0.001 ng/μL and 0.0088 ng/μL. It ceased to be used on 6 June 2022.

54. If test results are to be used in criminal proceedings, a scientist has to furnish a statement that will be given to police, prosecution and defence. This will ultimately constitute the basis for the oral evidence to be given by the scientist at the trial. Such a statement states the results of testing.

55. After the introduction of this new practice in February 2018, statements of scientists would, where applicable, state to the effect:

Insufficient DNA for analysis

56. Professor Linzi Wilson-Wilde is an internationally recognised expert in the field of DNA analysis. I commissioned her to give her opinion about whether, in

¹⁶ Queensland Health Forensic and Scientific Services, *Procedure for Case Management* (Doc No. 17117V19), pages 18-19.

¹⁷ Queensland Health Forensic and Scientific Services, *A review of the automatic concentration of DNA extracts using Microcon® Centrifugal Filter Devices: Options for QPS consideration*, page 9.

¹⁸ Queensland Health Forensic and Scientific Services, *Procedure for Case Management* (Doc No. 17117V19), page 19.

such cases, the statement “DNA insufficient for further processing” was appropriate. Professor Wilson-Wilde concluded as follows:¹⁹

1. The possibility of obtaining a profile from samples submitted for DNA analysis, with a quantitation result of between 0.001 ng/μL and 0.0088 ng/μL, cannot be excluded.
2. Samples in this quantitation range may contain:
 - insufficient DNA to develop a DNA profile, or
 - sufficient DNA to obtain a partial DNA profile, or
 - sufficient DNA to obtain a full DNA profile.
3. The statements *insufficient DNA for analysis* or *insufficient DNA for further processing* are without explanation or clarification in the Appendix.²⁰
4. Applied literally and without proceeding to amplification and analysis, the statements *insufficient DNA for analysis* or *insufficient DNA for further processing* cannot be substantiated.

57. I served each scientist who occupied a management position at FSS, as well as the Acting Director-General of Queensland Health, with a requirement under s 5(1)(c) of the *Commissions of Inquiry Act 1950* in the following terms:

Statement of possible findings by the Commission

- A. Immediately before early 2018, FSS would process samples submitted for Major Crime Casework that returned a quantitation value between 0.001 ng/μL and 0.0088 ng/μL by submitting them automatically to micro-concentration (referred to within FSS as ‘auto-microcon’), amplification, capillary electrophoresis and profiling.
- B. In early 2018, FSS began to process such samples in accordance with “option 2” referred to in paragraph 8 on page 9 of *A review of the automatic concentration of DNA extracts using Microcon® Centrifugal Filter Devices: Options for QPS consideration* dated January 2018 and submitted under the names of [Mr A and Ms B]. Attached hereto is a copy of that document.
- C. Option 2 provided as follows:

¹⁹ Professor Linzi Wilson-Wilde OAM PhD, Report to Commissioner of Inquiry into Forensic DNA Testing in Queensland (31 July 2022), page 2.

²⁰ Referring to the standard form Appendix attached to each Witness Statement prepared to be used as evidence.

Cease the 'auto-micron' process for Priority 2 (Major Crime) casework and report the exhibit result of 'DNA insufficient for further processing' based on Quantification result.

- D. The result of the adoption of this process was that samples for Priority 2 Casework that returned a quantitation value in the range between 0.001 ng/μL and 0.0088 ng/μL would:
- i. Not be processed further (unless expressly requested by QPS); and,
 - ii. Would be reported by a Reporting Scientist in his or her Witness Statement signed under section 110A(6C)(c) of the *Justices Acts 1886* for any court proceedings as containing "DNA insufficient for further processing" or words to similar effect.
- E. In fact, the possibility of obtaining a profile from such samples cannot be excluded because, although such samples might contain insufficient DNA to develop a DNA profile, such samples may contain:
- i. Sufficient DNA to obtain a partial DNA profile; or,
 - ii. Sufficient DNA to obtain a full DNA profile.
- Attached hereto is a report by Professor Linzi Wilson-Wilde OAM PhD concerning these matters.
- F. In the premises, a report in a Witness Statements that a sample contained "DNA insufficient for further processing", or words to a similar effect, was not true in the case of every sample so reported.
- G. Any Witness Statement expressing that opinion about samples within the said range of quantitation, merely because the samples were within that range, have, to that extent, been untrue.

Matters about which information is required from you:

1. State whether you agree or disagree with any of the matters in paragraphs A to G above.
2. If you disagree to any extent with any of the statements, state:
 - a. The nature of your disagreement; and,
 - b. Explain, in detail, your reasons for such disagreement.
3. If I conclude that the matters stated above are substantially correct, I may decide that I should make recommendations to the government about steps that ought to be taken as a result of the occurrence of such matters or some of them. One

recommendation that I might consider making is that FSS immediately withdraws any and all statements issued by it since 2018 that have stated that a sample contained “insufficient DNA for further processing” and that fresh statements be issued in all such cases reporting the actual facts referable to such samples.

4. Make any submission you wish concerning the nature of any recommendation that, in your view, I should make in the event that I conclude that the matters set out in paragraphs A to G are correct or are substantially correct.
58. As can be seen, a copy of Professor Wilson-Wilde’s opinion was furnished to each respondent. A copy is also included as Annexure 2 to this report.
59. Mr C holds the position of Senior Scientist at FSS. He holds the degree of Bachelor of Science, the degree of Master of Science, a diploma of Government Security and a diploma of Management. Mr C agreed with propositions A, B, C, D(i) and E.²¹ With respect to each and every other proposition, Mr C said that the matter fell outside the scope of his work at FSS²² so that he felt unable to comment.
60. Ms D holds the position of Senior Scientist at FSS. Relevantly, she holds the degree of Bachelor of Science (Molecular Biology), a post-graduate diploma in Forensic Science and a diploma in Management (Public Sector). She agreed with propositions A, B, C, D, E, F and G.²³
61. Ms E holds the position of Senior Scientist at FSS. Relevantly, she holds a PhD degree, a degree of Bachelor of Science and a diploma of Management. Ms E agreed with propositions A, B, C, D and E.²⁴ She said that she understood from “general laboratory discussions” that case managers had a discretion to process samples within the relevant range further if they desired. She said that the Standard Operating Procedures do not say that this is so, but she pointed out that they also do not say that that is not so.²⁵ In fact, the *Standard Operating Procedure - Procedure for Case Management* says in relation to these samples “Similarly, case managers may at their discretion order a rework in cases where the only results are low quant samples”.²⁶ Unfortunately, when the *only results* in a case are DIFP, a statement will rarely be required and, consequently, a case manager will not be called upon to give a profile or consider the case and will be unaware of the existence of the

²¹ Statement of Mr C declared 3 August 2022, [2], [3], [7] – [10], [12].

²² Statement of Mr C declared 3 August 2022, [11], [14], [17], [18].

²³ Statement of Ms D declared 9 August 2022, [2], [3], [7], [8], [11] – [15].

²⁴ Statement of Ms E declared 4 August 2022, [2], [3], [7] – [10].

²⁵ Statement of Ms E declared 4 August 2022, [9].

²⁶ Queensland Health Forensic and Scientific Services, *Procedure for Case Management* (Doc No. 17117V21), page 19.

sample or its result. Ms E made no comment about the propositions concerning the truth of witness statements on the ground that she is not a Reporting Scientist, that is to say, a profiler, and is, therefore, "not familiar with the detail of their procedures and processes".²⁷

62. Ms F is also a Senior Scientist at FSS. She holds the degree of Bachelor of Science and the degree of Master of Science (Forensic Science). Ms F agreed with propositions A, B and C.²⁸
63. Ms F disagreed with proposition D(i) on the footing that reporting scientists can decide to "rework" samples in the relevant range. She also said that defence counsel can request a "rework".²⁹ She also disagreed with proposition D(ii) on the basis that the phrase used in a witness statement in these cases is, according to Standard Operating Procedure 34006, "This sample contained insufficient DNA to be suitable for analysis and was not tested further".³⁰ As I have already said, and as the Acting Director General also pointed out, many similar expressions have been used to describe the result for these samples. Nothing turns upon fine distinctions of this kind.
64. As to Proposition E, Ms F agreed that "it is possible to obtain a DNA profile from a sample that has a quantitation value within the quantitation range of 0.001 ng/μL to 0.0088 ng/μL".³¹
65. Ms F did not agree with propositions F and G. In summary, her reasons are as follows.³²
 - a. She said that "the technicality of the language may be considered as not reflecting the intent of the statement".
 - b. "In hindsight" she "conceded that 'This sample contained insufficient DNA to be suitable for routine analysis and was not tested further' may be more suitable wording." She did not explain what she meant by "routine".
 - c. She said that "every professional discipline has its own vernacular or shorthand" and that the use of 'insufficient for DNA analysis' is commonly used to indicate that low levels of DNA were detected but was considered not suitable for routine work and that such

²⁷ Statement of Ms E declared 4 August 2022, [11].

²⁸ Statement of Ms F declared 9 August 2022, [2] – [4], [8].

²⁹ Statement of Ms F declared 9 August 2022, [10].

³⁰ Statement of Ms F declared 9 August 2022, [11].

³¹ Statement of Ms F declared 9 August 2022, [12].

³² Statement of Ms F declared 9 August 2022, [14].

language had been used to describe certain samples since at least 2013.

66. Ms F pointed out that Reporting Scientists who have put forward a statement containing this expression "are always available for case conference and or court evidence".³³ Otherwise, Ms F described how quantitation values are only estimates, that the ability to obtain "an interpretable DNA profile" has changed over time and that the "ability to review current capability is restricted" by certain factors.³⁴
67. None of these reasons given by Ms F is, in my respectful opinion, relevant to any of the questions that I posed.
68. As to paragraph 66 above, the availability of an opportunity to unmask the falsity of a statement, if such an opportunity existed, cannot change an untrue statement into a true statement.
69. Ms G holds the position of Team Leader in the Evidence Recovery and Quality Team at FSS. She holds the degree of Bachelor of Science and a degree of Master of Science in Forensic Science.³⁵
70. Ms G agreed with propositions A, B and C.³⁶ As to proposition D(i), Ms G said that both QPS and FSS staff could request further processing to be carried out.³⁷ Like Mr C and Ms E, Ms G offered no opinion about proposition D(ii) on the basis that this fell outside the scope of her role at FSS.³⁸
71. As to proposition E, Ms G accepted the "possibility that obtaining a suitable DNA profile from samples that fall within the quantitation range 0.001 ng/μL to 0.0088 ng/μL cannot be excluded".³⁹
72. Despite that acceptance, Ms G would not agree with proposition F. Her reason was that the relevant wording was "based upon workflow agreed by the QPS at the time" and, because of the way in which results were reported to QPS, the witness statements "were consistent with the understanding and application of the wording and the workflows at the time".⁴⁰
73. I do not regard these matters as relevant to the questions posed. The consistency of the DIFP Statement with "the workflow", or that QPS agreed

³³ Statement of Ms F declared 9 August 2022, [14(c)].

³⁴ Statement of Ms F declared 9 August 2022, [14(f), (g)].

³⁵ Statement of Ms G declared 9 August 2022, [2], [3].

³⁶ Statement of Ms G declared 9 August 2022, [7] – [9].

³⁷ Statement of Ms G declared 9 August 2022, [10].

³⁸ Statement of Ms G declared 9 August 2022, [11].

³⁹ Statement of Ms G declared 9 August 2022, [12].

⁴⁰ Statement of Ms G declared 9 August 2022, [16].

with that workflow and the consistency of the statement with “the understanding and application of wording and workflows at the time” cannot bear upon the question whether, when presented as evidence in a witness statement, to lawyers, witnesses, judges and juries, the statement was true or false.

74. Mr A holds the position of Team Leader at FSS. Relevantly, he holds the degree of Bachelor of Arts in Human Movement Science, the degree of Bachelor of Science in Molecular Biology, the degree of Master of Science in Forensic Science and a diploma of Management.⁴¹
75. Mr A agreed with proposition A but pointed out that the process referred to in that proposition applied to samples concerning Major Crime from November 2015 until 2018 and had applied to all samples in the range 0.00214 ng/μL to 0.0088 ng/μL until November 2015.⁴²
76. Mr A agrees with propositions B and C.⁴³
77. In relation to proposition D(i), Mr A disagreed to the extent, he said, that it was not only QPS who could request a rework. He said that FSS staff could do so as well.⁴⁴ It seems to me that the fact that staff could process the sample if they wished demonstrates that not every sample reported as DIFP actually contained insufficient for further processing.
78. As to proposition D(ii), Mr A described how the relevant expression came to be formulated and how it evolved over the period during which the Forensic Register was introduced into FSS.
79. Mr A said that staff were free to “edit” the words used in witness statements when writing them and that “ultimately, it is their statement that is a record of the findings in the case”. He added that such findings are then always reviewed by another “competent Reporting Scientist” who “has the opportunity for rewording”.⁴⁵
80. I understand Mr A to be saying that the language used in a witness statement was a matter for the scientist who wrote it. This issue of responsibility for what was said is immaterial to the immediate question of the truth of the statement.

⁴¹ Statement of Mr A declared 9 August 2022, [2], [3].

⁴² Statement of Mr A declared 9 August 2022, [7].

⁴³ Statement of Mr A declared 9 August 2022, [8], [9].

⁴⁴ Statement of Mr A declared 9 August 2022, [10], [11].

⁴⁵ Statement of Mr A declared 9 August 2022, [11].

81. Mr A said that the statements “describe the process that was current at the time”. It reflected the process adopted by QPS which was not to process these samples “as a standard process”. Mr A said:⁴⁶

This was not to say that there was insufficient DNA for a DNA profile, rather the process was that there was insufficient DNA for further processing or analysis as a workflow/triage process. Indeed, I believe that I was transparent in describing in the Options Paper that there was an ability to obtain DNA suitable for interpretation ...

82. As to proposition E, Mr A agreed that the possibility of obtaining a profile from these samples “cannot be excluded”. Mr A was not prepared to accept proposition E in the way it was expressed because he does not agree with the aptness of the terms “partial” and “full” in this context - for reasons that he gave.⁴⁷ In my opinion, nothing turns upon this qualification once it is accepted that a (useable) profile might be obtained from some of these samples.
83. Mr A disagreed that the statement “DNA insufficient for further processing” was not true in the case of every sample because, he said, that the statement is true because it “describes the processing workflow at the time it was approved by QPS”.⁴⁸ I do not think that the statement describes the workflow at FSS. It describes a result for a sample that has been tested.
84. Mr A said that the statement reflected “what was in the Standard Operating Procedure for Exhibit Results in 2012 and from 2018 ... and as suggested statement wording for the result type from 2013...”.⁴⁹ Customary practice cannot assist, in this case, in deciding truth or falsity.
85. Mr A repeated that it was “ultimately up to the individual Reporting Scientist to use wording that they feel most appropriate for the result”.⁵⁰ I have dealt with this point earlier.
86. Mr A said that, to his knowledge “there has not been feedback from clients requesting further wording to clarify the meaning of these results”.⁵¹ That may be so, whoever these “clients” may be, but it cannot determine the objective question of truth or falsity.
87. Ms B holds the position of Managing Scientist at FSS. She is the head of the DNA Analysis section of FSS. She holds the degree of Bachelor of Science, the

⁴⁶ Statement of Mr A declared 9 August 2022, [11].

⁴⁷ Statement of Mr A declared 9 August 2022, [14].

⁴⁸ Statement of Mr A declared 9 August 2022, [16].

⁴⁹ Statement of Mr A declared 9 August 2022, [16].

⁵⁰ Statement of Mr A declared 9 August 2022, [16].

⁵¹ Statement of Mr A declared 9 August 2022, [16].

degree of Master of Science (Forensic Science) and a certificate in Project Management.⁵²

88. Ms B agrees with propositions A, B and C.⁵³
89. In relation to proposition D, she referred to various parts of Standard Operating Procedures that apply to the processing of samples, the entry of data into the Forensic Register and those that concern making witness statements. Like Ms F and Mr A, Ms B said that, in her view, scientists were at liberty to rework samples if they considered it desirable to do so.⁵⁴ That might be so, but as I have earlier observed, the fact that scientists are at liberty to analyse these samples with the purpose of obtaining a useable profile demonstrates the falsity of the statement that the sample contains insufficient DNA for further processing.
90. Ms B referred me to a section of the Standard Operating Procedure entitled "*Explanation of Exhibit Results for Forensic Register 34229v2*". The document to which Ms B has referred explains that choosing the phrase "DNA insufficient for further processing" as the descriptor for the test result on the Forensic Register has the automatic consequence that the following also appears in the relevant entry on the Forensic Register:

DNA insufficient for further processing

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

91. In fact, the statement "insufficient for further processing (due to the limitations of current analytical and interpretational techniques)" is untrue. FSS was not limited by current techniques so as to prevent the obtaining of useable profiles in cases in which such samples were capable of producing them.
92. The contents of the Forensic Register are not generally available to police investigators. However, relevant information from the Forensic Register is also placed onto QPRIME, which is the database that is generally available to police officers. When the DIFP Statement has been entered into the Forensic Register it will also appear on QPRIME to report the result of testing. However, the accompanying note on QPRIME is not the same as the note on

⁵² Statement of Ms B declared 12 August 2022, [2], [3].

⁵³ Statement of Ms B declared 12 August 2022, [7].

⁵⁴ Statement of Ms B declared 12 August 2022, [9].

the Forensic Register. Indeed, it is substantially different. The note that investigating police see is this:

This item/sample was submitted for DNA analysis. Low levels of DNA were detected in this sample and it was not submitted for further 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.

93. It is immediately apparent that this statement, unseen by those in court, is at odds with the DIFP Statement.
94. Like Mr A, Ms B says that staff members may also “devise wording that is similar to the suggested wording in the Standard Operating Procedures and the wording used is accepted in the peer review process”.⁵⁵ That goes to the question of responsibility, with which I am not presently concerned.
95. Ms B did not distinctly state that she agreed with proposition D but neither did she state that she disagreed with it.
96. In relation to proposition E, Ms B accepted that one cannot exclude the possibility of obtaining an interpretable profile from these samples although, in her opinion, it is unlikely that the attempt would be successful.⁵⁶
97. Ms B's response to proposition F is that she “would not adopt the words ‘was not true’” but accepted that further clarification “is required”.⁵⁷ This is also her approach to proposition G.⁵⁸
98. Mr Shaun Drummond is the Acting Director General of Queensland Health. He agreed with propositions A, B, C, D(i)⁵⁹ and E.⁶⁰
99. With respect to propositions F and G, Mr Drummond accepted that “the use of the words ‘suitable for DNA analysis’ carries a latent ambiguity as to the content of the term ‘suitable’, and may convey the impression that further processing or analysis is not possible”.⁶¹

⁵⁵ Statement of Ms B declared 12 August 2022, [11].

⁵⁶ Statement of Ms B declared 12 August 2022, [4].

⁵⁷ Statement of Ms B declared 12 August 2022, [19].

⁵⁸ Statement of Ms B declared 12 August 2022, [20].

⁵⁹ Mr Drummond pointed out, correctly, that the expression “insufficient DNA for further processing” was not the only one used in witness statements. Mr Drummond set out other forms of expression that have been used. All of them are to the same effect as “insufficient DNA for further processing”.

⁶⁰ Statement of Shaun Drummond declared 5 August 2022, [1], [4] – [9].

⁶¹ Statement of Shaun Drummond declared 5 August 2022, [10].

100. I made inquiries of laboratories in other jurisdictions about the issue of thresholds of the kind under consideration here. I received the following information.
101. Western Australia does not apply any threshold to samples tested in investigations of Major Crime. Samples from all cases of serious crime, that is, not property crime, are all fully tested irrespective of the quantitation result. In property crime cases, low quants (below 0.0015 ng/μL) are not routinely tested and are described as "Due to low levels of DNA detected within this sample, DNA profiling was not performed".
102. New Zealand's Institute of Environmental Science and Research also applies no such threshold to samples in investigations of serious crime. For samples concerning Volume Crime, a quantitation of 0.0005 ng/μL or less results in the sample not being tested further and reported as "The presence of DNA could not be confirmed and therefore DNA profiling analysis has not been attempted". For samples just above that, between 0.0006 ng/μL and 0.003 ng/μL the report is "DNA profiling was not attempted because of the small amount of DNA detected in this sample."
103. The Northern Territory laboratory processes all samples, even those that return a quant of 0.000 ng/μL.
104. In South Australia samples with quants below 0.01 ng/μL undergo further processing at the discretion of the particular scientist performing the analysis. That discretion is exercised having regard to certain factors, such as the significance of the sample to the investigation, whether the sample is of a kind that is inherently likely to yield a result, such as blood or saliva, and whether it is thought that a technical issue within the lab might have affected the quant. From 2016 until 2022, samples that were not processed because of a low quant were described: "Sample contains very low amounts or no DNA and was not analysed. The group of profiles that fall into this bracket are the least likely to yield informative results." In early 2022 the description was changed to: "Insufficient DNA detected to proceed with further analysis. The group of profiles that fall into this bracket are the least likely to yield informative results." Recently, the wording used for general casework has become: "The DNA concentration is below the threshold set by FSSA for further analysis. These samples contain DNA concentrations that are least likely to yield informative results. This includes samples where DNA was not detected." Other, more specific, terminology is used in sexual offence cases in contexts that are not presently material.
105. New South Wales routinely leaves it to the discretion of the scientist reviewing the case to decide whether a sample below 0.004 ng/μL should undergo

further processing. If a decision is made not to process the sample, the result is reported as: "DNA testing was unsuccessful". An appendix to the report provides the following explanation:

A DNA result reported as "unsuccessful" could indicate one of several outcomes, such as there was not DNA detected; or the amount of DNA recovered from the sample was below the laboratory threshold for routine further DNA testing. "DNA testing was unsuccessful" will also be reported where routine further DNA testing has been carried out but no DNA profile was recovered; or a very limited amount of DNA profile information was recovered; and as such, the result is not suitable for meaningful comparison.

106. In Tasmania all samples that are confirmed or suspected to contain good sources of DNA, such as blood, semen and saliva, are processed fully if any DNA is detected at the quantification stage. For other kinds of samples, if the quant is 0.005 ng/ μ L or below, the responsible case officer, who is a forensic biologist, exercises a discretion whether the sample is worth testing further. In the latter case the result is reported as "Insufficient DNA to proceed further with testing" or words to the same effect. I observe that in such cases the description is used to report an actual judgment made by a responsible officer who has considered the question of suitability for processing.
107. I observe that no jurisdiction uses a description for untested samples that have not been individually considered that might mislead somebody into thinking that an actual judgment has been made that there was no DNA in the sample or that it was not possible to obtain a useable result.

CONCLUSIONS ABOUT DIFP STATEMENT

108. The facts set out in propositions A, B, C, D and E are really incontrovertible. Propositions A, B, C and D are documented historical facts, although it is true, as Ms F, Ms G, Mr A, Ms B and QPS have pointed out, that scientists in the laboratory might be in a position to request a reworking. However, that qualification is irrelevant to the present question which does not concern how such samples might come to be processed despite the reported result.
109. Proposition E has not been contested by anyone.
110. The real issue that I have to address is whether the DIFP Statement is true when used in a Witness Statement prepared for criminal proceedings.
111. One might expect that a statement by a scientist about a matter of science would be precise in its meaning and that, as a consequence, there would be

general agreement about its meaning among those who use it. The anomaly here is that:

- a. Mr C and Ms E, were not prepared to venture their understanding of what the DIFP Statement meant.⁶²
 - b. Ms F, said that it meant that there was insufficient DNA for “routine” analysis.⁶³
 - c. Ms G, did not offer an opinion about the meaning of the statement but said that the words used were “based upon workflow agreed by the QPS at the time”.⁶⁴
 - d. Mr A said that the statement “described the process”⁶⁵ and the process “was that there was insufficient DNA for further processing or analysis as a workflow/triage process”.⁶⁶
 - e. Ms B, the Managing Scientist also offered no opinion about the meaning of the statement but acknowledged that further clarification “is required”.⁶⁷
 - f. Nobody was willing to say that the DIFP Statement in its ordinary and natural meaning was true.
 - g. Only Ms D was willing to acknowledge that the DIFP Statement was untrue.⁶⁸
112. There was no agreement about what the statement meant by the scientists who used it and two FSS scientists would not even venture an opinion about the meaning.⁶⁹ This is remarkable.
113. Although a copy of Professor Wilson-Wilde’s opinion was furnished to each respondent, no respondent addressed anything that Professor Wilson-Wilde said.
114. In my opinion, no possible stretching of language can convert,
- This sample contained insufficient DNA to be suitable for analysis and was not tested further.

⁶² Statement of Mr C declared 3 August 2022; Statement of Ms E declared 4 August 2022.

⁶³ Statement of Ms F declared 9 August 2022, [14].

⁶⁴ Statement of Ms G declared 9 August 2022, [16].

⁶⁵ Statement of Mr A declared 9 August 2022, [18].

⁶⁶ Statement of Mr A declared 9 August 2022, [11], page 6.

⁶⁷ Statement of Ms B declared 12 August 2022, [20].

⁶⁸ Statement of Ms D declared 9 August 2022, [15].

⁶⁹ Mr C and Ms E.

into

This sample may contain sufficient DNA to obtain a useable profile but it was not tested to find out.

115. It must be borne in mind that witness statements issued by FSS over the signature of a qualified scientist contain two types of evidence. They contain evidence of fact, such as that a sample was received, that it underwent some testing and the objective result of that testing. They also contain opinion evidence. The DIFP Statements constitute evidence of the second kind.
116. The DIFP Statements represented that it was the expert opinion of the witness that the sample in question was unsuitable for any further analysis or processing. That has now been acknowledged by everyone not to be true in every case.
117. Section 95A of the *Evidence Act 1977* is a provision that permits many of these kinds of facts and opinions to be proved in a shorthand way by means of a certificate. It does so by making a certificate signed by a qualified expert evidence of the facts and opinions contained in it. The use of a certificate under the Act avoids the need for the Crown to lead direct evidence from many witnesses to prove that a sample was recovered, delivered, examined, tested and that it gave a particular profiling result. This is a good thing because most of these facts should be routinely accepted. The soundness of laboratory procedures is assumed and this assumption is the basis for the accepting of the conclusions offered about these matters by a witness who has no direct knowledge of the facts. The Act gives only very limited room for a defendant to question these statutory assertions. There is no room at all for victims of crime to do so.
118. In Queensland, rather than using statutory certificates to prove the facts, witness statements are routinely used. The section 95A certificates are more often used to deal with matters of handling and storage of samples when necessary. That is probably a better way of dealing with such evidence and nothing turns upon the use of this practice but for the present circumstances of the employment of DIFP Statements.
119. I am of the firm view that the statement "DNA insufficient for further processing", as well as its many analogues, was untrue in the way in which it has been used in witness statements since early 2018. That statement connotes the certainty that the sample cannot yield a useable profile when that is not known. Because the samples concerned had been quantified but not analysed, nobody could actually say that the sample could not yield a useable result nor did anybody ever actually reach that conclusion.

120. I emphasise that I am not presently concerned with whether the decisions made by FSS and QPS not to test a class of samples in investigations of major crime had a valid scientific basis. Nor am I presently concerned with any question of responsibility for the use in witness statements of the DIFP Statement.
121. Upon the establishment of this Commission, FSS recommenced testing samples within the range 0.001 ng/μL and 0.0088 ng/μL. As a consequence, the DIFP Statement ceased to be used for samples tested after 6 June 2022. However, witness statements containing the DIFP Statement that were issued before that date remain in circulation as evidence in the hands of those to whom they were given. Undoubtedly some of these will soon be the basis of evidence at a trial. Also, results within that range that were obtained before 6 June 2022 were to be reported as "DIFP" even after that date.
122. The discovery that witness statements have been issued that contain statements that are untrue is deeply concerning but not all of these statements will have had a material effect upon investigations or upon possible, intended or concluded criminal proceedings. By "material effect", I mean this:
- a. A participant in the criminal justice process has read a DIFP Statement and understood it to mean that the amount of DNA present was so low that there could be no further use in processing in the hope of obtaining a useable DNA profile.
 - b. Had that person known that further processing might usefully be undertaken, although the obtaining of a useable DNA profile was improbable, the person would have requested further testing.
 - c. The further testing would have resulted in a useable DNA profile.
 - d. The profile would have had significance for an actual or proposed investigation or for a possible, proposed or actual proceeding.
123. As presently advised, I am of the opinion that there would be few cases, fortunately, where there has been a miscarriage of justice due to a wrongful conviction. It must be borne in mind that a truthful statement would have informed the parties that, after more work is done, a DNA profile might be obtained but that that was unlikely. Non-use of the DIFP Statement would not have meant that all or any of these samples would have been tested. A request would still have had to be made that the sample be fully tested and who would have asked for that to be done? Practically speaking, in many cases, an accused person would not regard further DNA testing as a very good idea. The lack of DNA results is often an advantage to the defence.

124. A miscarriage by reason of a wrongful conviction would be likely to arise only if an unexamined sample would have been tested at the request of the defence or prosecution and if the result then obtained would have been that the convicted person had to be excluded as a possible offender. For practical reasons, this would be a rare case.
125. A more frequent, but still uncommon, case of potential miscarriage of justice might arise if the defence, knowing that further processing might yield an outcome, required that to be done and it was now established that some other person, known or unknown, might have been involved in the commission of the offence in a way that might have raised a reasonable doubt about guilt because another person's DNA appeared in a crime scene sample.
126. There are four kinds of cases in which the DIFP Statements might have had a material effect on outcome. First, the absence of DNA evidence when it was actually available might have resulted in a line of investigation by police being unnecessarily weakened or abandoned. Second, a prosecutor might have decided not to commence criminal proceedings or might have decided to discontinue proceedings because of the absence of such evidence when it might have been obtained. Also, a prosecutor might be inclined to accept a plea of guilty to a lesser offence because of the absence of such evidence which, if it had been obtained, would have sustained a conviction for a more serious offence. Third, the absence of evidence might have weakened the prosecution case significantly. In cases in which ignorance of the truth led to an actual acquittal, the laws of double jeopardy would, in most cases, preclude useful re-examination of the evidence. The chance of conviction is forever lost.
127. Finally, the absence of evidence of an offender's DNA in a sexual assault case in which, because of the circumstances of the offending, the offender's DNA was expected to be found, might compromise the credit of a truthful complainant to such a degree that he or she is (or a child complainant's parents are) no longer willing to pursue justice under such conditions.
128. I emphasise that these conclusions do not indicate that any DNA match reported by the laboratory was incorrect or that any conviction which involved DNA evidence is in doubt. These conclusions mean that persons or parties involved in criminal litigation may have taken a different course, but that does not of itself call into question any evidence given in court for other samples where testing was done and matches between crime scene samples and reference samples were obtained. That is the most common type of DNA evidence that supports a conviction.
129. The question is what is to be done now.

130. I invited submissions from certain stakeholders who may have had an interest in making submissions about this matter. Because of the short time frame that I set myself, this process was distinct from my general call for submissions about my terms of reference.
131. I received a submission from QPS who agreed with propositions A, B, C and E.⁷⁰
132. In relation to proposition D(i), like some others, QPS pointed out that there are occasions on which an FSS scientist might decide to process a sample further.⁷¹
133. In relation to proposition D(ii), QPS denied that the content of witness statements had been part of any agreement reached between QPS and FSS.⁷² Relevantly, the only agreement between the parties had been about the designation of results in the Forensic Register.
134. In relation to proposition F, QPS agreed that the statement was untrue in cases in which the relevant statement was "DNA insufficient for further processing" if that statement was applied to a sample just because it fell within the quant range 0.001 ng/ μ L to 0.0088 ng/ μ L.⁷³
135. QPS further submitted that in cases in which the applicable word was "analysis" rather than "processing", if a sample had been assessed using Quant Trio and, upon the interpretation of the results from Quant Trio⁷⁴ a conclusion had been reached that the sample was not suitable for further analysis, then the statement was true.⁷⁵
136. I do not need to consider this possibility because it has not been suggested to me by anybody in FSS, who are in a position to know the truth about the reasons for the use of statements of various types, that this might be an explanation for what has been said in witness statements. Accordingly, I do not consider this further in this report.
137. The Bar Association of Queensland submitted that if I accepted Professor Wilson-Wilde's opinion, then the DIFP Statement as used in witness

⁷⁰ Queensland Police Service, QPS Submissions to the Commissioner Regarding Proposed Interim Findings (12 August 2022), pages 1 - 2.

⁷¹ Queensland Police Service, QPS Submissions to the Commissioner Regarding Proposed Interim Findings (12 August 2022), page 1.

⁷² Queensland Police Service, QPS Submissions to the Commissioner Regarding Proposed Interim Findings (12 August 2022), page 1.

⁷³ Queensland Police Service, QPS Submissions to the Commissioner Regarding Proposed Interim Findings (12 August 2022), page 2.

⁷⁴ "Quant Trio" is a particular technology that FSS uses for quantitation.

⁷⁵ Queensland Police Service, QPS Submissions to the Commissioner Regarding Proposed Interim Findings (12 August 2022), page 2.

statements was objectively misleading and that it was likely that counsel did not understand that some samples might have contained sufficient DNA for further processing.⁷⁶ The Bar Association expressed its concern that it was likely that available lines of inquiry, for prosecution and defence, were not pursued in criminal matters when they should have been. The Bar Association also pointed out that in about 10% of cases there may have been a failure to perform the duty of disclosure in relation to a discoverable DNA result.⁷⁷ In 1.45% of cases there may have been a failure to disclose a previously unknown suspect's contribution to a crime scene sample. The Bar Association submitted that these non-disclosures might have affected the outcome of trials and might have allowed an undetected offender to remain undetected.⁷⁸ The Bar Association submitted that all witness statements containing the DIFP Statement should be corrected.⁷⁹

138. In a carefully considered submission, Legal Aid Queensland ("LAQ") pointed out that if publicity is given to this issue by the publication of a report, the largest ramification would be for cases in which, in reliance on such statements, no charges were laid or in which a prosecution has been discontinued, cases in which such statements may yet to be tendered in imminent cases and cases in which there has been an acquittal and in which such evidence might have been material to the acquittal.⁸⁰ I agree. It was submitted that cases might also appear in which such statements might give rise to inquiries leading to the discovery of a wrongful conviction but these are less likely than the other category of cases.
139. One objection that LAQ raised to the delivery of this report is that the short time frame for this report to be completed risks compromising the ability to ensure that all affected cases are identified.⁸¹ That task of identifying such cases cannot be done by me within the time available before the final report is due and, in any event, it can be done more efficiently by others.
140. LAQ has also raised a question whether it is efficient for me to consider and report upon this single issue at this point when there is potential for other

⁷⁶ Letter from the Bar Association of Queensland to Commissioner Walter Sofronoff QC dated 15 August 2022, page 1.

⁷⁷ Letter from the Bar Association of Queensland to Commissioner Walter Sofronoff QC dated 15 August 2022, page 1.

⁷⁸ Letter from the Bar Association of Queensland to Commissioner Walter Sofronoff QC dated 15 August 2022, page 2.

⁷⁹ Letter from the Bar Association of Queensland to Commissioner Walter Sofronoff QC dated 15 August 2022, page 2.

⁸⁰ Legal Aid Queensland, Commission of Inquiry into Forensic DNA Testing in Queensland – Proposal for Interim Report regarding Explanation of "Insufficient DNA" in Statement of a Witness (12 August 2022), page 3.

⁸¹ Legal Aid Queensland, Commission of Inquiry into Forensic DNA Testing in Queensland – Proposal for Interim Report regarding Explanation of "Insufficient DNA" in Statement of a Witness (12 August 2022), page 3.

related issues to come to light.⁸² I do not think that this is a concern. The issue that I have addressed in this report is a very narrow one. It is whether or not a particular expert opinion expressed about a certain category of crime scene samples was false. I am not concerned presently with questions about how that came about nor whether anyone was responsible. These are matters that are yet to be investigated.

141. LAQ and Queensland Law Society ("QLS") have both pointed out the potentially large disruption that this interim report might provoke and the short time for this particular aspect to be examined and reported. They submitted that the Commission will not have the benefit of submissions from every potentially interested party. For those reasons they both cautioned against dealing with these issues in this report. They both submitted that the issue should await consideration in my final report.⁸³
142. I must respectfully reject those submissions. The report of Professor Wilson-Wilde and the responses from FSS managers point inexorably towards a single conclusion. These statements have been discovered to be untrue and that will not change. Their use over the last four years has large ramifications for the fate of trials, the integrity of police investigations of serious offences and decisions about whether to commence proceedings and for victims of serious offences and that, also, will not change.
143. I am of the opinion that the practice of putting forward these untrue statements as true expert evidence is a profound issue for the administration of criminal justice, for the integrity of police investigations and for decisions made by victims of crime. The belief in the truth of these statements should not be permitted to continue for a day longer. Steps should be taken promptly to retrieve the position where necessary and where rectification is still possible. Indeed, this is the course that must be adopted as long as there is a chance that there has been even a single case of miscarriage of justice, whether that is because there has been a wrongful conviction or whether that is because there has been a failure to bring an offender to justice. Postponement of action cannot change the aftermath. I see no reason to delay acting.

⁸² Legal Aid Queensland, Commission of Inquiry into Forensic DNA Testing in Queensland – Proposal for Interim Report regarding Explanation of “Insufficient DNA” in Statement of a Witness (12 August 2022), page 4.

⁸³ Legal Aid Queensland, Commission of Inquiry into Forensic DNA Testing in Queensland – Proposal for Interim Report regarding Explanation of “Insufficient DNA” in Statement of a Witness (12 August 2022), page 3; Queensland Law Society, Explanation of “Insufficient DNA” in Statement of a Witness (11 August 2022).

144. LAQ submitted that if the matters discussed above do not constitute valid objections to the issue of a report upon this question, it supports the issue of such a report as soon as possible.⁸⁴
145. QPS submitted that all incorrect statements should be withdrawn.⁸⁵ Like LAQ, QPS has drawn my attention to the practical ramifications that will follow should that step be taken. QPS submitted that, in relation to current criminal litigation, notification should be given promptly about the potential effect of this issue to Police Prosecution Corps, the Office of the Director of Public Prosecutions, the QLS, the Bar Association of Queensland, LAQ and the Aboriginal and Torres Strait Islanders' Legal Service.⁸⁶
146. QPS submitted that, in relation to concluded matters, notification has to be given to all parties who may have an interest in knowing the truth. This can best be done by a process of consultation between the parties referred to above and also FSS, the Department of Justice and Attorney-General, victim support groups and, potentially, other parties.⁸⁷
147. QPS submitted that consideration has to be given for further testing of samples whose results may have a material effect having regard to other evidence in a case.⁸⁸ That is a matter for QPS, the DPP and FSS.
148. QPS undertook to commit necessary resources and will collaborate with other parties to ensure a just outcome.⁸⁹
149. The DPP cautioned against describing the DIFP Statement as "not true" on the basis that that description would tend to "skew the complex issue and [suggest that] an element of deliberation or dishonestly (*sic*) that is not found in a proper understanding of the circumstances".⁹⁰ The DPP submitted:

It fails to make clear, or recognise, that the words used in the Witness Statements were the consequence of a decision made in the context of what I anticipate to have been workload pressures and were designed to

⁸⁴ Legal Aid Queensland, Commission of Inquiry into Forensic DNA Testing in Queensland – Proposal for Interim Report regarding Explanation of "Insufficient DNA" in Statement of a Witness (12 August 2022), page 3.

⁸⁵ Queensland Police Service, QPS Submissions to the Commissioner Regarding Proposed Interim Findings (12 August 2022), page 3.

⁸⁶ Queensland Police Service, QPS Submissions to the Commissioner Regarding Proposed Interim Findings (12 August 2022), page 3.

⁸⁷ Queensland Police Service, QPS Submissions to the Commissioner Regarding Proposed Interim Findings (12 August 2022), page 3.

⁸⁸ Queensland Police Service, QPS Submissions to the Commissioner Regarding Proposed Interim Findings (12 August 2022), page 3.

⁸⁹ Queensland Police Service, QPS Submissions to the Commissioner Regarding Proposed Interim Findings (12 August 2022), page 3.

⁹⁰ Letter from the Office of the Director of Public Prosecutions to Commissioner Walter Sofronoff QC dated 17 August 2022, page 4, [13].

improve efficiency in processes whilst achieving an outcome which remained, I conclude, within acceptable scientific tolerances. The wording of the finding fails to put in proper context the complexity of the issues driving the decision to adopt the subject methodology and risks an unwarranted undermining of public confidence not only in the scientists, but in the science, with a wide-reaching detrimental effect upon the criminal justice system. It also fails to reflect the statistically small number of samples (not cases) that may have provided a result despite not meeting the threshold, and the fact that even those which *may* have produced a further result does not suggest that the result was of further utility in the context of the investigation, nor that there remained the opportunity for further testing to be conducted upon request (although, perhaps this ability for further testing was not widely known and known only to the police).⁹¹

150. As I explain below, I am not presently concerned with the reasons why this policy was adopted. I do not pause now to consider whether it is possible to justify declining to do a statistical proportion of otherwise essential work as a method of alleviation of workplace pressures when that work bears upon the administration of criminal justice in individual cases of serious violent offences. At present I am concerned only with the question whether the past use of the DIFP Statement was prone to mislead and whether its continued use has that proclivity. The aims at which the Options Paper was directed, as well as the justifiability as well as the soundness and rationality of those aims, await further consideration.
151. In any event, I do not accept that the words “true” and “false”, when applied to the character of the DIFP Statement, connote a moral element; they are terms of logic. I address this further below.
152. The DPP’s concerns about the potential effect of a finding that the DIFP Statement is untrue is largely based, it seems to me, upon the assumption that, as the submission puts it, “it is overwhelmingly likely that the subject sample will contain insufficient DNA to develop a DNA profile [and that the] figure given [in the Options Paper is] 1.45% of all ‘auto-microcon’ samples.”⁹²
153. Since that assumption constitutes the basis for the DPP’s important submission that I make no finding about the untruth of the statement, I have to consider it carefully.

⁹¹ Letter from the Office of the Director of Public Prosecutions to Commissioner Walter Sofronoff QC dated 17 August 2022, page 5, [15].

⁹² Letter from the Office of the Director of Public Prosecutions to Commissioner Walter Sofronoff QC dated 17 August 2022, page 4, [12].

154. The Options Paper posits that 10.6% of samples meet the criterion of "success".⁹³ The terms "Fail" and "Success" were defined as follows:
- Fail:** In this report, this is DNA profile information that was not suitable for comparing to reference DNA profiles and other casework samples. This word was used to filter the data into two possible outcomes (fail/success).
- Success:** In this report, this is DNA profile information that was obtained that was suitable for comparing to reference DNA profiles and other casework samples. This word was used to filter the data into two possible outcomes (fail/success).
155. Later in the Options Paper its authors considered the extent to which samples within this range gave rise to an identification of an *unknown suspect* by reference to the national DNA database. Only 1.86% of samples gave rise to such a "cold-link" identification. Such intelligence is vital, of course, in cases in which a killer or rapist is unknown and there is no suspect or obvious person of interest. However, the problem is that in many, and perhaps in most, homicides and sexual offences there is a known suspect or, at least, persons of interest. In such cases police are not looking for an unknown offender whose profile might be on the national DNA database. That category of samples that give rise to a useable profile that links to a *known person* makes up part of the 10.6% of samples which were categorised as "success" in the Options Paper.
156. The proportion of samples that were capable of generating a useable profile was not 1.86%. It was 10.6%.⁹⁴ Some of these expert opinions may have been critical to an investigation of a serious offence, a decision to prosecute or the outcome of a trial. Such statements continue to circulate - with a potentially operative effect upon investigators and upon tribunals of fact. I do not accept that, having discovered this to be so, it is acceptable to do nothing.
157. Nor can I accept that fears of the effect upon public confidence of this practice could justify the suppression of this truth. This would involve the knowing perpetuation of the use of misleading evidence. Public confidence in the system of the administration of criminal justice can only be maintained by the actual integrity of its administration.
158. The State Coroner, Mr Terry Ryan, submitted that, if I accepted Professor Wilson-Wilde's opinion, it was open to me to make the findings in propositions A to E.⁹⁵ In his view, having regard to the significance of the issue, it was preferable for me to submit a report now rather than to await the

⁹³ See page 3.

⁹⁴ This figure is itself controversial but that is immaterial for present purposes.

⁹⁵ Letter from Terry Ryan, State Coroner, to Commissioner Walter Sofronoff QC dated 20 August 2022, page 1.

final report.⁹⁶ He agreed that the DIFP Statement, where it was used in Witness Statements, should now be corrected.⁹⁷

NO DNA DETECTED

159. All scientific measuring instruments have their limitations. The instrument and the associated equipment used for quantitation is not an exception.
160. The manufacturer of the technology currently used by FSS specifies a “Limit of Detection” of 0.001 ng/μL.⁹⁸ This means only that, if the quant value returned is below that value, the result cannot be regarded as signifying that DNA is present or that it is not present. The technology offers no answer at such readings. As I described earlier, the process employs a technique whereby a laser is applied to a chemically treated sample and, if the laser generates fluorescence in the sample, that fluorescence generally demonstrates the presence of DNA. Sufficiently intense fluorescence demonstrates the presence of DNA and the instrument uses the light intensity as a factor to determine the concentration of DNA in the sample. However, other substances might also generate low levels of fluorescence under the same conditions and, if the levels of fluorescence detected are very low, there may be no way of telling whether such fluorescence is due to the presence of small quantities of DNA or small quantities of other substances. It will be recalled that we are here concerned with quantities of molecular material below one thousandth of one billionth of a gram in mass.
161. In such a case a scientist might rightly observe that DNA has not been detected in the sample. In this context, such a statement is not intended to imply that there is an absence of DNA but only that, literally, the scientist has not been able to determine whether there is or is not any DNA in the sample.⁹⁹
162. As a consequence of this common scientific use of language, FSS has arranged its system of reporting so that such results are recorded on the Forensic Register as “No DNA detected”.¹⁰⁰ If, in due course, a witness statement is prepared for use in criminal proceedings, the same statement is employed to report the result.

⁹⁶ Letter from Terry Ryan, State Coroner, to Commissioner Walter Sofronoff QC dated 20 August 2022, page 1.

⁹⁷ Letter from Terry Ryan, State Coroner, to Commissioner Walter Sofronoff QC dated 20 August 2022, page 2.

⁹⁸ Quantifiler HP and Trio DNA Quantification Kits USER GUIDE, Publication Number 4485354, Revision G.

⁹⁹ This reflects the difference between classical logic, which deals with statements that are either true or false and intuitionist logic which is interested in whether a statement is refutable or provable or “not substantiated” as an expression used by Professor Wilson-Wilde.

¹⁰⁰ *Queensland Health Forensic and Scientific Services Procedure for Case Management*, version 21, page 12.

163. The expression has been used to report results in which quants of, say, 0.00086 ng/μL and 0.00059 ng/μL have been reported. However, it is uncontroversial that some samples with quants between 0.00 ng/μL and 0.001 ng/μL have been known to result in useable profiles although the probability of achieving this outcome may be low. As has already been noticed, labs in some jurisdictions routinely process such samples.
164. The choice of particular language depends, fundamentally, upon the intent of the speaker. The intent of a scientist using technology in an attempt to determine whether or not DNA is present in a sample is, in this case, to report that the testing has been unable to determine whether DNA is present. So, "I have not been able to find whether there is any DNA" becomes, when the passive voice is used, "No DNA detected".
165. As with the use of the DIFP Statement, I served requirements upon management figures in FSS to provide information.
166. Ms E and Ms D both agreed that samples with quants below 0.001 ng/μL might generate a useable profile.¹⁰¹ Ms B and Mr A said that that possibility could not be excluded.¹⁰² Ms G referred me to the manuals that state that quants at those levels might undergo certain further tests, such as micro-concentration.¹⁰³ I took that to be an implied acceptance of the proposition. Ms F said that she did not know but opined that the number of such quants was "trivial".¹⁰⁴
167. Nobody asserted that it was not possible to obtain profiles from samples in that category although it was common ground that the prospect of doing so is low. Very recently, QPS has conducted a review of "No DNA detected" results. After selecting 205 samples in which that result appeared anomalous, for example, samples of presumptive blood, QPS required full testing and achieved a partial or full profile in 49 cases. Of these, 27 gave results that were capable of being usefully uploaded to the national DNA data base or returned a profile with a ratio of over 100 billion to one likelihood that a particular person contributes to the profile.¹⁰⁵
168. The likelihood of obtaining a useable profile from samples with such low quantities of DNA, or possibly no DNA, does not concern me. I have two concerns.

¹⁰¹ Statement of Ms E declared 24 August 2022, [12]; Statement of Ms D declared 24 August 2022, [10].

¹⁰² Statement of Ms B declared 25 August 2022, [12]; Statement of Mr A declared 25 August 2022, [21].

¹⁰³ Statement of Ms G declared 25 August 2022, [19] – [23].

¹⁰⁴ Statement of Ms F declared 24 August 2022, [16] – [17].

¹⁰⁵ Statement of Mr H declared 8 September 2022, [1] – [4].

169. First, when given as evidence in a criminal trial, a scientist's conclusion that there was no DNA detected in a sample is apt to be regarded as asserting the absence of any DNA. That fact may be crucial in many kinds of cases. It is capable of misleading a jury in a circumstantial case. It is capable of impugning the credibility of a complainant whose evidence implied that DNA should have been present. Second, when reported to a police investigator or a victim of a serious crime, it is equally apt to be misunderstood as proof that the offender's DNA was not present when, on the complainant's account, it ought to have been present;¹⁰⁶ or that the complainant's DNA was not present where it ought to have been present.¹⁰⁷
170. Several respondents who have furnished their statements to me have urged that the statement is true in its scientific sense and that, in any case, "police" knew what it meant. QPS submitted to the same effect.¹⁰⁸ That does not address the problem. The word "police" refers to many different people, a few of whom undoubtedly knew what was meant by FSS; but many front-line QPS investigators might not have known. Moreover, nobody suggested that this particular meaning was ever made plain to anyone else, such as counsel, judges or juries. It is also unlikely, and nobody suggested, that any victim of crime to whom a police officer reported such a result was given a conceptual scientific explication.
171. The choice of language has been unfortunate. It has been in use for a long time. It should not be used any longer.
172. Ms F submitted that, if FSS was required to issue addendum statements to correct every witness statement in which the phrase was used, FSS would be severely impeded in its ability to do its current work.¹⁰⁹ She submitted that the cost involved in such a course, in terms of time and effort, would substantially outweigh any benefit that might be obtained in the rare case or cases in which the effect of the statement was material.¹¹⁰ She also submitted that the issue of addendum statements was apt to confuse the courts.¹¹¹
173. I do not accept that the rectification of the current situation, in which some parties may have been materially misled about the evidence, involves an oppressive burden upon the resources of FSS. I do not accept that it is

¹⁰⁶ As when, for example, a complainant says that offender ejaculated within her but the test result for a vaginal swab searching for a suspect's DNA is "No DNA detected".

¹⁰⁷ As when, for example, a complainant says that the offender penetrated her but the test result for a penile swab searching for the complainant's DNA is "No DNA detected".

¹⁰⁸ Queensland Police Service, QPS Submissions to the Commissioner Regarding Topic IR1B: Explanation of 'No DNA' in statement of a witness (26 August 2022), pages 1 – 2.

¹⁰⁹ Statement of Ms F declared 24 August 2022, [19].

¹¹⁰ Statement of Ms F declared 24 August 2022, [20].

¹¹¹ Statement of Ms F declared 24 August 2022, [21].

impossible to achieve the necessary correction by efficient means. I am unpersuaded that it is better to save FSS the work involved than it is to ensure that there has been no miscarriage of justice in any individual cases, even if that is only a single case. Nor can I take seriously the suggestion that a correction of a misleading statement put forward in court might itself mislead a court.

RECOMMENDATIONS

174. I therefore recommend as follows:

- a. Every Witness Statement issued by FSS since February 2018 in which a sample has been reported under the rubric "DNA insufficient for further processing" or any similar expression, and in which a sample has been reported as "No DNA detected" be identified by FSS without delay in a manner that will ensure ease of production of a list of such statements and, if required, the production of the statements themselves and the due provision of quants that were the basis for such statements.
- b. For every such statement, a further statement be prepared by FSS stating that:
 - i. In each case in which the DIFP Statement has been used, that the statement was not correct and that the sample contains a low level of measurable DNA which, if fully processed, might produce an interpretable profile.
 - ii. In each case in which the statement "No DNA detected" has been used, that the statement was not correct and that the sample returned a quantitation result below the level of detection but that further work might result in a useable profile but that that is unlikely.
- c. That the Queensland Government take steps to ensure that public bodies and publicly funded bodies that require additional funds or other resources to investigate, consider and resolve these issues be furnished with the necessary funds and resources so that any miscarriages of justice are resolved as promptly as is practicable.



Walter Sofronoff QC
Commissioner
Commission of Inquiry into Forensic DNA Testing in Queensland
15 September 2022

*ANNEXURE 1: A review of the automatic concentration of DNA extracts using
Microcon Centrifugal Filter Devices: Options for QPS Consideration*



HealthSupport Queensland

A review of the automatic concentration of DNA extracts using Microcon[®] Centrifugal Filter Devices: Options for QPS consideration.

January 2018

Mr A and **Ms B**

A review of the automatic concentration of DNA extracts using Microcon® Centrifugal Filter Devices: Options for QPS consideration.

Published by the State of Queensland (Queensland Health), January 2018



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1. Abstract

All casework DNA extracts that underwent a concentration step using the Microcon® process were evaluated and categorised into whether there was meaningful information obtained or not. This evaluation primarily focussed on samples that underwent an 'auto-microcon' process in 2016.

The findings of this evaluation are presented for the Queensland Police Service to advise on whether they would prefer their Priority 2 samples to continue with the 'auto-microcon' process, or to cease this automatic step and notify the laboratory if particular samples are requested to be reworked.

These options relate to Priority 2 (Major Crime) samples only, as the process developed in 2012 for Priority 3 (Volume Crime) samples will be reinstated with the operationally-required move to process these samples using PowerPlex® 21 system (PP21).

2. Definitions

DNA Profile Intelligence: DNA profile information available for interpretation by Forensic DNA practitioners that is able to be provided to clients.

Fail: In this report, this is DNA profile information that was not suitable for comparing to reference DNA profiles and other casework samples. This word was used to filter the data into two possible outcomes (fail/success).

NCIDD: National Criminal Investigation DNA Database.

QPS: Queensland Police Service.

Success: In this report, this is DNA profile information that was obtained that was suitable for comparing to reference DNA profiles and other casework samples. This word was used to filter the data into two possible outcomes (fail/success).

3. Introduction

Microcon® Centrifugal Filter Devices desalt and concentrate macromolecular solutions such as DNA-containing solutions. They employ Amicon's low binding, anisotropic, hydrophilic regenerated cellulose membrane^[1].

The use of Microcon® filters to concentrate extract has been a standard post-extraction process within Forensic DNA Analysis to reduce the volume of

extract from approximately 100uL to $\leq 35\mu\text{L}$ for amplification with PowerPlex[®] 21 system.

Since the implementation of PP21 amplification kit within Forensic DNA Analysis for casework samples in December 2012, extracts with low Quantification values were recommended to be concentrated. Templates of $<0.132\text{ng}$ (Quantification $<0.0088\text{ng/uL}$) were found to exhibit marked stochastic effects after amplification [2]. Consequently, a workflow that directed extracts automatically to a concentration step based on Quantification value was implemented ('auto-microcon' process) for Priority 2 samples.

A workflow for Priority 3 samples remained within active Standard Operating Procedures to have the DNA extracts not amplified, nor automatically concentrated with Microcon[®] filters, but to be held after Quantification and QPS informed that low levels of DNA were obtained that were insufficient for further processing at that stage [3][4].

Anecdotally, the suitability to provide QPS with DNA profile Intelligence from extracts that have been concentrated has been noted to be limited, and added to scientist's time and availability to direct resources to samples with more DNA detected.

4. Data interrogation

The 'auto-microcon' data was interrogated by assessing the DNA profile outcome results reported as Exhibit Report lines as a function of the Quantification value.

The Exhibit lines were interrogated and grouped into two interpretation outcomes as follows:

1. 'Fail': DNA profile interpretation outcomes of 'Complex unsuitable for interpretation', 'No DNA profile', 'Partial unsuitable for interpretation', 'No DNA Detected';
2. 'Success': All other DNA profile outcomes including single source DNA profiles matching assumed known contributors or different reference DNA profiles, mixtures that were suitable for comparison to reference DNA profiles, DNA profiles that were suitable for loading to NCIDD.

NB. These descriptions were used to filter the data. A 'fail' does not mean there was a Quality failure in the process; a 'success' does not necessarily mean a DNA match.

5. Assessment of 'auto-microcon' results

Intent

Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 through the 'auto-microcon' workflow.

Data Analysis

The samples applicable to this experiment had Quantification values in the range 0.001ng/ μ L to 0.0088ng/ μ L, and a total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value. A percentage of samples that fell into these categories was determined.

The 'auto-microcon' data could be expressed as a function of Quantification value.

The percentage of samples that had an 'auto-microcon' process and led to an NCIDD upload was obtained. This data could be filtered further into the outcome from the NCIDD load, at the time of data collection.

6. Datamine of the difference in pre- and post- Microcon[®] Quantification values

Intent

Evaluate the difference between the Quantification values obtained for samples prior to the 'auto-microcon' step, and then after the 'auto-microcon' process. This is to assess, through the Quantification data, the effectiveness of the Microcon[®] step in concentrating the DNA extract.

As this is purely a datamining experiment, only the samples that yielded a result of 'success' were examined.

Data Analysis

The samples applicable to this experiment had Quantification values above 0.001ng/ μ L and less than 0.015ng/ μ L where the final result was 'success'.

This range was considered by the author to be able to provide a sufficient demonstration of the trend of the data (N=278 samples).

7. Results and Discussion

7.1 Assessment of 'auto-microcon' results

There were N=1449 samples in the 'auto-microcon' Quantification range, excluding certain samples as per Section 5.

The percentage of samples that resulted in a determination of 'fail' was 89.4% (Fig 1). As expected, the number of 'fails' increased when the Quantification decreased and approached the Limit of Detection of Quantification ie. 0.001ng/ μ L (Fig 2). This was considered to be due to there being less DNA detected in the extract, and therefore less DNA to concentrate.

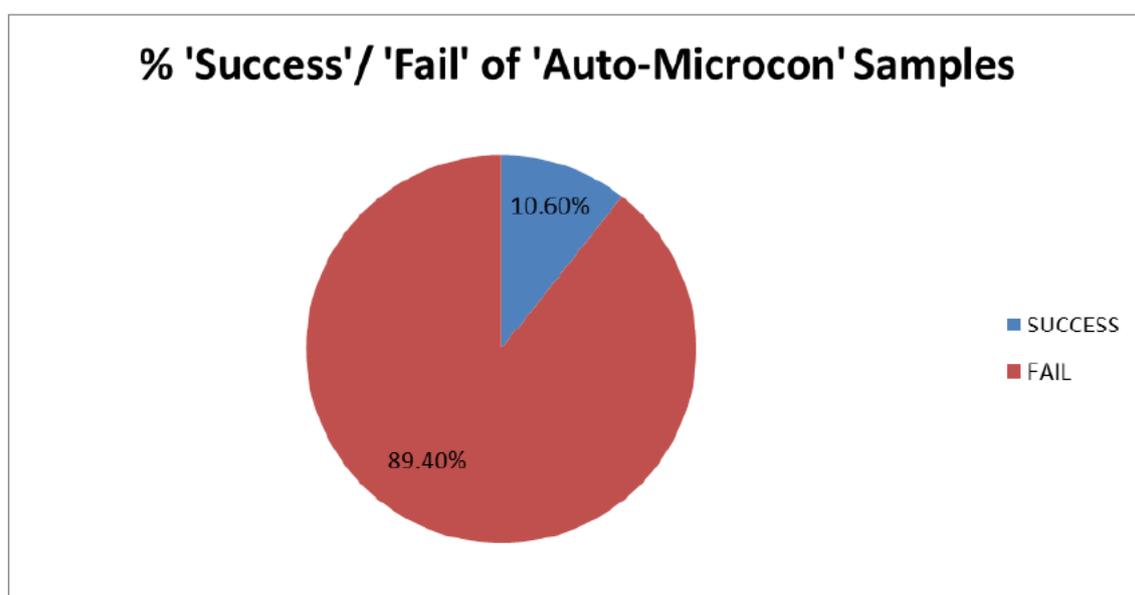


Figure 1: Percentage 'Success'/'Fail' of 'Auto-Microcon' samples.

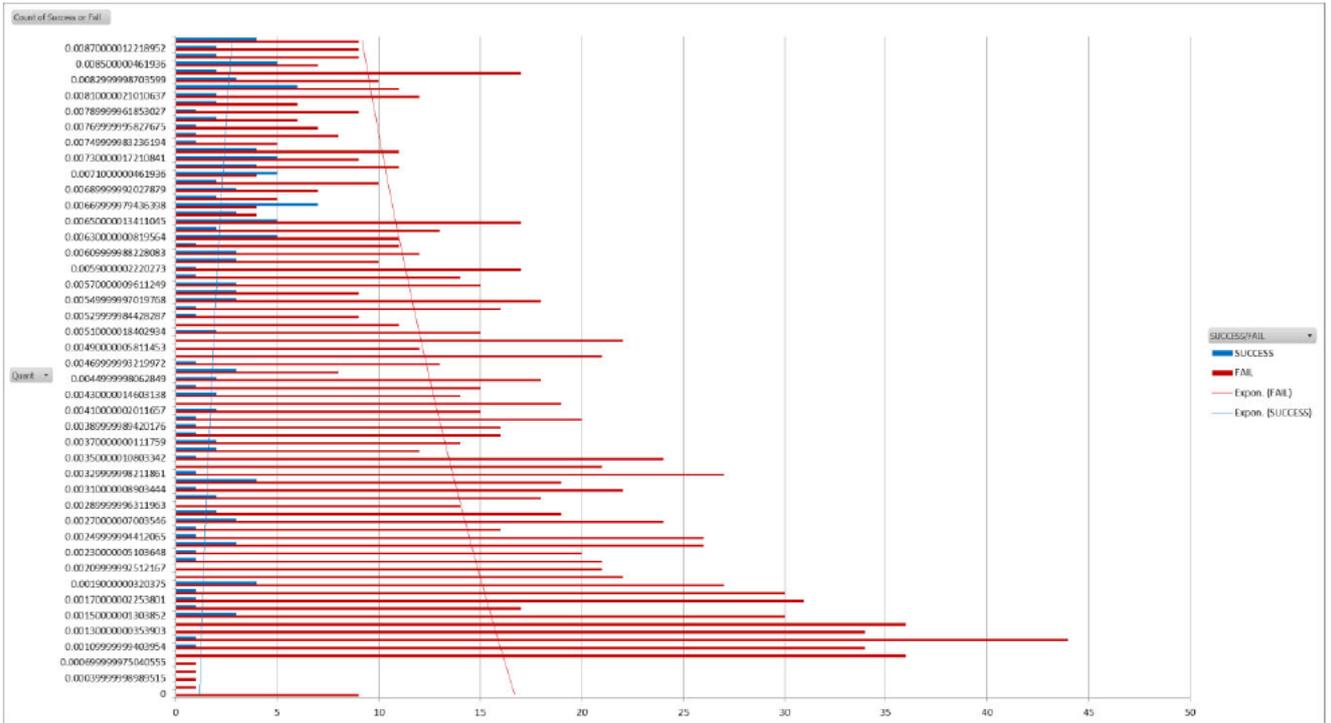


Figure 2: Spread of data and categorised as 'Success'/'Fail' for 'Auto-Microcon' samples.

If samples were not processed through the 'auto-microcon' process, what DNA Intelligence would the client miss out on? To evaluate this, the 'success' data was drilled down to the samples that had some NCIDD interaction and in particular, where they were the only samples in the case that were NCIDD-suitable for that particular profile. This represented 1.86% of all 'auto-microcon' samples. In looking at samples that provide *new* Intelligence, that is DNA information available for future linking, or has provided a cold-link, this equated to 1.45% of all 'auto-microcon' samples (Fig 3)..

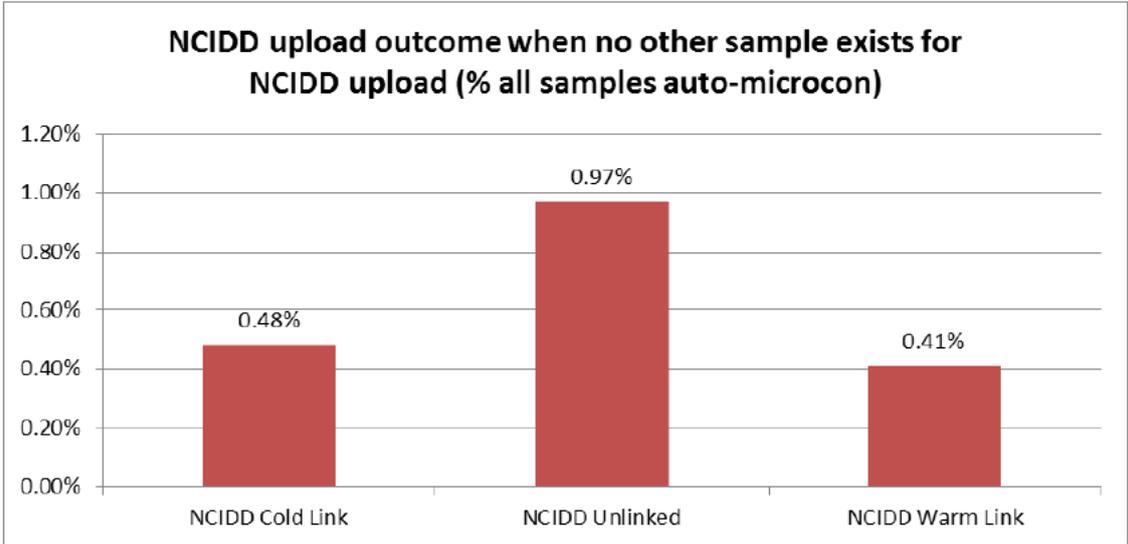


Figure 3: NCIDD outcome for samples that were loaded to NCIDD

This 1.45% of 'auto-microcon' samples is considered to be the pertinent value for the client to assess if the 'auto-microcon' process was not performed.

7.2 Datamine of the difference in pre- and post- Microcon® Quantification values

The samples applicable to this experiment had Quantification values above 0.001ng/μL where the final result was 'success'.

As the Microcon® process concentrates the DNA extract from approximately 100uL to approximately 35μL, in theory it would be a reasonable expectation to obtain approximately two to three-fold increases in DNA Quantification after concentration. Figure 4 shows the plot of the differences found for samples that resulted in 'success'.

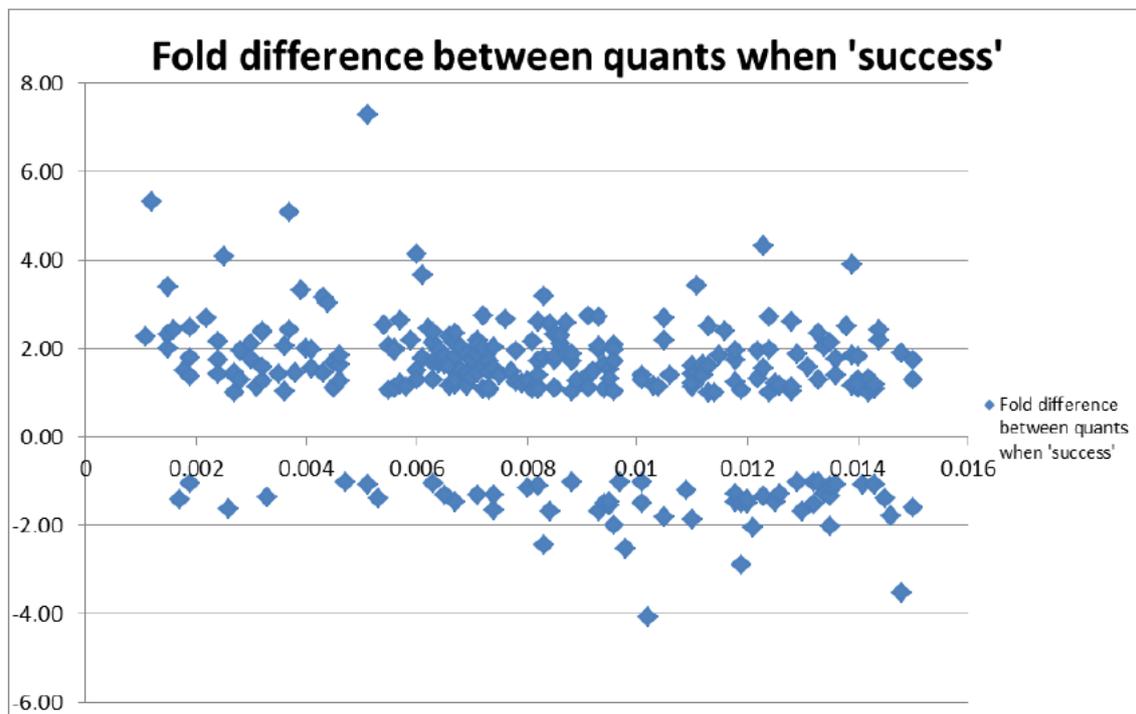


Figure 4: Quantification differences pre and post concentration

The findings are not unexpected as the scatter focusses mostly around two-fold increases in Quantification. It was also not unexpected to observe the variable results. Anecdotally, variability in success rates is found at profile management stage when assessing results of samples that have had this concentration step.

DNA can be lost in the process as seen in Fig 4 where the Quantification values decreased after concentration (below the horizontal axis). Variability in results could be attributed to a number of things, including but not limited to the slight

differences between operators and instrumentation, the differences in substrate type and level of degradation, and the variability in Quantification result.

8. Options for consideration

The options to consider are:

1. Continue with 'auto-microcon' process for Priority 2 (Major Crime) casework; or,
2. Cease the 'auto-microcon' process for Priority 2 (Major Crime) casework and report the exhibit result of 'DNA insufficient for further processing' based on Quantification result.
 - a. Priority 1 samples could proceed with the 'auto-microcon' process. If a DNA concentration rework is required, the Microcon® process can be ordered manually by the scientist.

In considering continuing or discontinuing the automatic concentration of DNA extracts for Priority 2 (Major Crime) samples, some key elements to consider include, but are not limited to:

- The opportunity to link DNA profiles on NCIDD would not be initially possible (without automatic concentration) for approximately 1.45% of samples that would qualify for this process. Of the 'auto-microcon' data set (N=1449 samples) evaluated, 1.45% equates to 21 samples;
- Time and cost for processing all samples in the 'auto-microcon' range, including batch preparation, Quality checking and control;
- Time and cost for processing these samples further with additional rework options, as one would expect with low levels of DNA detected initially;
- The ability to potentially reallocate staff time currently allocated to processing, interpreting and reporting 'auto-microcon' samples, to samples with higher DNA yield, thus improving the turnaround time for results on these samples;
- The opportunity to conserve DNA extract for further processing with other technologies should that be considered (eg. Y-STR analysis, Low Copy Number analysis);

- The improved ability to provide quick results to QPS (using the Forensic Register at Quantification stage) indicating low levels of DNA detected, thus enabling QPS to employ further strategies at their discretion (eg. further sampling of items, request the rework);
- The continued ability to process the DNA extract upon client request or depending on priority (eg Priority 1 – Critical Priority).

9. References

- [1] QIS 19544v11 – Concentration of DNA Extracts Using Microcon Centrifugal Filter Devices
- [2] PowerPlex® 21– Amplification of Extracted DNA Validation. ██████████, ██████████, ██████████. December 2012. Forensic DNA Analysis.
- [3] QIS 23008v15 – Explanation of EXR/EXH Results
- [4] QIS 24012v13 – Miscellaneous Analytical Section Tasks

ANNEXURE 2 - Report by Professor Linzi Wilson-Wilde OAM PhD

REPORT

Report to: Walter Sofronoff QC, Commissioner
Commissioner of Inquiry into Forensic DNA Testing in Queensland

Report Date: 31 July 2022

Request: To advise:

- Whether it is true or untrue that a sample with a quantitation of between 0.001 ng/uL and 0.0088 ng/uL contains “insufficient DNA for analysis” or “insufficient DNA for further processing”;
- How would you accurately describe the suitability for DNA profiling of a sample with a quantitation of between 0.001 ng/uL and 0.0088 ng/uL.

Information Reviewed:

Document	Date Issued
Letter from W Sofronoff to L Wilson-Wilde in relation to expert opinion about insufficient DNA	27.07.2022
Statement of [REDACTED]	03.09.2020
Statement of [REDACTED]	22.07.2021
Statement of [REDACTED]	22.07.2021
Statement of [REDACTED]	05.08.2021
Statement of [REDACTED]	14.09.2021
Statement of [REDACTED]	22.09.2021
Statement (unsigned) of [REDACTED]	No issue date
Statement of [REDACTED]	28.10.2021
Statement of [REDACTED]	26.11.2021
Statement of [REDACTED]	26.11.2021
Statement of [REDACTED]	24.01.2022
Statement of [REDACTED]	18.03.2022
Statement of [REDACTED]	25.03.2022
Statement of [REDACTED]	21.04.2022
Statement (unsigned) of [REDACTED]	No issue date
Statement of [REDACTED]	12.05.2022
Statement of [REDACTED]	25.05.2022

Document	Date Issued
Statement of [REDACTED]	25.05.2022

Findings

Considering the request and after reviewing the information listed above, the following observations can be made:

1. The possibility of obtaining a profile from samples submitted for DNA analysis, with a quantitation result of between 0.001 ng/uL and 0.0088 ng/uL, cannot be excluded.
2. Samples in this quantitation range may contain:
 - insufficient DNA to develop a DNA profile, or
 - sufficient DNA to obtain a partial DNA profile, or
 - sufficient DNA to obtain a full DNA profile.
3. The statements *insufficient DNA for analysis* or *insufficient DNA for further processing* are without explanation or clarification in the Appendix.
4. Applied literally and without proceeding to amplification and analysis, the statements *insufficient DNA for analysis* or *insufficient DNA for further processing* cannot be substantiated.

A more accurate description for samples in this quantitation range would be:

The sample contains a low level of quantifiable DNA, which is below the laboratory threshold permitted for further analysis.

[For use where the laboratory maintains a “hard bar” quantitation threshold]

or

The sample contains a low level of measurable DNA, which is below the laboratory threshold recommended for further analysis.

[For use where the laboratory permits scientist discretion when considering further DNA analysis. Note: the term *measurable* has been provided as an option to simplify the language, other similar terms may also be suitable.]

The above definition should be accompanied by further clarification in the Appendix as follows:

1. A description of the quantitation method (Quant Trio) should be added.
2. Descriptions for the following terminology should be added.
 - DNA was not detected
[Example definition: The laboratory quantitation method was unable to detect any DNA in the sample]
 - The sample contains a low level of quantifiable DNA, which is below the laboratory threshold permitted for further analysis
[Example definition: Samples that contain quantitation results below the laboratory threshold for further testing. These samples are more likely to contain insufficient DNA to develop a DNA profile, but in a small number of cases, there may be sufficient DNA to obtain a partial or full DNA profile. Note: this example definition does not preclude the addition for further explanatory information.]


Professor Linzi Wilson-Wilde OAM