STATEMENT OF JUSTIN HOWES

I, Justin Howes, care of Queensland Health Forensic and Scientific Service, Team Leader, do solemnly and sincerely declare that:

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

2. I hold the position of Team Leader at QHFSS at Coopers Plains.

3. I hold a Master of Science in Forensic Science (Griffith University -2000), a Bachelor of Arts in Human Movement Science (University of Qld – 1997), and a Bachelor of Science in Molecular Biology (University of Qld -1995). I also have a Diploma of Management (TAFE Qld – 2015) and a Certificate IV in Workplace Training and Assessment – 2005.

4. On 2 August 2022, I was requested to provide a statement as to whether I agree or disagree with a number of matters as set out in paragraphs A to G contained within Notice 2022/00068 "Statement of possible findings by the Commission" ('the statement'). If I disagree to any extent with any of the matters, I have been requested to state the nature of my disagreement and to explain in detail the reasons for such disagreement.

5. I have also been asked to make a submission concerning any recommendation that, in my view, ought be made in the event the Commissioner Sofronoff QC, concludes that the matters set out in Paragraphs A to G are substantially correct, including in particular a recommendation as follows:

   (a) *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.*

6. As part of my response I have read the following:

   (a) The statement;

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DEPARTMENT OF JUSTICE AND ATTORNEY-GENERAL
Reg. No. 6728

[redacted]

Justin Howes

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Witness

CELINA DA SILVA
9/8/2022

(b) A document entitled: "A review of the automatic concentration of DNA extracts using Microcon Centrifugal Filter Devices: Options for OPS consideration dated January 2018 and submitted under the names of Justin Howes and Cathie Allen"; and

(c) A document entitled: "Report" by Professor Linzi Wilson-Wilde OAM PhD dated 31 July 2022.

Responses to paragraphs A to G

Paragraph A

Immediately before early 2018, FSS would process samples submitted for Major Crime Casework that returned a quantitation value between 0.001ng/µL and 0.0088ng/µL by submitting them automatically to micro-concentration (referred to within FSS as 'auto-microcon'), amplification, capillary electrophoresis and profiling.

7. AGREE for Major Crime samples from November 2015 until March 2018; prior to that, this workflow applied to samples with quantitation values between 0.00214ng/µL and 0.0088ng/µL. Further, a point of clarification is that the samples had a second quantitation process after the 'auto-microcon'. This can be seen in Figure 4 of the Options Paper.

Paragraph 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 OPS consideration dated January 2018 and submitted under the names of Justin Howes and Cathie Allen. Attached hereto is a copy of that document

8. AGREE

Paragraph C

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Reg. No. 6728

[redacted]

Justin Howes

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Witness CELILIA DE SANTO
9/8/2022

Option 2 provided as follows: 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.

9. AGREE although there is a typo: 'auto-microcon' is the term used.

Paragraph 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 0.001ng/µL and 0.0088ng/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.

10. DISAGREE

11. I partly agree with the two points (i) and (ii) in Paragraph D, but given an omission in detail and context required, my opinion overall is to disagree.

The process described in Paragraph D (i) is partly correct in that as per the information from QPS when Option 2 was approved, samples could be requested by QPS for further testing (**JH-1**). Samples may also be requested to be processed through DNA analytical processes by QHFSS case managers/Reporting Scientists at their discretion (**JH-2 section 6.5.5 and 11.1**).

Suggested statement wording was provided by me to staff on 7 February 2018 (**JH-3**). This suggested statement wording was: 'Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling'. This suggested wording was formed after consultation with senior scientists where I asked them to consider the suggested wording (above), and to compare with wording that was already in existence (**JH-4-JH-6**).

The wording for the exhibit result line 'DIFP - DNA Insufficient for Further Processing' was first created at implementation of the PowerPlex 21 DNA amplification kit to describe a workflow for volume crime samples. This result line is a short explanation of the result that

was within character length requirements for the field in AUSLAB (Laboratory Information System at the time) that was used to report results to QPS. In 2013, Reporting Scientists worked together on standardised wording for statements based on the results reported in exhibit result form. This wording was developed and shared with staff by being available on the network within a 'Reporting Guidelines' subfolder (**JH-13-JH-14**). This wording was added to the next version of the SOP QIS17119v13 that contained suggested statement wording for all results (**JH-9**).

Suggested statement wording is largely based on the result information reported to QPS via Exhibit Result Lines. An excerpt from the Standard Operating Procedure (SOP) QIS 23008v13 that was the next version of this document post-implementation of PowerPlex 21 amplification kit and creation of the exhibit result line is below (**JH-7- section 4.9.4**), and was based on the spreadsheet created for all results that served as a working copy between QHFSS and QPS (**JH-15**):

The following comment is used when the quantitation value falls below the point at which the results would be considered unreliable for interpretation. These samples will not proceed to amplification. See 17117 *Procedure for Case Management* for details.

1 **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 DNA Analysis if further information is required.
Mnemonic = DIFP
(PP21)

Exhibit result wording is devised through collaboration between QHFSS and QPS where a mnemonic (eg. 'DIFP'), exhibit result line (eg. 'DNA Insufficient for Further Processing'), and an expanded comment are used to explain all results reported to QPS. The expanded comment is the explanation of what every mnemonic and result line mean, and my understanding is that this is the wording that appears to the QPS DNA Management Section when viewing the Forensic Register after result review by QHFSS. My understanding is that this expanded comment is either added in part or full to Q-PRIME for Investigating Officers to review (**JH-1**).

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Justin Howes Witness CECILIA DE SANTO

9/8/2022

This line was used within the workflow at that time (from 2013) and was similarly applied in 2018 to samples in the quantitation range between 0.001ng/µL and 0.0088ng/µL. The SOP QIS17119v15 that was active at the time of the Options Paper in 2018 contained suggested statement wording that was based on this original exhibit result wording (**JH-8**).

In March 2018, QPS informed QHFSS that the expanded comment for 'DIFP – DNA Insufficient for Further Processing' was changed slightly by QPS (**JH-17**). This wording was added as a record to the spreadsheet of exhibit results that was in use at the time (**JH-18**). This spreadsheet shows the expanded comment from a QHFSS perspective - that is also reflected in the SOP QIS34229v2 that was the next version after this comment change (**JH-19**) - and the wording change from QPS. It is my understanding this edited wording is what was then made available in Q-PRIME for Investigating Officers to review.

I provided all Reporting staff with suggested statement wording for 'DIFP - DNA Insufficient for Further Processing' at the time of implementation of the QPS-approved workflow in 2018. I reiterated this suggested wording in April 2018 to certain staff working on a project to simplify statement wording (**JH-16**). Staff were allocated to work on a project to improve statement wording as a measure to continuously improve the statement product (**JH-11-JH-12**).

At the time of development of the Forensic Register (FR) for use at QHFSS, Subject Matter Experts were involved in assisting the vendor with providing wording for statements for certain result types (**JH-20**). The wording supplied (date unknown but the last modification date by the author was 03 February 2016) was as follows: 'This sample contained insufficient DNA to be suitable for analysis and was not tested further'[1]. My understanding was this wording was supplied to the FR developers presumably in 2016 or 2017 prior to the implementation of the FR at QHFSS in July 2017, and therefore prior to the Options Paper in 2018. However, this wording was not developed (by the FR developers) at the time to a level where it would be automatically added by the FR for results of this type; therefore, for these results, Reporting Scientists manually add wording to their Witness Statements. The wording supplied at the time to the FR developers, is the same wording that was added to the SOP and was active at the time

[1] JH-20, p.5

of implementation of Option 2 from the Options Paper **(JH-8)**. Since the Options Paper release, there are examples of where the Reporting Scientist has used the wording suggested by me in February 2018 **(JH-10)**, or alternative wording as follows: 'This sample contained insufficient DNA for further processing and was not tested further.' **(JH-21)** and 'This sample contained insufficient DNA to be suitable for DNA analysis, therefore it was not tested further' **(JH-22)**.

Although there was suggested wording provided by me, the wording in statements can be edited by the Reporting Scientist when writing their Witness Statements as ultimately, it is their statement that is a record of the findings in the case. It is then available for review by another competent Reporting Scientist and therefore has the opportunity for rewording. This is evidenced by the slight variation in statement wording between the relevant SOP and example statements.

While there are these slight variations, the meaning of the various lines in my opinion, describe the process that was current at the time. The process, as approved by QPS in 2018, was not to process further at that time as a standard process. 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 I was transparent in describing in the Options Paper that there was an ability to obtain DNA suitable for interpretation and provided percentages of findings around that, and that the first key consideration was for QPS to be mindful of the percentages of profiles that might be suitable for loading and matching on the National Criminal Investigation DNA Database (NCIDD). Further, in my suggested wording to staff **(JH-3** and **JH-12)**, I suggested that 'Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling' and this was consistent with the exhibit result reports sent to QPS **(JH-18)**. This demonstrates that it isn't as simple as describing the result as 'DNA insufficient', rather all wording suggested or used describe the workflow process, not the suitability for interpretation of any potential DNA profile.

12. ***Paragraph E***

COMMISSIONER FOR DECLARATIONS
DEPARTMENT OF JUSTICE AND ATTORNEY-GENERAL
Reg. No. 6728

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Justin Howes Witness Celina De Sano

9/8/2022

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.

13. DISAGREE

14. I partly agree with the two points (i) and (ii) in Paragraph E, but given the context required, my overall opinion is to disagree.

It is true that the possibility of obtaining a profile from such samples cannot be excluded. It is clearly described in the Options Paper that there is a possibility to obtain DNA profiles in the quantitation range described. The probability of obtaining a suitable versus unsuitable DNA profile for interpretation is also presented. It is also presented in the section relating to key considerations for the QPS, that there isn't just a possibility of obtaining a DNA profile but there might be DNA information obtained that could be used for searching on NCIDD. Similar information was also presented in a previous internal study from 2015 on quant ranges and ability to obtain DNA profiles for interpretation (**JH-23**).

Since the introduction of PowerPlex 21 DNA amplification kit and STRmix to assist the interpretations in 2012, the terminology in Paragraph E: 'partial DNA profile' and 'full DNA profile' was reserved for DNA profiles where there was no indication of more than one contributor ie. single-source DNA profiles. This is due to the drop-out of DNA information within DNA profiles and how that can lead to partial DNA profiles (**JH-29**). Extending this to mixed DNA profiles, with the possibility of drop-out within DNA profiles, it can be difficult to determine whether the DNA information observed (alleles) are the only alleles in the DNA profile, or if there are other alleles not displaying due to stochastic behaviour in low-level profiles. This stochastic behaviour was observed within the testing that resulted in the PowerPlex 21 validation (**JH-30**) where it was reported that:

'Stochastic effects were obvious in this experiment in data from templates below 0.132ng. Stochastic effects are the result of random, uneven amplification of heterozygous allele pairs

from low template samples (SWGDAM 2010 interpretation) which is displayed by low peak heights or allele/locus dropout.'

This is reflected in the exhibit result spreadsheet in 2012 that was developed when writing the expanded comments for exhibit results that are reported to QPS (**JH-24**). In this spreadsheet, the use of partial/incomplete or full DNA profiles, are only mentioned for single-source DNA profile interpretations. This information is also mentioned in the comments against the SOP QIS23008v13 which mentions that there are no partial and full DNA profiles (**JH-25**). This information is also reflected in the Appendix to accompany Witness Statements from 2012 (**JH-26 – JH-27**). After the creation of the exhibit report expanded comments, and the relevant Witness Statement Appendix, a further body of work on updated suggested statement wording was created (**JH-14**). This wording was mentioned in meeting minutes to have been externally checked by Dr Duncan Taylor and Dr Jo-Anne Bright (**JH-28**). There is no mention in the suggested statement wording of the use of 'partial', or 'full' DNA profiles.

In summary, to address Paragraph E, I would have to disagree due to the clarification of wording for DNA profile interpretations. Please note that 'partial' and 'full' terminology is only used in single-source DNA profile interpretations and while I understand these words, as it was used prior to implementation of PowerPlex 21, it is not current to the DNA profile reporting vernacular. Further, (i) and (ii) can be interpreted to mean that these DNA profiles are suitable for interpretation. The Options Paper describes the chance of obtaining suitable vs unsuitable DNA profiles from the dataset assessed, and even if processing led to what can be termed 'partial' or 'full' DNA profiles, this does not mean that the profile would be suitable for interpretation.

Paragraph 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

15. DISAGREE

COMMISSIONER FOR DECLARATIONS
DEPARTMENT OF JUSTICE AND ATTORNEY-GENERAL
Reg. No. 6728

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Justin Howes Witness CELLMA DR JAMO

9/8/2021

16. I disagree to this paragraph on the basis that in my view, the reporting of 'DNA insufficient for further processing' is correct as it describes the processing workflow at the time it was approved by QPS in 2018.

It must be noted that the workflow in 2018 was not a new workflow. The workflow was devised in 2012 for the implementation of PowerPlex 21 and STRmix (**JH-31**). In the workflow, it demonstrates when volume crime (Priority 3) samples would be reported in short as 'DNA Insufficient'. This same result line was reactivated in 2018 for the use in volume and major crime (Priority 2) results after the approval of the workflow by QPS.

Reporting 'DNA insufficient for further processing' in Witness Statements is not incorrect and is a reflection of what was in the Standard Operating Procedure for Exhibit Results in 2012 and from 2018 (**JH-7, JH-24, JH-18**), and as suggested statement wording for the result type from 2013 (**JH-13, JH-14**). While I had provided some alternative statement wording to staff in 2018 (**JH-3**), it is ultimately up to the individual Reporting Scientist to use wording that they feel most appropriate for the result. When written in a statement, this wording undergoes a review where another competent Reporting Scientist checks the results reported in the statement prior to release. In my opinion, if staff requested alterations to wording suggested by me, or from the collective teamwork on statement wording in 2013, they have had the ability to add comments to the relevant SOPs to suggest any alternative wording. It is not uncommon to suggest edits, as evidenced by the slight wording changes to Statement Appendices as demonstrated by some slight changes in the last two versions: **JH-33** and **JH-34**. Not having comments registered in the Quality System to alter wording for low level results shows in my view that the wording is reflective of the understanding of the workflow. Further, to my knowledge there has not been feedback from clients requesting further wording to clarify the meaning of these results.

On 05 August 2022, a Memorandum was released by the Acting Director General Shaun Drummond (**JH-32**). The Memorandum contained wording that was directed to be added to Witness Statements for any result that was reported to QPS as 'insufficient DNA for analysis' or 'insufficient DNA for further processing'. The new wording contains the same wording as the original wording that I suggested to Reporting Scientists in 2018 (**JH-3**) plus some additional explanatory information around what the result means. This is not to say that the

wording reported in statements before 5 August 2022 was incorrect, it was that the new wording provides further information to the results reported. This direction has now been adopted and incorporated into the relevant SOP, initially added as a comment (**JH-35**).

Paragraph 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

17. DISAGREE

18. In my opinion, the wording used was not incorrect and therefore, anything reported in statements has been true. The wording accurately described the workflow process approved at the time.

Submissions on recommendations

19. I will accept any recommendation that the Commission makes. Currently, an immediate change to wording in Witness Statements has been implemented as evidenced by a comment against the relevant SOP (**JH-35**). and the insertion of a line in the Change Management Minor Change Register (**JH-36**). This is to be applied to all statements in draft and released from the time of receipt of the Memorandum from the A/DG Health (**JH-32**). In my opinion, the second line of information that is now added to statements provides further explanatory information on what the result means. The first sentence in the updated wording is exactly the same as my suggested wording to staff in 2018 and is consistent with the wording supplied to QPS in exhibit report format in every instance where results in the quantitation range have been reported.

    My view is that the wording used in statements has not been made untruthfully as it is not incorrect. It has always been open for questioning in court or in pre-trial conference and I am not aware if any wording has caused confusion to the courts in any particular matter.

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Justin Howes Witness CECILIA DA SILVA

9/8/2022

All the facts and circumstances declared in my statement, are within my own knowledge and belief, except for the facts and circumstances declared from information only, and where applicable, my means of knowledge and sources of information are contained in this statement.

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

TAKEN AND DECLARED before me at Brisbane in the State of Queensland this ninth day of August 2022

[redacted] [redacted]

Justin Howes Witness

CECILIA DE SANTO

COMMISSIONER FOR DECLARATIONS
DEPARTMENT OF JUSTICE AND ATTORNEY-GENERAL
Reg. No. 6728

Attachments Index

JH-1 - Email thread 02022018_includes QPS comms

JH-2 - 17117V20_post implementation and reworking

JH-3 - Email thread to staff members after QPS decision_07022018

JH-4- Email from KDR with statement wording_07022018

JH-5- Email from SMJ with statement wording_07022018

JH-6 - Email from TEN with statement wording_07022018

JH-7 - 23008V13 _ Explanation of EXR EXH Results_active10122012

JH-8 -17119V15_active at time of Options paper based on 2013 wording

JH-9 - 17119V13_original statement wording_insufficient_2014

JH-10 - QP1701341538_TEN_Final Statement

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Justin Howes Witness CECILIA DE SANTO

C.dec 6728

9/8/2022

JH-11 -Email to seniors for working party_wording_04042018

JH-12 -Email to staff working on wording_21052018

JH-13 - Example Statement Wording_May2013

JH-14 - Example Statement Wording_Aug2013

JH-15 - EXH_2012_v2.0_QPS

JH-16 -Email_insufficient suggested statement wording_18042018

JH-17 - Email to seniors after email from QPS with changed exp comment_insufficient_02032018

JH-18 - EXH_2018_current full list_strmix2.6 and 4p_21112019

JH-19 - 34229V2_next version after 2018 change

JH-20 - FR statement wording_PP21

JH-21 - QP2101743266_EJC_Final Statement

JH-22 - QP2102108673_ARM_Final Statement

JH-23 - Project #163 _final report_signed

JH-24 - EXHs_2012_v4

JH-25 - Comments against SOP 23008v13_partial

JH-26 - APPENDIX 6 Draft_most recent_191012_FINAL_HSSA

JH-27 - 17119V12_active Dec2012_appendix wording

JH-28 - FRIT_22082013

JH-29 - Bright 2016 Developmental validation of STRmix

JH-30 - PowerPlex®21 - Amplification of Extracted DNA Validation final SIGNED

JH-31 - 17117V16_case mgt at time of PP21_2012

Justin Howes

Witness CECILIA DAL SANTO

C. dec 6728

9/8/2021

JH-32 - DG Memo - Urgent Amendment to Standard Operating Procedure required

JH-33 - APPENDIX_current_JAH16052022

JH-34 - APPENDIX_current_JAH27042021

JH-35 - comment to SOP 34006v4_08082022

JH-36 - Change Register - Minor Changes and emerging or novel practices

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Reg. No. 6728
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9/8/2022