From: Neville.DavidH[OSC]
Sent: Fri, 1 Apr 2022 15:55:57 +1100
To: Cathie Allen
Cc: Lara Keller;McNab.BruceJ[OSC]
Subject: RE: Testing thresholds

Dear Cathie
Previously you indicated that you would provide a report in response to issues raised by QPS around the thresholds used to triage continuation of DNA testing. I spoke to Bruce who indicated that he has not received this as yet (unless he missed it amongst his many emails).

In any case, can you confirm whether or not this has been provided yet, please. If not, do you have an expected date of release. Bruce has also requested that the report be provided to me as the responsible officer for DNA in the QPS, please.

Regards

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

From: Neville.DavidH[OSC]
Sent: Wednesday, 16 March 2022 14:28
To: Cathie Allen [redacted]
Cc: Lara Keller [redacted] McNab.BruceJ[OSC]
[redacted]
Subject: RE: Testing thresholds

Hi Cathie
I have been continuing to track success rates of samples that were originally reported as 'DNA Insufficient for further processing' but then yielded a useable profile when QPS requested testing to continue. I am still seeing a similar success rate of nearly 30%. This high success rate with lower quant samples shows the very good work done by your lab which is much appreciated.

The results are included in the attached spreadsheet. The features of the spreadsheet are as follows:

- Tabs 1 and 2 includes previous provided data for January – September 2021
- Tab 3 relates to the raw data download for the period 1 October 2021 – 15 March 2022 outlining exhibits that were submitted for further processing and the results that were obtained.
- Tab 4 is a pivot table grouping the results that have been returned from the requested reworks.

Of note, in relation to the data for 1 October – 15 March, there are a total of 155 samples that have finalised testing. Breakdown of results as follows:

- 43 samples obtained a useable result (Single source; 2, 3, and 4 person mixed DNA profiles)
- 2 samples returned a quality control failure result
- 110 samples did not return a useable result.

The remainder of samples that were submitted for further processing for this period (47 samples), are still undergoing testing at QHFSS, therefore it is unknown at this time what results will be returned on these samples.

I have provided this information as it may assist with the report that you are preparing as discussed in previous emails. It would be very interesting to see how the quant and degradation values correlate with success of further processing. It may also assist with any review of thresholds as requested by QPS. This is provided for information only.

Kind regards

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

From: Cathie Allen [redacted]
Sent: Monday, 7 March 2022 16:47
To: Neville.DavidH[OSC] [redacted]
Cc: Lara Keller [redacted]; McNab.BruceJ[OSC]
[redacted]
Subject: RE: Testing thresholds

Hi David

Thank you for your email.

My clarification only related to the figure of 1.86% and 'uploadable' profiles to the NCIDD.

I'll work with Lara on how this is best resolved and we'll provide a recommendation/s in the follow-up report.

Cheers
Cathie

Cathie Allen BSc, MSc (Forensic Science) (She/Her*)
Managing Scientist
Social Chair, Organising Committee for 25th International Symposium of the
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From: Neville.DavidH[OSC] [redacted]
Sent: Thursday, 3 March 2022 2:26 PM
To: Cathie Allen [redacted]
Cc: Lara Keller [redacted] McNab.BruceJ[OSC]
[redacted]
Subject: RE: Testing thresholds

Hi Cathie
Without doubting your obvious expertise, I think you may be misinterpreting the data in the paper. In your response you indicated that *"The value of 1.86% refers to DNA profiles that are able to be uploaded to the NCIDD ('loadable profile')."* However, in part 4 of the paper it describes 'success' as what appears to be a loadable profile and figure 1 indicates this is 10.6% (See below).

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.

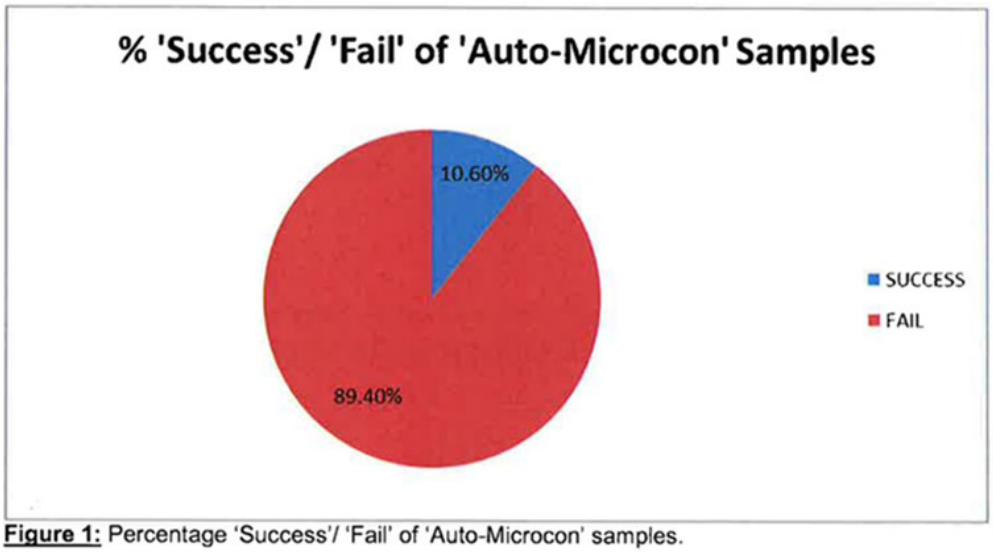

Figure 1: Percentage 'Success'/ 'Fail' of 'Auto-Microcon' samples.

The 1.86% refers to where 'success' occurred and it was the only sample in the case that was NCIDD-suitable for that particular profile. In other words, there were no other samples in the case that yielded the same profile. Again, this is problematic because the probative value of samples varies as outlined in my last email to you.

In relation to the spreadsheet you mentioned, we do not have access to quant values and no such spreadsheet exists. This is why I am requesting that you make this information visible to us in addition to degradation values.

I agree that the scientist are best positioned to make a determination as to whether microcon or further testing should occur. I would much rather this decision be made by an expert with access to

all of the data, but my understanding is that this does not occur at the moment. Rather, testing is automatically ceased and it is left up to the QPS to make a request without access to any of the information.

I also agree absolutely that any change should be evidence based. I would request that the options paper give consideration to lowering the threshold value. I look forward to report and hope that the current weather does not impact on you or your team

Regards

David Neville

From: Cathie Allen [redacted]
Sent: Thursday, 3 March 2022 12:34
To: Neville.DavidH[OSC] [redacted]
Cc: Lara Keller [redacted]; McNab.BruceJ[OSC]
[redacted]
Subject: RE: Testing thresholds

Hi David

Thank you for the recognition of being experts in the area of DNA profiling and workflow surround it – I really appreciate it. The Queensland Government has made a significant investment in the expertise and skills of all staff in Forensic DNA Analysis in our area of DNA profiling and interpretation and it's great that they are recognised for that.

I'd like to clarify a point regarding the interpretation of the data in the Options Paper from 2017. This was discussed with the Supt and Inspector at the time. The value of 1.86% refers to DNA profiles that are able to be uploaded to the NCIDD ('loadable profile'). The more alleles available within a profile, the greater the chance that any matches could be considered a true match, rather than an adventitious match. This should be borne in mind when considering additional resources being put towards a sample with a low quant value (ie return on investment). Achieving more than 12 alleles for a sample is the aim so that matches on the NCIDD can be made and intelligence results delivered to the QPS.

The Commissioner delegates the responsibility for DNA testing and reporting to FSS. We're aware that a spreadsheet is used within the QPS DNA Management regarding quant values etc. To enable FSS to provide an even higher standard of service to the QPS, could we please gain access to the spreadsheet, with the view to incorporating it into the FR? We feel that if we could incorporate this, we will be able to provide recommendations for the QPS to consider, as you've rightly pointed out 'there is a lot to assimilate when you don't work in the field'. As we're across this and how the profile behaves, this would allow us to provide that information to the QPS that assists with any future decision making on a collaborative basis.

The data generated within the Options Paper was from 2017. Given a large number of samples have been processed since then, which would include any changes in sampling made by both organisations, FSS would prefer that any proposed changes are done using evidence based research. Gathering more data will assist in decision making regarding the processing of DNA samples, whilst also making an assessment on the best use of resources for both organisations. We anticipate providing a follow-up paper to Supt McNab in approx two weeks (given the current weather event being experienced and affecting a number of people). Please bear in mind that any changes to the FR workflow will also require an FR enhancement (which at this time will be within the new version of the FR, given how close it is to implementing).

Cheers
Cathie

Cathie Allen BSc, MSc (Forensic Science) (She/Her*)
Managing Scientist
Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022
Police Services Stream, Forensic & Scientific Services
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From: Neville.DavidH[OSC] [redacted]
Sent: Thursday, 24 February 2022 1:21 PM
To: Cathie Allen [redacted]
Cc: Lara Keller [redacted] Frieberg.DaleJ[OSC] [redacted]
Subject: RE: Testing thresholds

Hi Cathie,
Thanks for the reply and also for the paper discussing the micro-con success rates. I have read the paper previously, however the explanation in your email sent yesterday made this a lot clearer. It was really helpful because there is a lot to assimilate when you don't work in the field.

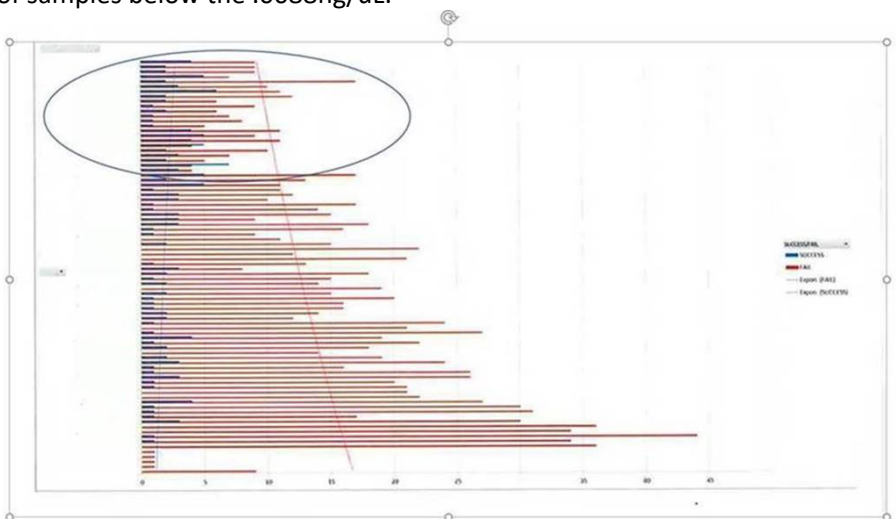
I wondered if you can clarify my understanding of the paper? The success rate of <2% relates to the likelihood of the process resulting in a new link rather than the likelihood of obtaining a profile. The actual success rate of obtaining a profile is roughly 10% overall according to Figure 1.

I'll be honest, using the number of new links to measure the value of analysis is very problematic because the probative value of the evidence will vary hugely depending on the sample type and location. Although I can see the logic, it does over simply the situation.

10% is much closer to 30% which is what we observed and our selection process may explain part of the gap in our success values. More importantly, I did some calculations based on the success rate shown in Figure 2 for samples with a quant value of over .006ng/uL. Above this quant the success rate is 24% which is even closer to our observation.

The current system of reporting places an onus on the QPS to make a decision as to whether testing should continue for samples under .0088ng/uL of DNA. Investigators are advised to let the DNA Management Section know if they seek for this to occur. This is problematic for members of the QPS to make a decision as to whether testing should proceed because they do not have access to information about the quality and quantity of DNA present. For this to actually work we need to have visibility over the quant and degradation values to make an informed decision. This could easily be resolved through a change in the FR. For a short time QPS members had visibility of this information due to a programming error, but it was switched off. I believe it is essential that this limited information be made available again for the current regime of reporting is to remain.

According to Figure 2, the likelihood of success appears to be much greater for samples above .006ng/uL (approx. 24%). Its also interesting to note that this accounts for relatively low proportion of samples below the .0088ng/uL.



Based on the information in this graph, I wondered if it might be worthwhile lowering the threshold.

I am not supportive at this point of returning to automatic processing of all of the samples above .001ng/uL. I think that would be a retrograde step and unnecessarily tie up the scientists. But I am very supportive of fine tuning the threshold.

In any case, your email has been incredibly helpful and it does resolve some of my concerns. However it also highlights a need for us to modify our practices. Can you please provide advice on the practicality of the suggestions I have made? Alternatively I would be very interested in any improvement suggestions you may have.

Thanks again and I look forward to hearing your thoughts.

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

From: Cathie Allen [redacted]
Sent: Thursday, 24 February 2022 08:37
To: Neville.DavidH[OSC] [redacted]
Cc: Frieberg.DaleJ[OSC] [redacted] Lara Keller
[redacted]
Subject: RE: Testing thresholds

Hi David

The laboratory has conducted an extensive validation process prior to the implementation of the current quantitation process. The validation outcomes were in line with the manufacturer's specification. From August 2018 onwards, if a sample obtains a quantitation value of 0.001 ng/uL or below, the laboratory reports this to the QPS as 'No DNA Detected'. If a sample obtains a quantitation value between 0.001ng/uL and 0.0088ng/uL, the laboratory reports this to the QPS as 'DNA insufficient for further processing' (expanded QPRIME results supplied below). These values are listed in the Options paper attached that was provided to the QPS. Samples that obtain a quantitation value greater than 0.0088ng/ug are processed through the DNA profiling step and results obtained are reported. Its FSS's understanding that forensic officers review DNA results within the context of the case and can request testing or submit additional items for testing.

No DNA detected
This item/sample was submitted for DNA analysis; however no DNA was detected above the limit of detection at the quantitation stage. No further processing was conducted on this item.

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.

The theoretical values regarding human cells to derive a DNA profile are not used within the laboratory. The laboratory uses values obtained from the quantitation process that provide the approximate amount of human DNA available within the sample.

Each year, the forensic laboratories will exchange information regarding profiling kit and equipment used, however details regarding quantitation values has not been exchanged or collated so I'm unable to comment or draw comparisons to other jurisdictions. Validation studies conducted within each laboratory ensures that the method or equipment is fit for purpose within that laboratory environment, so it's not unexpected that different laboratories would have slightly different thresholds for quantitation or limit of detect for DNA profiles (as different equipment and kits are used in the different laboratories).

The in-house validation of the current QuantiFiler Trio system showed that the laboratory could reliably detect DNA down to concentrations of 0.001ng/uL, however the manufacturer has reported that the system has single source sensitivity only down to 0.005ng/uL. At these lower concentrations of DNA, there are more stochastic effects that can occur and thereby affect the interpretation of the DNA profile. Quantity and quality of the DNA obtained from a sample determines the ability to obtain a DNA profile.

If the QPS request a 'DNA insufficient' sample to be processed, it first undergoes a concentration step then amplification and associated DNA interpretation (excluding Priority 1 samples). The concentration step is required to give the sample the best opportunity to obtain a 'useful' DNA profile (ie useful to load to the NCIDD or meaningful comparison to other profiles obtained within the case).

Once we've received the quote from bdna regarding when an enhancement can be added to the FR for data extraction, we will be able to provide a timeframe regarding analysis of the data and provision of a report.

Cheers
Cathie

Cathie Allen BSc, MSc (Forensic Science) (She/Her*)
Managing Scientist
Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022
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From: Neville.DavidH[OSC] [redacted]
Sent: Wednesday, 23 February 2022 8:51 AM
To: Cathie Allen [redacted]

Cc: Frieberg.DaleJ[OSC] [redacted]>; Lara Keller [redacted]
Subject: RE: Testing thresholds

Dear Cathie

Thank you for your reply to my email, however the response does not address the main query posed. I am seeking information from you in relation to the comments in the Australian claiming that the thresholds in Queensland are twice that of other states and three times higher than the manufacturer's recommended value. These claims in the national newspaper come at a time when the QPS has raised similar concerns around testing triage thresholds. Unfortunately the gears have shifted since our meeting on 1 February due these claims in the media and I am being asked questions in relation to these very issues.

I need to also further clarify my comment that the QPS had 'cherry picked' samples. The dataset that was provided included the barcodes of samples that the QPS requested to continue testing after receiving a result 'insufficient DNA for further testing'. Some of these were selected because we found it unusual for the sample type to yield low DNA. This included samples from blood and a used condom. The fact that these produced low quant values is concerning to some extent. However, the majority of them were selected due to the probative value of the sample rather than the sample type. For [redacted] alone, this included 33 samples with 10 later providing a full profile. Yes, the sample selection may have had some impact, however it could not explain the vast difference between >2% and 30% success rate.

Having said this, I do appreciate the work that you have done so far in reviewing the dataset. I understand that this may not be a simple task. I know that we share a common interest in ensuring the effectiveness of DNA in enhancing community safety. To that effect, could you please provide an estimated timeframe for completion.

For clarity, could you please provide advice on the threshold values used with QHFSS as a matter or priority including how they accord with other jurisdictions. I assume that this information will be readily available within your procedures.

Kind Regards

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

From: Cathie Allen [redacted]
Sent: Tuesday, 22 February 2022 16:32
To: Neville.DavidH[OSC] [redacted]
Cc: Frieberg.DaleJ[OSC] [redacted] Lara Keller [redacted]
Subject: RE: Testing thresholds

Hi David

During the Bi-Monthly QPS / QHFSS meeting on the 1st of February, I provided a verbal update to you and Supt Frieberg regarding this. Minutes from this meeting are yet to be circulated (it was recorded), I have detailed notes that I took during the meeting and I've referred to those for this email.

I advised that due to the community transmission of COVID-19 affecting Forensic DNA Analysis staff members and the two urgent cases that the QPS requested we process (a number of items), slow progress had been made on this request. At the meeting, you provided an assurance that you understood the situation that both the QPS and FSS were in due to the community transmission of COVID-19 affecting the workforces.

During the meeting, you advised that you were aware that the QPS had 'cherry-picked' particular samples to be tested further, and that this may be the reason behind the results that were achieved.

The data that is required to be analysed is within the FR, and FSS have submitted a request to bdna for a quote to extract the data required. Once we have received the quote and approved it, and then received and analysed the data, we will provide a report to the QPS regarding this.

Cheers
Cathie

Cathie Allen BSc, MSc (Forensic Science) (She/Her*)
Managing Scientist
Social Chair, Organising Committee for 25th International Symposium of the Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022
Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health
p [redacted]

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From: Lara Keller [redacted]
Sent: Monday, 21 February 2022 11:22 AM
To: Neville.DavidH[OSC] [redacted]
Cc: Frieberg.DaleJ[OSC] [redacted]; Cathie Allen [redacted]
Subject: RE: Testing thresholds

Good morning David

Cathie is off duty today, so I have asked for an update from within the team today. I do know that Cathie has been following this up already.

Thanks and Kind Regards
Lara

Lara Keller B App Sc (MLS), Grad Cert Health Mgt, MAIMS, CMgr FIML
A/Executive Director
Forensic and Scientific Services
Prevention Division, Queensland Health
[redacted]

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From: Neville.DavidH[OSC] [redacted]
Sent: Monday, 21 February 2022 10:21 AM
To: Cathie Allen [redacted]
Cc: Frieberg.DaleJ[OSC] [redacted]; Lara Keller [redacted]
Subject: FW: Testing thresholds

Dear Cathie
I understand the difficulty of the ongoing coverage by the *The Australian* of the [redacted] case. This must be causing significant stress for you and your staff.

Unfortunately I have been drawn into comment internally on peripheral matters raised by the outlet on 18 February 2022.

article.

It claims that the Queensland lab requires crime scene samples to have the equivalent of at least 22 cells to be fully tested, otherwise they are deemed to have insufficient DNA. It claims that the threshold is double the 11 cells required in NSW, and almost three times the eight cells that the product manufacturer has used to obtain good quality DNA profiles.

I know you are busy, but since 1 December 2021 I have raised concerns in relation to the truncating of testing based on DNA quant values because of the significant number of below threshold samples yielding a profile when testing is continued. This remains a high priority matter for the QPS. To date I have not received any feedback or explanation as to difference between the predicted (<2%) and observed success rates (30%) for samples that reportedly contained a low concentration.

Could you please provide advice as to how the Queensland threshold for testing accords with other jurisdictions. Can you also please advise the outcome of any internal review that you have undertaken based on the information I provided. I need this information as a matter of urgency to brief the executive in relation to this matter.

Regards

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

From: Neville.DavidH[OSC] [redacted]
Sent: Friday, 17 December 2021 17:23
To: Cathie Allen [redacted]
Cc: Frieberg.DaleJ[OSC] [redacted]; 'Lara [redacted]
Subject: Re: [redacted]

Hi Cathie
Thanks for the clarification. That was my understanding too. I was of the belief that QHFSS stopped doing this as a matter of routine for low quant samples because there was a lower than 2 percent chance of success. However, QPS has found the success rate to be 30 percent when we requested this to be done. It is the difference between these success rates that I am interested in.

Have a good weekend

David Neville
Inspector, FSG
[redacted]

From: Cathie Allen [redacted]
Sent: Friday, December 17, 2021 5:06 pm

To: Neville.DavidH[OSC]
Cc: Lara Keller; Frieberg.DaleJ[OSC]
Subject: RE: [redacted]

Hi David

Thank you for the follow-up email regarding samples within this case.

To ensure that we're all on the same page, I'd like to clarify the process. If samples that have been deemed 'insufficient DNA for further processing' are processed further, they all first undergo a concentration step, followed by amplification. This is in contrast with samples that are not deemed in this range, as these samples amplification, without a concentration step. Just wanted to draw to your attention that there is additional work undertaken on the DNA extract to attempt to achieve a DNA result for the samples deemed 'insufficient DNA for further processing'.

Cheers
Cathie

Cathie Allen BSc, MSc (Forensic Science) (She/Her*)
Managing Scientist
Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022
Police Services Stream, Forensic & Scientific Services
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[redacted] *acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.*
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From: Neville.DavidH[OSC] [redacted]
Sent: Friday, 17 December 2021 12:04 PM
To: Cathie Allen [redacted]
Cc: Lara Keller [redacted]; Frieberg.DaleJ[OSC]
[redacted]
Subject: RE: [redacted]

Hi Cathie
In addition to the items on the list provided previously, last week we requested a blood swab [redacted]) to be retested which was originally reported as "insufficient DNA for further testing". This sample was taken from blood on a broken shard of glass as depicted in the photo below.

Given the nature of the stain and inert substrate, we were surprised with the original result which is what prompted the request to further test. Today we were advised that subsequent testing yielded a single source 20 loci profile. This was an excellent result solving the crime which would have been otherwise missed.

The image below is attached to the exhibit screen which was visible to the laboratory staff. The results of presumptive testing are also included on that screen. I wondered if lab staff use this information when making a decision on stopping testing?

Forwarded for you information and consideration along with the other material provided.

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

From: Neville.DavidH[OSC] [redacted]
Sent: Thursday, 16 December 2021 12:56
To: Cathie Allen [redacted]
Cc: Frieberg.DaleJ[OSC] [redacted]; Lara Keller
[redacted]
Subject: Re: [redacted]

Hi Cathie
Thanks, this is a high priority for us, we would appreciate advice as soon as possible please.

David Neville
Inspector, FSG
[redacted]

From: Cathie Allen [redacted]
Sent: Thursday, December 16, 2021 12:42 pm
To: Neville.DavidH[OSC]
Cc: Frieberg.DaleJ[OSC]; Lara Keller
Subject: RE: [redacted]

Hi David

Thank you for your email and feedback regarding this. We will review scientific data available to us and will provide further advice to the QPS in due course.

Cheers
Cathie

Cathie Allen **BSc, MSc (Forensic Science) (She/Her*)**
Managing Scientist
Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022
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From: Neville.DavidH[OSC] [redacted]
Sent: Monday, 13 December 2021 2:06 PM
To: Cathie Allen [redacted]
Cc: Harris.LibbyA[OSC] [redacted]
Subject: RE: [redacted]

Hi Cathie
Since sending you my last message I found some correspondence from February 2018 where QHFSS made a recommendation to QPS that testing of samples that contained less than 0.008ng/uL of DNA should discontinue because the chance of obtaining a profile was less than 2%. Samples below this threshold were previously micro concentrated in an effort to attain a profile. Based on the advice from QHFSS, the QPS agreed to discontinue testing including micro concentration under such circumstances and the result would be reported as "DNA Insufficient for further testing" (DIFFT). I am assuming this is the information I was seeking in the below request.

Based on the results obtained for [redacted], I asked my staff to undertake a wider review of the success rate of further testing of items that were originally reported as DIFFT during 2021. This revealed 51 out of 160 samples provided a profile when the QPS requested testing to continue. These items are listed in the attached.

On 14 November 2018 I raised similar concern in relation to [redacted] after 3 out of 4 samples yielded a result when QPS requested testing to continue. At that time QHFSS provided reassurance that the success rate would be lower than 2% and that the matter should be treated as an aberration. As a result the QPS agreed to continue the truncation of testing for items below the threshold quantity of DNA and limit automated micro concentration to P1 samples only.

Given the result of the recent cases where continued testing was successful, might it be timely to review the practice of truncating testing of lower quant items? For instance, is the threshold value still valid? Also, with the implementation of the latest version of STRMix that can deconvolute more complex mixtures, is it more likely to get a result now?

I think the 30% success rate of retesting warrants a little further examination to make sure we are maximising our chances of solving crime, particularly for major crime matters.

I look forward to discussing this further with you.

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

From: Neville.DavidH[OSC]
Sent: Friday, 3 December 2021 10:07
To: Cathie Allen [redacted]
Subject: RE: [redacted]

Thanks Cathie
I appreciate the timely feedback. Based on our conversation the other day, I am assuming these discussions occurred in 2008. Is there any correspondence that was provided to base this decision on that you can provide, please? For our refence and moving into the future, what is the actual percentage that your dataset has indicated? Obviously this information will be helpful in guiding future requests for retesting.

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

From: Cathie Allen [redacted]
Sent: Friday, 3 December 2021 09:55
To: Neville.DavidH[OSC] [redacted]
Cc: Justin Howes [redacted]
Subject: RE: [redacted]

Hi David

Thanks for the additional information on those samples from that particular case. We'll have a look into them and get back to you when we can.

After we had conducted a review of a large dataset, it was found that below a particular quantitation threshold and in line with manufacturer's specifications, a very small percentage of samples may

provide some type of DNA profile, if they proceeded through DNA processing. This information was provided to the QPS, and the QPS advised that it would prefer that those samples that didn't exceed the quant threshold were not processed through to a DNA profile. We've monitored this and have found that with a larger dataset, the small percentage didn't vary.

We'll provide advice for this particular case when we're able to.

Cheers
Cathie

Cathie Allen BSc, MSc (Forensic Science) (She/Her*)
Managing Scientist
Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022
Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health
[redacted]

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

*If you're wondering about the use of pronouns She/Her on this signature block, I encourage you to read some resources available here

From: Neville.DavidH[OSC] [redacted]
Sent: Wednesday, 1 December 2021 1:48 PM
To: Cathie Allen [redacted]
Cc: Justin Howes [redacted]
Subject: RE: [redacted]

Hi Cathie
To provide further context, it has been raised with me that 33 items were examined with advice being received, "DNA Insufficient for further testing". A request was made for these items to be further worked. Ten of these then returned a result with persons being identified with LRs of >100 billion. I have attached a spreadsheet that includes the results. II wondered if there was a particular reason for this case as to why approx. 30% of the samples yielded a result after the work was requested. Can you please advise what the actual threshold is and advice as to whether this needs to be reviewed.
Finally, sorry to sound demanding, can you also provide information on your expected likelihood of success in normal casework (i.e the likelihood of DNA insufficient samples yielding a result if testing is continued).

Cheers

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

From: Neville.DavidH[OSC]
Sent: Wednesday, 1 December 2021 10:24
To: Cathie Allen [redacted]
Subject: [redacted]

Hi Cathie
I wondered if you might be available at some time today to have a brief chat about some results from [redacted] If Justin was available too, that might be helpful. Can we teams please?

David Neville
Inspector
Biometrics
Forensic Services Group
Operations Support Command
[redacted]

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