# STATEMENT OF EMMA-JAYNE CAUNT

I, **Emma-Jayne Caunt,** of Queensland Health at the Forensic and Scientific Services, 39 Kessels Road, Coopers Plains, do solemnly and sincerely declare that:

## Background

1. I was awarded a Bachelor of Science with Honours from the University of Manchester Institute of Science and Technology (UMIST), UK.
2. I started my career in 1997 as an Assistant Forensic Scientist in the drugs department at the Forensic Science Service in the United Kingdom. In 1999 I became a Reporting Scientist in the Forensic Biology department having been trained by leading experts in the field. I was employed by the Forensic Science Service until 2006.
3. In 2007 I began working for Queensland Health at Forensic and Science Services (FSS) as a Reporting Scientist in Forensic DNA Analysis. I am still employed in this position currently.
4. The duties of my current role include the interpretation and reporting of DNA profiling results to the Queensland Police Service (QPS) and the judiciary.
5. From 2008 until 2013, I acted in a Senior Scientist position, which is equivalent to a Health Practitioner Level 5 (HP5). During this time, I also acted in the position of Team Leader of the Forensic Reporting and Intelligence Team (Health Practitioner Level 6) on several occasions totalling just over 7 months.

## STRmix expertise

6. In 2010, I joined a statistics working group created through the Australia New Zealand Policing Advisory Agency (ANZPAA) National Institute of Forensic Science (NIFS). The role of this working group was to standardise DNA profile interpretation across Australasia. The working group consisted of approximately ten to fifteen representatives from all jurisdictions of Australia and New Zealand. I was the only representative from Queensland.
7. As a result of that working group, 'STRmix' was created by Drs Duncan Taylor, Jo-Anne Bright and John Buckleton, which later became a commercial product. I attended the STRmix training course and, later, the STRmix Train the Trainer course provided by

Duncan Taylor, Jo-Ann Bright and John Buckleton; it became my role in FSS to implement STRmix into the laboratory. Annexed and marked EC-01 is a copy of an email from Cathie Allen (Cathie) advising that I was taking on the project of implementing the changes to the way statistics are reported.

8. In 2012 I undertook the validation of STRmix for use with PowerPlex® 21 (PP21) and trained everyone in Forensic DNA Analysis in the use of STRmix for the interpretation of PP21 profiles. I received advice from Duncan Taylor during this time.
9. Once STRmix was implemented, I became a mentor, trouble-shooter, and subject matter expert for STRmix within Forensic DNA Analysis.

**Issues with current processes**

10. I am concerned about the following issues:
    a) The concentration/amplification process,
    b) Reworks on DIFP samples,
    c) Inaccurate statements for court, and
    d) No DNA detected samples.

Concentration/amplification process

11. Prior to 2018, the process for Priority 1 and 2 samples with quant values between 0.001ng/µL and 0.0088ng/µL was that they automatically underwent a microcon concentration where the extract was concentrated to approximately 35µL. Priority 3 samples were amplified using Profiler Plus (without microcon concentration) until 22 January 2018 when they began being amplified using PP21.
12. Between 2018 and 2022, the process for Priority 2 and 3 samples with quant values between 0.001ng/µL and 0.0088ng/µL was that processing was ceased and they were reported as "DNA insufficient for further processing" (DIFP). Priority 1 samples continued to undergo the automatic microcon process. The QPS and reporting scientists were able to request further processing of Priority 2 and 3 samples where it was deemed appropriate. A routine request for further processing by the QPS prompted a microcon concentration to 35µL.
13. I held concerns about the validation of the DIFP result line. On 8 February 2018, I emailed Justin Howes (Justin) after the Options Paper was presented and asked how the validation process for 'DNA insufficient for processing' samples would be managed.

In my opinion, the line should not be validated until the whole case had been assessed to see if processing of the sample would be of benefit, particularly if the quant reaches the upper range. Justin responded to my question verbally and told me that the DIFP process will continue as per the 'no DNA detected' process so samples would not be assessed taking into account the circumstances of the case. I raised this issue with Kylie Rika, who agreed with me that this was a concern.

14. That same day, I emailed Kylie Rika to highlight an example of a sexual assault case ([redacted]) that could have been impacted by the DIFP process. Semen was not detected on any of the intimate swabs and all DNA profiles obtained from them matched the victim. A DNA profile was obtained from a shoe located in a park that matched the defendant, however this result does not support the allegation of sexual assault. There was one other sample in the case, a swab from the victim's underwear. Semen was not detected in the spermatozoa fraction obtained from this swab, and it was not tested further. The epithelial fraction gave a quant value of 0.0083ng/µL (which is in the DIFP quant range of 0.001ng/µL to 0.0088ng/µL) and a DNA profile with a Likelihood Ratio (LR) of greater than 100 billion favouring the presence of DNA from the defendant. This was the only sample in the case that addressed the allegation of sexual assault. This sample was processed before the DIFP process commenced, however if it had been processed afterwards that evidence would not have come to light.
15. Kylie responded to say that she had brought this up in her feedback of Project #184 but had not had a response. Annexed and marked EC-02 is a copy of the email chain dated 7 - 9 February 2018.

Reworking of DIFP samples

16. Recently I picked up a sample from a high vaginal swab that was an exhibit in an alleged rape case (sample [redacted] from [redacted]). This sample was reported as DIFP in 2019 and the QPS recently requested a rework. The rework was completed in the week starting 25 July 2022.
17. The first quant value was 0.004ng/µL and the new quant value is 0.006ng/µL.
18. As a result of this rework, a DNA profile was produced that provided an LR of greater than 100 billion in favour of the presence of DNA from one of the reference samples in the case. This has been identified three years later.

19. Fortunately, this case had other items that provided results in 2019 that addressed the allegation, including a DNA profile from the low vaginal swab that provided an LR of greater than 100 billion in favour of the presence of DNA from the same reference sample as the high vaginal swab. Although the DIFP process did not directly affect the overall results in this case, it demonstrates the risk that that DIFP process posed.
20. In November 2021, I began identifying samples that had a quant value between 0.001ng/µL and 0.0088ng/µL that were reprocessed and obtained a usable profile. I have kept records of some of these samples in an Excel spreadsheet created by Kylie Rika and Adrian Pippia and stored in the G:/drive.
21. Since QPS started requesting reprocessing of samples previously reported as DIFP, I believe I have seen at least 30-40 samples now showing useable profiles. I believe there are hundreds of samples formerly in the DIFP range that would have a useable profile if reworked.
22. My view is that all samples previously reported as DIFP should be reprocessed.
23. On 25 May 2022, I emailed my line manager Sharon Johnstone (Sharon) about a sample where sperm were detected, and the sample was reported as DIFP. Following a request from the QPS, the sample was microconned to 35µL and amped at 14µL (due to an FR bug), and I believed a better outcome would have been obtained if the sample had been microconned to full and amplified at 15µL. I wondered if we should consider microcon to full as a default for reworking DIFP samples. Annexed and marked EC-03 is a copy of the email to Sharon dated 25 May 2022. I did not receive a response from Sharon.
24. On 20 July 2022, I advised a colleague that they might obtain a usable profile for a sample if they microconned to full. My colleague had doubts about the microcon, however a rework was performed, and a reportable DNA profile was obtained. Annexed and marked EC-04 is a copy of the email chain dated 21 July 2022. Annexed and marked EC-05 is a copy of the email chain dated 28 July 2022.

*Introduction of the 3500xL*

25. In 2021, during the verification of STRmix v2.7 for the interpretation of DNA profiles generated on the 3500xL Genetic Analyser (3500) (Project #219) it was noted that the peak heights of DNA profiles were much higher than those obtained from the 3130xl Genetic Analyser (3130). This indicated an increase in sensitivity in that minor DNA

profiles that had not previously been detected on the 3130 were now being detected on the 3500.

26. I recall a conversation I had with Justin where I suggested that maybe we should be reassessing the DIFP threshold as the 3500s were more sensitive. He responded to say something along the lines of sensitivity is related to the amplification kit and not the capillary electrophoresis instruments and therefore the DIFP threshold is related to PP21. He suggested that the DIFP threshold could be reconsidered with the implementation of the VeriFiler Plus amplification kit. This kit is still in the process of being validated.

27. In my view, the introduction of the 3500xL should have resulted in a reconsideration of the DIFP threshold because the increased sensitivity was an indication that samples in the DIFP range may produce interpretable DNA profiles.

*6 June decision*

28. On 6 June 2022, the process for Priority 2 and 3 samples with quant values between 0.001ng/µL and 0.0088ng/µL changed so that all samples in that range were directly amplified rather than being microcon concentrated.

29. I consider there were issues with the process in place from 6 June 2022:

*Wasting sample*

a) When a sample has a low quant value, it is important to maximise the use of the sample. After extraction, most samples will have approximately 90µL of extract. Amplification of samples with low quant values requires 15µL of extract; this is approximately 17% of the sample.

*Poor/interfering results*

b) Amplification of samples with low quant values without microcon concentration can result in poor profiles because there is less DNA in the amplification reaction than there would be if the sample had been concentrated.

c) If I obtained a poor result from a sample with a low quant value on the first amplification, I would then concentrate the sample using microcon concentration.

d) This microcon concentration may not be as successful because part of the sample (approximately 17%) would have been used (and therefore lost) in the first amplification.

e) If the first amplification provides a poor result, and a second amplification following microcon concentration provides a good result, the first poor result may confuse and/or complicate the interpretation. This could potentially lead to the profile result being written off as too complex for interpretation due to the differences between the two results.

f) As there is no guidance provided to reporting scientists on this matter, there is reluctance to disregard the first result.

30. There are two different microcon processes within Forensic DNA Analysis:

g) Standard Microcon: a sample is concentrated to approximately 35µL, which allows a quantification with 2µL and enough remaining to amplify twice at 15µL each.

h) Microcon to full: a sample is concentrated to approximately 15µL and the whole sample is amplified without a quantification.

31. If QPS request further testing after a DIFP result (for a sample processed before 6 June 2022), the request is sent to Luke Ryan who is the Senior Scientist in the Analytical section, and he orders a standard microcon.

32. I consider the process of ordering a standard microcon for every sample to be an issue. For example, if I have a sample with a quant value of 0.0086ng/µL, I would microcon to 35µL, but if I have a sample with a quant value of 0.002ng/µL, I would microcon to full. I believe that the decision to microcon to 35µL or to full should be made on a case-by-case basis by a reporting scientist.

33. I consider the decision to microcon before amplification should be made by a reporting scientist. I believe the automatic standard microcon process after a DIFP result should have been stopped and changed to allow a reporting scientist to assess all information relevant to the sample after quantification and before further processing; a standard microcon may not have been the best course of action for a particular sample.

34. I consider the decision made on 6 June 2022 to amplify samples between 0.001ng/µL and 0.0088ng/µL without microcon concentration to be sub-optimal.

35. For Priority 3 samples, our agreement with the QPS is that minimal reworks are to be requested after the initial amplification and that microcon concentration should not be performed as per Section 6.3.6 of QIS 17117v21 *Procedure for Case management*.

Since the decision made on 6 June 2022, Priority 3 samples are now progressing directly to amplification without a microcon concentration step, which often results in poor profiles. Those profiles are subsequently labelled as "*complex mixed profile unsuitable for interpretation or comparison*" (CMPU) instead of "*insufficient DNA for further testing*" (DIFP). When a result is reported to the QPS as CMPU, this could simply mean that there is insufficient information to interpret the profile, however the QPS are unable to distinguish this from a result reported as CMPU where the profile has too much information to enable interpretation. In the absence of any information indicating the quant value of the sample, QPS are not being provided with information to suggest that retesting may be of benefit, so retesting is not requested.

*Inhibitors*

36. One of the advantages of the DNAIQ extraction process is that inhibitors are removed; this was not the case with the previous Chelex extraction process. Previously, if a DNA profile indicated inhibition in the sample a Nucleospin could be performed, which is a process where the sample is added to a column and the DNA binds to a membrane. This process is not common anymore, and I have ordered maybe one or two Nucleospins in the last ten years.
37. Due to the implementation of the DNAIQ extraction process, there is limited risk of concentrating inhibitors with the microcon process.

*Familiarity with low quants*

38. I believe that the laboratory has lost familiarity with interpreting DNA profiles obtained from low quant samples. Forensic DNA Analysis staff have not previously interpreted PP21 DNA profiles obtained from samples with quant values between 0.001ng/µL and 0.0088ng/µL without performing a microcon as it has not been the process. Previously samples with quant values in this range were either submitted for an automatic microcon or reported as DIFP.

*Reworks*

39. When QPS requested a DIFP sample be reworked, the default process was to order a microcon to 35µL. On or around 28 July 2022, a sample which had an original quant value of 0.00135ng/µL had been microconned to 35µL, and the profile was not quite

interpretable. I believed that if the sample had been microconned to full, we may have been able to interpret the result. On 28 July 2022, I emailed Sharon asking that this process be changed so that the microcon ordered (either 35µL or full) is more appropriate for the original quant value obtained. Annexed and marked EC-06 is a copy of the email dated 28 July 2022. I did not receive a response from Sharon.

*Raising concerns*

40. On 7 June 2022, I emailed Sharon Johnstone, Kylie Rika and Justin Howes asking why we were sending samples with quant values in the range of 0.001ng/µL and 0.0088ng/µL directly for amplification rather than for auto microcon. Following this email, I had a brief conversation with Sharon where she said words to the effect of "I have tried but this is what Cathie wants". Annexed and marked EC-07 is a copy of the email dated 7 June 2022. I did not receive a response from Justin or Kylie.

*A/Director-General decision – 19 August 2022*

41. On 19 August 2022, I received an email from Helen Gregg, the Acting Executive Director attaching a memorandum from the Acting Director-General. This memo requested that the workflow revert to the concentration process for Priority 1 and Priority 2 samples stipulated in Standard Operating Procedure 17117V19 (which was the process prior to 2018). This means that all Priority 1 and 2 samples in the DIFP range are now being concentrated down to a volume of 35µL and undergo quantification and one amplification process.
42. Justin Howes sent a further two emails to the reporting scientists outlining the process following this memo. Annexed and marked EC-08 is a copy of the emails dated 19 August 2022 and 1 September 2022.
43. I discussed my concerns with Kylie Rika and we created a list of concerns about the current process:
    a. microcon concentrating a sample to full (thereby consuming the sample) is a process that has been carried out in the laboratory for at least the last 15 years and, as far as I am aware, consuming the sample has never been raised by the QPS as a concern.
    b. The workflow does not provide the scientist the ability to assess everything in relation to the sample to get the best result. It may be that the sample could be pooled (or combined) with another sample in the case to maximise the amount of DNA, or if the

sample was at the higher end of the quant range, the scientist might want to try amplifying first rather than performing a microcon concentration, particularly if conserving sample is a consideration.

c. Undue restrictions are now being placed on the scientist trying to obtain the best result for the sample due to the requirement for permission from the QPS to perform a second amplification. The QPS may not necessarily be in the position to determine whether a second amplification might make a profile interpretable.
d. The workflow does not enable the scientist to assess which rework strategy would be the best based on their scientific knowledge and the circumstances of the case.
e. The workflow places emphasis on conserving sample for future testing, however in doing so reduces the ability of the scientist to get the best result for the case now. Perhaps the better option would be for the QPS to let us know if any particular sample requires conserving before testing commences.
f. Submitting all samples with quant values between 0.001ng/µL and 0.0088ng/µL for a microcon to 35µL is not appropriate for those samples at the lower end of the quant range. Experience tells us that these samples would benefit from a microcon to full and that a microcon to 35µL for these samples is less likely to yield an interpretable result.
g. One process for all samples is not appropriate. Each sample should be assessed on its own merits.
h. One process for all samples compromises quality to obtain short turnaround times.
i. Although a microcon to 35µL was deemed appropriate when the process was implemented prior to 2018, our knowledge and processes have changed. This process is outdated particularly since the improvement of STRmix modelling allowing STRmix to better model low level profiles and the implementation of the more sensitive 3500xL Genetic Analyser.
j. Under this 'new' process, all Priority 3 samples are not being microcon concentrated; they are still being amplified at 15µL. Priority 3 samples should be treated the same as Priority 2 samples; it is a waste of sample to do this.
k. Cold case samples in this range are held after quant to enable the scientist to make a decision on further processing. This should be the case for all samples.

44. I have not raised my concerns with management because I know that if I was to say I am not happy with the decision, the response would be that it was the Director-General's decision, and we have to do it.

Statements

45. Prior to 6 June 2022, samples that returned quant values between 0.001ng/µL and 0.0088ng/µL were reported as having "insufficient DNA for further processing" in statements provided to the QPS.
46. On 6 June 2022, Sharon Johnstone emailed the reporting scientists advising that any sample that has already returned a result of DIFP is to be continued to be reported as such at statement stage, and if QPS wish to have them restarted they will let us know. Annexed and marked EC-09 is a copy of the email from Sharon dated 6 June 2022.
47. There is nothing within the statement to prompt further requests for testing by QPS or DPP.
48. Pre-June 2022, reporting scientists were generally able to request a rework of a sample at the statement stage, with or without a request from QPS.
49. I hold concerns about the results being provided to the courts, given that a rework may provide a useable DNA profile, but we have been told not to rework them by Sharon Johnstone (as per paragraph 46).

No DNA detected

50. It is my opinion that there is a possibility that the samples with quant values less than 0.001ng/µL and therefore reported as 'no DNA detected' could have provided interpretable results.
51. There have been instances of samples with quant values less than 0.001ng/µL having spermatozoa sighted on microscope slides. Due to the 'no DNA detected' threshold and the automatic list system in the Forensic Register (FR), once "no DNA" has been detected, the sample populates a list for validation. The validator, who is a member of the Analytical team and not a Reporting Scientist from the Reporting team, may not look at the records in the FR to determine whether spermatozoa were observed and therefore whether further processing may be appropriate.
52. I consider the detection of spermatozoa or the suggestion of an item being 'blood stained' to be reason enough for further work, regardless of what quant value is reported.

53. I am unaware of the thresholds other laboratories use to determine whether a sample has no DNA detected.

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 by and virtue of the provisions of the Oaths Act 1867.

**TAKEN AND DECLARED** before me at Brisbane in the State of Queensland this 16th day of September 2022.

.....[redacted]..... .....[redacted]..... JUSTICE OF THE PEACE (QUALIFIED) Reg.No.: 123943 DEPT. OF JUSTICE & ATTORNEY-GENERAL

Emma-Jayne Caunt Witness Rene [redacted] (JP Qual.)

.....[redacted]..... .....[redacted..... JUSTICE OF THE PEACE (QUALIFIED) Reg.No.: 123943 DEPT. OF JUSTICE & ATTORNEY-GENERAL

Emma-Jayne Caunt Witness

**Schedule of Exhibits**

| | |
|---|---|
| EC-01 | Email from Cathie Allen, Subject: Staff movements, 24 November 2010 |
| EC-02 | Email thread, Subject: RE: Auto-microcons, 9 February 2018 |
| EC-03 | Email from Emma Caunt, Subject: DIFP samples, 25 May 2022 |
| EC-04 | Email from Jacqui Wilson, Subject: RE: [redacted], 21 July 2022 |
| EC-05 | Email from Jacqui Wilson, Subject: RE [redacted], 28 July 2022 |
| EC-06 | Email from Emma Caunt, Subject: Requests for reprocessing, 28 July 2022 |
| EC-07 | Email from Emma Caunt, Subject: RE: DNA Insufficient – Quant transition to Amp, 7 June 2022 |
| EC-08 | Email from Justin Howes, Subject: RE: Process following A/DG memo, 1 September 2022 |
| EC-09 | Email from Sharon Johnstone, Subject: FW: DNA Insufficient – Quant transition to Amp, 6 June 2022 |

[redacted]

Emma-Jayne Caunt

[redacted]

Witness

JUSTICE OF THE PEACE (QUALIFIED) QUEENSLAND GOVERNMENT Reg.No.: 103943 DEPT. OF JUSTICE & ATTORNEY-GENERAL

# EC-01

**Emma Caunt**

**From:** Cathie Allen <[redacted]>
**Sent:** Wednesday, 24 November 2010 12:42 PM
**Subject:** Staff movements
**Attachments:** Cathie Allen.vcf

Hi Everyone,

I just wanted to advise you of the following staff movements from Monday, 29th of November:

Emma Caunt will be moving into the Project Officer - Biostatistics position. The Stats Scientific Working Group (set up by the Biology Specialist Advisory Group) is really ramping up on changes that will be made nationally, and will affect the way that we report statistics. To ensure that we are across all of those changes prior to implementation, I've asked Emma to take on this project, and she has agreed. It is anticipated that the project will be for 6 months. Emma will still have a caseload during this period.

As Emma moves into this position, I've asked Kylie Rika to move across into the Reporting Team 2 for this period.

As Kylie moves, we have asked Tim and Lisa to act in the role of Senior Scientist of the Intelligence Team, and they've agreed. Tim will act until the end of Feb (with Lisa acting on Wednesdays) and Lisa will act from the end of Feb until the end of May.

And lastly, Robert Morgan will move into his permanent reporting role in Reporting Team 2.

If you have any questions, please don't hesitate to email me or chat with Kylie or Paula.
Cheers,
Cathie

Cathie Allen
A/Managing Scientist, DNA Analysis Unit,
'Best Practice in State Govt' Award Joint Winner for
2010 IPAA Qld Public Sector Excellence Awards
Forensic and Scientific Services

Clinical and Statewide Services Division | Queensland Health

[redacted]
Web: [redacted]

# EC-02

**Emma Caunt**

**From:** Kylie Rika
**Sent:** Friday, 9 February 2018 9:24 AM
**To:** Emma Caunt
**Subject:** RE: Auto-microcons

Thanks Emma

I had mentioned this type of thing in my feedback on project 184. I have not had a reply to my final feedback and it seems the executive decision has been made.

I will discuss this example with Justin as this is definitely a concern

thanks

**Kylie Rika Dip Mgt BSc PGrad Dip (Forensic)**
Senior Reporting Scientist – Forensic Reporting and Intelligence Team

Forensic DNA Analysis | Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

[redacted]



**From:** Emma Caunt
**Sent:** Thursday, 8 February 2018 4:56 PM
**To:** Kylie Rika
**Subject:** RE: Auto-microcons

Hi Kylie

I understand from a conversation with Justin that the DNA Insuff process will continue as per the no DNA detected process so samples won't be assessed taking into account the circumstances of the case. I just want to pass on one example.

Rape case
Nothing on the SAIK
Underpants – EFRAC had auto microcon and gave 2 pers mixture of complainant and defendant
Only other sample in the case was defendant on a shoe found in a park
In this case the auto-microcon gave the only evidence to substantiate the claims of the complainant
[redacted]

Thanks

Emma

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**From:** Emma Caunt
**Sent:** Thursday, 8 February 2018 9:37 AM
**To:** Justin Howes
**Cc:** Kylie Rika
**Subject:** RE: Auto-microcons

Hi Justin

I've been thinking about this a bit more. I want to say from the outset that I am not necessarily opposed to stopping the auto-microcon process, but I do think that there is a risk that we are able to manage.

I am assuming that the 'DNA insuff for processing' line will be added automatically and that it will be added to a list for validation. My question is, how will the validation process be managed?

My personal opinion is that the line should not be validated until the whole case has been assessed to see if processing of this sample would be of benefit, particularly as the quant value reaches the upper range. Obviously at the statement stage, the reporter can assess these samples, but the gap will be if no statement is requested. Since we case manage on a sample by sample basis the 'DNA insuff' results won't be monitored during the normal case management process.

Thanks

Emma

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**From:** Justin Howes
**Sent:** Wednesday, 7 February 2018 4:14 PM
**To:** Emma Caunt
**Cc:** Kylie Rika
**Subject:** RE: Auto-microcons

Hi, yes I will be changing the expanded comment as I know it is not exactly what we mean. The wording will be similar to the statement wording and making it clear that requests can be actioned.

QPS will have their processes expanded to enable this as well as including how to request further work. The expanded comment change will be added to the current SOP as a comment.

JAH

**Justin Howes**
Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

[redacted]

**HSQ's vision** | Delivering the best health support services and solutions for a safer and healthier Queensland.

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

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**From:** Emma Caunt
**Sent:** Wednesday, 7 February 2018 4:07 PM
**To:** Justin Howes
**Cc:** Kylie Rika
**Subject:** RE: Auto-microcons

Hi Justin

I've had a look at the reports for this and, NCIDD aside, it shows that 10% of samples that went through the auto-microcon gave interpretable results.

The expanded comment for the 'DNA Insufficient for further processing' line states the following:

> 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.

This indicates to scientific staff that there is nothing further that can be done with this sample, which is not the case for 10% of samples. It also does not give them the option to request for this sample to be processed further. Can I request that we update the expanded comment to be clear that there may be a chance of getting a usable profile and that they have the option of requesting this? We should probably bring this expanded comment in line with your suggested statement wording as they say different things.

Thanks

Emma

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**From:** Justin Howes
**Sent:** Wednesday, 7 February 2018 3:18 PM
**To:** Adrian Pippia; Alicia Quartermain; Allison Lloyd; Amanda Reeves; Angela Adamson; Angelina Keller; Anne Finch; Cassandra James; Claire Gallagher; Deborah Nicoletti; Emma Caunt; Hannah Pattison; Helen Williams; Ingrid Moeller; Jacqui Wilson; Josie Entwistle; Justin Howes; Kylie Rika; Lisa Benstead; Matthew Hunt; Penelope Taylor; Rhys Parry; Sharon Johnstone; Susan Brady; Thomas Nurthen; Timothy Gardam
**Subject:** Auto-microcons

Hi all
On the back of case manager's anecdotal feedback and our lab's second round of datamining of samples that underwent the auto-microcon process, an Options Paper was presented to QPS Superintendent of Forensic Services Dale Frieberg on ways forward for QPS to consider – continue with auto-microcon process, or cease auto-microcons.

QPS have advised the laboratory that they do not wish for our efforts to be put to the auto-microcon process (including the efforts in interpretation) for Priority 1 or 2 samples.

This means samples in the range 0.001ng/uL (LOD) - 0.0088ng/uL will be reported at Quant stage as 'DNA Insufficient for Further Processing'. This is consistent with the process in place for P3 samples. The manual Microcon process may be performed upon QPS request.

To report in a statement, the following wording could be used:

*Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling.*

This is slightly different to the wording written in 2012/13 for these samples (P3) but after some consultation, appears a good starting point.

An enhancement has been requested to enable this to occur from 12 February. Reactivating samples for further post-extraction processing, if requested from QPS, will be directed to Luke via an FR Request. If there are changes to the 12 February date, I will let you know. As usual, appropriate comments to SOPs will follow.

Regards
Justin

**Justin Howes**
Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

[redacted]

# EC-03

## Emma Caunt

**From:** Emma Caunt
**Sent:** Wednesday, 25 May 2022 10:35 AM
**To:** Sharon Johnstone
**Subject:** DIFP samples

Hi Sharon

I have noticed a number of DIFP samples where QPS have requested reprocessing. One example is [redacted] where sperm were detected. This sample was m'conned to 35uL and then only amped at 14uL due to the FR bug. A 2p mix was obtained which is low level but interpretable however I think that a much better profile would have been obtained if :

1. The sample had been m'conned to full
2. The sample had been amped at 15uL

Personally I request a m'con to full for most DIFP samples that I rework and find that this works well. I wonder if we could consider this as a default for reworking DIFP samples. Additionally it would be really helpful if the FR bug where samples are only amped at 14uL was fixed asap as I think it could have a detrimental impact on the processing of low quant samples.

Thanks

Emma

**Emma Caunt**
Scientist

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

[redacted]

***Please note that I may be working from a different location during the COVID-19 pandemic. The best contact method is via email.***

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

# EC-04

## Emma Caunt

**From:** Jacqui Wilson
**Sent:** Thursday, 21 July 2022 11:00 AM
**To:** Emma Caunt
**Subject:** RE: [redacted]

**Follow Up Flag:** Follow up
**Flag Status:** Flagged

Hi Emma

I'm not convinced that a microcon will do the trick given the quant, it's a mix and the lack of information at numerous loci.

That said, I have ordered the rework.

Thanks
Jacqui

---

**From:** Emma Caunt <[redacted]u>
**Sent:** Wednesday, 20 July 2022 3:36 PM
**To:** Jacqui Wilson <[redacted]>
**Subject:** [redacted]

Hi Jacqui

I think you might get a usable profile for this one if you m'con to full.

Thanks

Emma

**Emma Caunt**
Scientist

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

[redacted]

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# EC-05

## Emma Caunt

**From:** Jacqui Wilson
**Sent:** Thursday, 28 July 2022 2:39 PM
**To:** Emma Caunt
**Subject:** RE: [redacted]

😊 Thanks!

I did ponder it for some time given the number of subs and I had to get onto GM to check them out.

I was happier when I did the STRmix and figured it is probably the dude's own house anyway 😝

**From:** Emma Caunt <[redacted]>
**Sent:** Thursday, 28 July 2022 2:37 PM
**To:** Jacqui Wilson <[redacted]>
**Subject:** RE: [redacted]

Great result!

I have reviewed 😊

**From:** Jacqui Wilson <[redacted]>
**Sent:** Thursday, 28 July 2022 2:19 PM
**To:** Emma Caunt <[redacted]>
**Subject:** [redacted]

Hi Emma

I've run this one as a 2MX.

Let me know what you think 😊

Thanks
Jacqui

**Jacqui Wilson B App Sc. M Sc.**
Reporting Scientist

**Forensic DNA Analysis, Forensic and Scientific Services**
Prevention Division, Queensland Health

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[redacted]

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# EC-06

## Emma Caunt

**From:** Emma Caunt
**Sent:** Thursday, 28 July 2022 10:18 AM
**To:** Sharon Johnstone
**Subject:** Requests for reprocessing

Hi Sharon

When QPS request a DIFP sample to be reprocessed it appears that the default is to order a m'con to 35uL. This may not always be the best rework strategy. For example, sample [redacted] had an original quant value of 0.00135ng/uL and had a m'con to 35uL. The profile obtained looks like it's probably 2p but is not quite interpretable. I think that if this sample had ben m'conned to full we may have been able to interpret the result.

Are we able to look at having the process changed so that the m'con ordered (either 35 or full) is more appropriate for the original quant value obtained?

Thanks

Emma

**Emma Caunt**
Scientist

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

[redacted]

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# EC-07

## Emma Caunt

**From:** Emma Caunt
**Sent:** Tuesday, 7 June 2022 8:39 AM
**To:** Sharon Johnstone; Kylie Rika; Justin Howes
**Subject:** RE: DNA Insufficient - Quant transition to Amp

Hi

Before the DIFP process was implemented, all PP21 samples in the quant range of 0.001 – 0.0088 ng/uL were sent for an automatic microcon (as per QIS 17117v19). Now that the DIFP process has been stopped, I was wondering why are we sending these samples straight for amp rather than for auto microcon?

Thanks

Emma

---

**From:** Sharon Johnstone <[redacted]>
**Sent:** Monday, 6 June 2022 3:13 PM
**To:** Adrian Pippia <[redacted]>; Alicia Quartermain <[redacted]>; Angela Adamson <[redacted]>; Anne Finch <[redacted]>; Cassandra James <[redacted]>; Emma Caunt <[redacted]>; Jacqui Wilson <[redacted]>; Josie Entwistle <[redacted]>; Kerry-Anne Lancaster <[redacted]>; Rhys Parry <[redacted]>; Allan McNevin <[redacted]>; Angelina Keller <[redacted]>; Claire Gallagher <[redacted]>; Deborah Nicoletti <[redacted]>; Ingrid Moeller <[redacted]>; Matthew Hunt <[redacted]>; Penelope Taylor <[redacted]>; Tegan Dwyer <[redacted]>; Thomas Nurthen <[redacted]>
**Cc:** Kylie Rika <[redacted]>; Allison Lloyd <[redacted]>; Luke Ryan <[redacted]>
**Subject:** FW: DNA Insufficient - Quant transition to Amp
**Importance:** High

Hi all,
Please see below instructions stemming from today's announcements. These have been agreed to by QPS.
Please also note that any sample that has already been DNA insufficient is to be continued to be reported as such at statement stage. These results are known to the QPS. If it is their wish to have them restarted they will let us know.

Regards,
Sharon

**Sharon Johnstone**
Senior Scientist – Forensic Reporting and Intelligence Team

**Forensic DNA Analysis, Police Services Stream**
Prevention Division, Queensland Health

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[redacted]

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**From:** Justin Howes <[redacted]>
**Sent:** Monday, 6 June 2022 1:55 PM
**To:** Kylie Rika <[redacted]>; Sharon Johnstone <[redacted]>
**Cc:** Paula Brisotto <[redacted]>
**Subject:** FW: DNA Insufficient - Quant transition to Amp
**Importance:** High

Hi
Please note the DIFP process is currently suspended (the range correction to below is 0.001-0.0088ng/uL). Any new samples in this range will go directly for amp.

Previously reported DIFP that are requested for a restart, will go to microcon as per current process.

P3 samples will continue to be case managed in the same way as always – without rework unless not amped at max (of which the samples in the pertinent range will be amped at max).

Regards
Justin

**Justin Howes**
Team Leader - Forensic Reporting and Intelligence Team

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

[redacted]

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**From:** Paula Brisotto <[redacted]>
**Sent:** Monday, 6 June 2022 1:23 PM
**To:** Justin Howes <[redacted]>
**Subject:** FW: DNA Insufficient - Quant transition to Amp
**Importance:** High

FYI

**From:** Luke Ryan <[redacted]>
**Sent:** Monday, 6 June 2022 1:20 PM
**To:** Adam Kaity <[redacted]>; Alanna Darmanin <[redacted]>; Amy Cheng <[redacted]>; Belinda Andersen <[redacted]>; Biljana Micic <[redacted]>; Generosa Lundie <[redacted]>; Lai-Wan Le <[redacted]>; Lisa Farrelly <[redacted]>; Maria Aguilera <[redacted]>; Melissa Cipollone <[redacted]>; Nicole Roselt <[redacted]>; Pierre Acedo <[redacted]>; Sharelle Nydam <[redacted]>; Tara Prowse <[redacted]>
**Cc:** Paula Brisotto <[redacted]>; Cathie Allen <[redacted]>
**Subject:** DNA Insufficient - Quant transition to Amp
**Importance:** High

Afternoon All
The premier has requested we test (amp) all samples in the current DNA Insufficient Range (i.e. above 0.001 – 0.088 ng/µL).

**When transitioning Quant batches, please ensure all samples in the DNA Insufficient range are transitioned to the Amp WL. We are not reporting DNA Insufficient result lines as of now.**

Please also ensure when reviewing No DNA Detected samples, look for samples with the DNA Insufficient result which have not been transitioned to the Amp WL. Please reallocate these to the Amp WL. I will go through the No DNA review list now and allocate these to the Amp WL.

There is no change to rules for No DNA Detected samples.

FR will be modified so that these rules are incorporated into the Quant transition page, but this will be a manual process until these changes are made.

Thanks
Luke

**Luke Ryan**
Senior Scientist – Analytical Team

**Forensic DNA Analysis, Forensic and Scientific Services**
Prevention Division, Queensland Health

[redacted]

Integrity | Customers and patients first | Accountability | Respect | Engagement

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# EC-08

## Emma Caunt

**From:** Justin Howes
**Sent:** Thursday, 1 September 2022 3:25 PM
**To:** Allison Lloyd; Cathie Allen; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone; Wendy Harmer; Adrian Pippia; Alicia Quartermain; Allan McNevin; Allison Lloyd; Angela Adamson; Angelina Keller; Anne Finch; Cassandra James; Claire Gallagher; Deborah Nicoletti; Emma Caunt; Ingrid Moeller; Jacqui Wilson; Josie Entwistle; Kerry-Anne Lancaster; Matthew Hunt; Penelope Taylor; Rhys Parry; Tegan Dwyer; Thomas Nurthen
**Subject:** RE: Process following A/DG memo

Hi all
QPS have requested additional information to be provided to Request/Tasks when seeking approval for testing that might exhaust the DNA extract.

Firstly, the Request/Task is to be directed to Action Unit: 'FLU'. From there, my understanding is the Investigating Officer will be contacted and approval will be considered.

The additional information required is below. Also provided is suggested wording that took on Kylie and Sharon's feedback.

*Hello, a DNA profile has been obtained from the linked crime scene sample. I am seeking approval for additional work to be undertaken on the sample, in an attempt to obtain a suitable DNA profile for interpretation. Please be advised if this additional work is approved, the DNA extract will be consumed. This means there will be no opportunity for further processing in this laboratory, or elsewhere if alternative technologies are under consideration. We understand that consultation with the Investigating Officer may be necessary and will await the outcome of those discussions. Once finalised, please advise via return Request/Task if the additional work is approved. If approval is not provided, the DNA profile obtained will be reported.*

*Additional information to assist:*

- *Quant value:*
- *Undergone concentration (Microcon): No/Yes*
- *Current Volume Remaining: uL*
- *Further Processing Requested eg. Microcon to full, additional amplification*
- *Will further processing exhaust the sample: No/Yes*
- *Description of DNA profile obtained to date: eg. Low level DNA profile difficult to interpret, complex DNA profile, Low level profile that may not be suitable for interpretation*
- *Scientific Opinion on the likelihood that further internal testing may provide additional probative information: eg. further work is likely to/ may assist in the confirmation of information currently obtained. Further work may also confirm that the profile is too complex to interpret.*
- *Recommendation as to whether the sample may be better tested by an external service provider: If this item is critical to the outcomes of the case then a discussion is requested to explore all possible options.*

This has been added to 17117 SOP which is in review.

Please add the extra information to all Request/Tasks when seeking approval that might exhaust the DNA extract.

Regards
Justin

**Justin Howes**
Team Leader - Forensic Reporting and Intelligence Team

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

[redacted]

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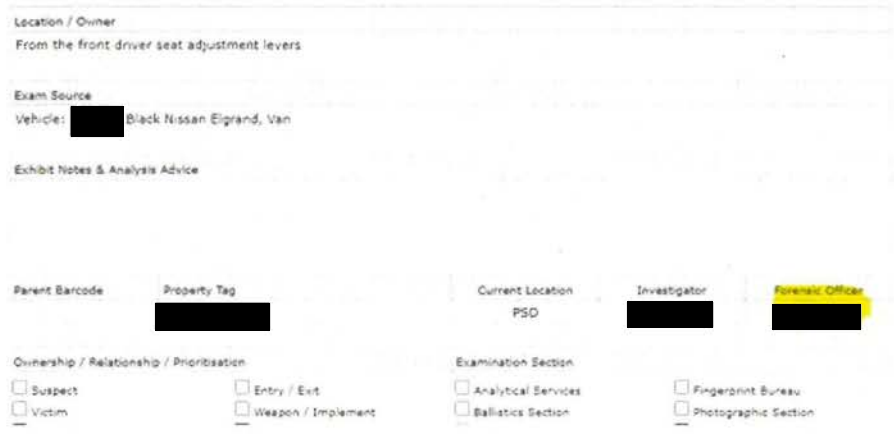
**From:** Justin Howes <[redacted]>
**Sent:** Friday, 19 August 2022 4:54 PM
**To:** Allison Lloyd <[redacted]>; Cathie Allen <[redacted]>; Kirsten Scott <[redacted]>; Kylie Rika <[redacted]>; Luke Ryan <[redacted]>; Paula Brisotto <[redacted]>; Sharon Johnstone <[redacted]>; Wendy Harmer <[redacted]>; Adrian Pippia <[redacted]>; Alicia Quartermain <[redacted]>; Allan McNevin <[redacted]>; Allison Lloyd <[redacted]>; Angela Adamson <[redacted]>; Angelina Keller <[redacted]>; Anne Finch <[redacted]>; Cassandra James <[redacted]>; Claire Gallagher <[redacted]>; Deborah Nicoletti <[redacted]>; Emma Caunt <[redacted]>; Ingrid Moeller <[redacted]>; Jacqui Wilson <[redacted]>; Josie Entwistle <[redacted]>; Justin Howes <[redacted]>; Kerry-Anne Lancaster <[redacted]>; Matthew Hunt <[redacted]>; Penelope Taylor <[redacted]>; Rhys Parry <[redacted]>; Tegan Dwyer <[redacted]>; Thomas Nurthen <[redacted]>
**Subject:** Process following A/DG memo

Hi all
Following this memo, the information below will be added to 17117 which will be sent to review early next week:

When seeking written approval from QPS for additional work if considered beneficial, send a Request/Task via the Forensic Register to the relevant Forensic Officer found by the field below. Add the Forensic Officer's ID number to the Action Officer field, and link the relevant crime scene barcode to the Request/Task.


Location / Owner
From the front driver seat adjustment levers

Exam Source
Vehicle: [redacted] Black Nissan Elgrand, Van

Exhibit Notes & Analysis Advice

Parent Barcode | Property Tag [redacted] | Current Location PSD | Investigator [redacted] | Forensic Officer [redacted]

Ownership / Relationship / Prioritisation
☐ Suspect ☐ Victim ☐ Entry / Exit ☐ Weapon / Implement

Examination Section
☐ Analytical Services ☐ Ballistics Section ☐ Fingerprint Bureau ☐ Photographic Section

Suggested Template for wording:

*Hello, a DNA profile has been obtained from the linked crime scene sample. I am seeking approval for additional work to be undertaken on the sample, in an attempt to obtain a suitable DNA profile for interpretation. Please be advised if this additional work is approved, the DNA extract will be consumed. This means there will be no opportunity for further processing in this laboratory, or elsewhere if alternative technologies are under consideration. We understand that consultation with the Investigating Officer may be necessary and will await the outcome of those discussions. Once finalised, please advise via return Request/Task if the additional work is approved. If approval is not provided, the DNA profile obtained will be reported.*

When sending the Request/Task, the exhibit result line *SOHAA – Sample on hold, awaiting advice* should be added, and validated by a second operator.

When QPS respond, the exhibit result line *TRQ – Testing restarted on advice from QPS* should be added irrespective of whether approval for further processing has been granted or not. The result will either be reported based on the one amplification result, or will be reported after the further processing.

Regards
Justin

**Justin Howes**
Team Leader - Forensic Reporting and Intelligence Team

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

[redacted]

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**From:** Helen Gregg <[redacted]>
**Sent:** Friday, 19 August 2022 3:33 PM
**To:** Abigail Ryan <[redacted]>; Adam Kaity <[redacted]>; Adrian Pippia <[redacted]>; Alanna Darmanin <[redacted]>; Alicia Quartermain <[redacted]>; Allan McNevin <[redacted]>; Allison Lloyd <[redacted]>; Amy Cheng <[redacted]>; Amy Morgan <[redacted]>; Angela Adamson <[redacted]>; Angelina Keller <[redacted]>; Anne Finch <[redacted]>; Belinda Andersen <[redacted]>; Biljana Micic <[redacted]>; Cassandra James <[redacted]>; Cathie Allen <[redacted]>; Cecilia Flanagan <[redacted]>; Chantal Angus <[redacted]>; Chelsea Savage <[redacted]>; Cindy Chang <[redacted]>; Claire Gallagher <[redacted]>; Dasuni Harmer <[redacted]>; Deborah Nicoletti <[redacted]>; Emma Caunt <[redacted]>; FSS.FDNA.Admin <[redacted]>; Generosa Lundie <[redacted]>; Helen Williams <[redacted]>; Ingrid Moeller <[redacted]>; Jacqui Wilson <[redacted]>; Janine Seymour-Murray <[redacted]>; Josie Entwistle <[redacted]>; Julie Brooks <[redacted]>; Justin Howes <[redacted]>; Kerry-Anne Lancaster <[redacted]>; Kevin Avdic <[redacted]>; Kim Estreich <[redacted]>; Kirsten Scott <[redacted]>; Kristina Morton <[redacted]>; Kylie Rika <[redacted]>; Lai-Wan Le <[redacted]>; Lisa Farrelly <[redacted]>; Luke Ryan <[redacted]>; Madison GULLIVER <[redacted]>; Maria Aguilera <[redacted]>; Matthew Hunt <[redacted]>; Melissa Cipollone <[redacted]>; Michael Goodrich <[redacted]>; Michael Hart <[redacted]>; Michelle Margetts <[redacted]>; Naomi French <[redacted]>; Nicole Roselt <[redacted]>; Paula Brisotto <[redacted]>; Penelope Taylor <[redacted]>; Phillip McIndoe <[redacted]>; Pierre Acedo <[redacted]>; Rhys Parry <[redacted]>; Ryu Eba <[redacted]>; Sandra McKean <[redacted]>; Sharelle Nydam <[redacted]>; Sharon Johnstone <[redacted]>; Stephanie Waiariki <[redacted]>; Suzanne Sanderson <[redacted]>; Tara Prowse <[redacted]>; Tegan Dwyer <[redacted]>; Thomas Nurthen <[redacted]>; Valerie Caldwell <[redacted]>; Vicki Pendlebury-Jones <[redacted]>; Wendy Harmer <[redacted]>; Yvonne Connolly <[redacted]>
**Cc:** Alison Slade <[redacted]>; FSS Corro <[redacted]>; Lara Keller <[redacted]>; Keith McNeil <[redacted]>; Petra Derrington <[redacted]>
**Subject:** FW: C-ECTF-22/13557 - DG MEMO - from Dr David Rosengren, Acting Director-General, Queensland Health - Subject of memorandum

Good afternoon everyone,

Please see attached memo. I have asked for an enhancement to FR to assist with this change.

Please hold all quants effective immediately, until the FR enhancement is complete. Paula has specific details for the analytical team.
For batches that have already progressed beyond quant, proceed as per this morning's processes.

Could you please update SOPs asap.

Contact me if you have any queries.

Regards
Helen

**Helen Gregg**
A/Executive Director

**Forensic and Scientific Services**
Prevention Division, Queensland Health

[redacted]

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---

Good Afternoon

Please see attached the Memorandum from Dr David Rosengren, Acting Director-General, Queensland Health, for your attention.

Should you have any questions in relation to this advice, please contact Professor Keith McNeil, Acting Deputy Director-General on telephone [redacted].

Kind Regards

Queensland Government

Ministerial & Executive Services Unit, Office of the Director-General | Queensland Health

E [redacted]
W health.qld.gov.au

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# EC-09

## Emma Caunt

**From:** Sharon Johnstone
**Sent:** Monday, 6 June 2022 3:13 PM
**To:** Adrian Pippia; Alicia Quartermain; Angela Adamson; Anne Finch; Cassandra James; Emma Caunt; Jacqui Wilson; Josie Entwistle; Kerry-Anne Lancaster; Rhys Parry; Allan McNevin; Angelina Keller; Claire Gallagher; Deborah Nicoletti; Ingrid Moeller; Matthew Hunt; Penelope Taylor; Tegan Dwyer; Thomas Nurthen
**Cc:** Kylie Rika; Allison Lloyd; Luke Ryan
**Subject:** FW: DNA Insufficient - Quant transition to Amp

**Importance:** High

Hi all,
Please see below instructions stemming from today's announcements. These have been agreed to by QPS.
Please also note that any sample that has already been DNA insufficient is to be continued to be reported as such at statement stage. These results are known to the QPS. If it is their wish to have them restarted they will let us know.

Regards,
Sharon

**Sharon Johnstone**
Senior Scientist – Forensic Reporting and Intelligence Team

**Forensic DNA Analysis, Police Services Stream**
Prevention Division, Queensland Health

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[redacted]

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**From:** Justin Howes <[redacted]>
**Sent:** Monday, 6 June 2022 1:55 PM
**To:** Kylie Rika <[redacted]>; Sharon Johnstone <[redacted]>
**Cc:** [redacted]

**Subject:** FW: DNA Insufficient - Quant transition to Amp
**Importance:** High

Hi
Please note the DIFP process is currently suspended (the range correction to below is 0.001-0.0088ng/uL). Any new samples in this range will go directly for amp.

Previously reported DIFP that are requested for a restart, will go to microcon as per current process.

P3 samples will continue to be case managed in the same way as always – without rework unless not amped at max (of which the samples in the pertinent range will be amped at max).

Regards
Justin

**Justin Howes**
Team Leader - Forensic Reporting and Intelligence Team

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

[redacted]

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**From:** Paula Brisotto <[redacted]>
**Sent:** Monday, 6 June 2022 1:23 PM
**To:** Justin Howes <[redacted]>
**Subject:** FW: DNA Insufficient - Quant transition to Amp
**Importance:** High

FYI

**From:** Luke Ryan <[redacted]>
**Sent:** Monday, 6 June 2022 1:20 PM
**To:** Adam Kaity <[redacted]>; Alanna Darmanin <[redacted]>; Amy Cheng <[redacted]>; Belinda Andersen <[redacted]>; Biljana Micic <[redacted]>; Generosa Lundie <[redacted]>; Lai-Wan Le <[redacted]>; Lisa Farrelly <[redacted]>; Maria Aguilera <[redacted]>; Melissa Cipollone <[redacted]>; Nicole Roselt

<[redacted]>; Pierre Acedo <[redacted]>; Sharelle Nydam
<[redacted]>; Tara Prowse <[redacted]>
**Cc:** Paula Brisotto <[redacted]>; Cathie Allen <[redacted]>
**Subject:** DNA Insufficient - Quant transition to Amp
**Importance:** High

Afternoon All
The premier has requested we test (amp) all samples in the current DNA Insufficient Range (i.e. above 0.001 – 0.088 ng/µL).

**When transitioning Quant batches, please ensure all samples in the DNA Insufficient range are transitioned to the Amp WL. We are not reporting DNA Insufficient result lines as of now.**

Please also ensure when reviewing No DNA Detected samples, look for samples with the DNA Insufficient result which have not been transitioned to the Amp WL. Please reallocate these to the Amp WL. I will go through the No DNA review list now and allocate these to the Amp WL.

There is no change to rules for No DNA Detected samples.

FR will be modified so that these rules are incorporated into the Quant transition page, but this will be a manual process until these changes are made.

Thanks
Luke

**Luke Ryan**
Senior Scientist – Analytical Team

**Forensic DNA Analysis, Forensic and Scientific Services**
Prevention Division, Queensland Health

[redacted]