From: Allan McNevin

Sent: Friday, 10 June 2022 8:21 AM

To: **Justin Howes** Cc: Paula Brisotto Subject: RE: docs

Hiya,

I've had a look over everything again (mostly looking at the changes) – all good, I think the report reads a lot better too

I was thinking today a little about the chart on page ten with quant ranges, and how the highest range it flips to more suitable than unsuitable, and it occurred to me that the total numbers for each range are interesting, how the total numbers decrease as the quant value goes up ... I would have thought that more samples with quants closest to the threshold would have been chosen for further work, rather than more samples close to the LOD. Just an odd observation.

Cheers

Αl

From: Justin Howes

Sent: Thursday, 9 June 2022 3:05 PM

To: Allan McNevin Cc: Paula Brisotto

Subject: RE: docs

HI all

Some amendments to the report have been made and I tracked the changes.

For consistency, I removed the NA from the criteria so we are only looking at 650 results. This impacted some graphs etc.

I looked at the 4p numbers and found to be 9 of the 165 samples (suitable).

I removed the point on 3500 altogether as although I had written 'might', I just don't have data at all so can keep assumptions out.

I changed uL to µL throughout.

I updated charts throughout.

Agree and addendum could be done on sample type and information obtained. This is a first pass assessment of data in the questioned range.

I have removed the options and just added considerations from here. A separate Options paper will be drafted.

Attached are: spreadsheet post review, doc accompanying spreadsheet, report with changes tracked, final report(v2). Justin



Justin Howes

Team Leader - Forensic Reporting and Intelligence Team

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

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From: Allan McNevin

Sent: Wednesday, 8 June 2022 12:20 PM

To: Justin Howes
Cc: Paula Brisotto

Subject: RE: docs

Hiya,

I have had a read of the review report – there are some wording suggestions, typos etc. but I haven't written hem down as I'm not sure that was the purpose of me having a read and I don't know how much of a draft it is. Sorry if you've already thought of what I have noted, it's just what springs to mind.

Some thoughts though – page 8 "The data in Project #184 did not include interpretations where the DNA profile result was deemed to have come from at least four contributors. (and remaining paragraph)" This makes me think that for the 167 samples that were suitable, we should go back through them to look at how many were 4P (might was well compare numbers of 1, 2, 3 contribs as well) as this is something that can covered clearly with data rather than make some caveat statements

Also page 8 – discussion on 3500 v 3100 results, have we seen a reduction in CMPU since going to 3500? Or increase? Or not looked at that? I know that increased signal strength means more information, which could make some previous CMPU reportable, and other formerly reportable now CMPU, so may not be relatable, but if we have the data ...

Since this report was written, it has obviously come out about the specific claim regarding SA cases / samples, so maybe going back and looking at the 167 samples and breaking them down with a bit more details so assess this specific element – one of the things that got me thinking as I was looking in the spreadsheet at profiles suitable for NCIDD or not – so we re-process an intimate swab from a complainant or suspect, we may not get an upload (because it is a complainant in a SA case that get's separated out / minor is suspect) but it could still be informative (example swabs

from suspect's intimate location, stat for remaining >100 bill to complainant, but no upload as suspect already uploaded from other intimate swab). The flipside was how many un-informative profiles there were i.e. suitable for interpretation but not giving any useful information (particularly intimate swabs that end up SS assumed contrib, or low level minors where even someone matching the few additional peaks give very low LRs) – this could all be an addendum to what has been done as it is just more detail on the same data.

Looking at the options for consideration, options 2 and 4 seem out of sync with the data. I.e. there is no data being presented for samples over the DIFP quant value regarding suitable v unsuitable, whether m'con has proved useful (increase in suitable, decrease in unsuitable in the subset that has been through m'con) etc. They're not silly ideas, but a bit of data would be needed e.g. looking at quants up to say 0.025 or could choose 0.0333 (15uL amp at max value) as anything less has sub optimal template.

I hope my input is useful to you

Cheers

Αl



Allan McNevin

Scientist - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic and Scientific Services

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From: Justin Howes

Sent: Friday, 3 June 2022 3:56 PM

To: Allan McNevin **Cc:** Paula Brisotto

Subject: docs

Hi

Thanks for working on this. If possible, please work in 611 or 6103 or at home.

Here is the source data, and draft reports. The Exec summary was written by Cathie, based on the other doc.

Please review and add details to a doc/xls..

We are aiming for Tues COB.

Thanks

Justin



Justin Howes

Team Leader - Forensic Reporting and Intelligence Team

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



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