Kylie Rika

From: Kylie Rika
Sent: Wednesday, 3 June 2020 8:23 AM
To: Justin Howes
Subject: RE: [redacted]

Thanks Justin

My full conversation (as original reviewer) with the PDA analyst is listed in the emails I sent on:

6 Feb 2020
11 March 2020
24 April 2020
27 April 2020
14 May 2020
2 June 2020

Please let me know if you don't have all of them and I will send to you so you can add in the FR notation.

Thanks
Kylie

From: Justin Howes [redacted]
Sent: Tuesday, 2 June 2020 4:11 PM
To: Kylie Rika [redacted]
Subject: RE: [redacted]

Hi Kylie
Thankyou for your information below. The information provided is part related to a particular sample and its reporting, and part related to process. This email is to address the sample component only and will complete this thread on this sample – I will add it to the FR as a sample notation in due course.

I will have the profile looked at by an additional person and through that process, they will naturally communicate with the PDA entry scientist to determine what path the sample could take from there. Thankyou for your information on this sample; your assistance on this sample is not required from here.

After the sample has progressed, I will add this thread to the FR so as not to influence the further interpretation. Please note that I have my reply here, and your last email, added to the last communication that I provided you on 1 May 2020 which was a reply to your email on 27 April 2020; this is to complete the entire thread on this sample.

Thanks
Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream
Forensic & Scientific Services, Health Support Queensland, Queensland Health

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

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From: Kylie Rika [redacted]
Sent: Thursday, 14 May 2020 12:08 PM
To: Justin Howes [redacted]; Allan McNevin [redacted]
Subject: RE: [redacted]

Hi both

I have used the relevant SOPs and guidelines to finalise the review of this sample.

There are many aspects that I consider when interpreting a DNA profile. One cannot simply "not see" other peaks that are below LOD and they do help build a picture of the profile as a whole, however I would never use this alone to make a call on a DNA profile. In fact with this DNA profile ([redacted] if I was simply blind to peaks below LOD, my call on this DNA profile is that it is still complex unsuitable due to the followings reasons:

Degradation – is observed and according to the number of contributors guidelines, the sample should be reworked
Stochastic range – at least two of the contributors in this sample are within the stochastic range (below ~300 rfu) and according to the number of contributors guidelines, further investigation may be required in this scenario
Allelic Imbalance – this is observed within this DNA profile and according to the number of contributors guidelines, the sample should be reworked
Reworking – according to the number of contributors guidelines, this is the type of sample that should be reworked despite it being a P3 sample

As a reviewer it is my opinion that either this sample is reworked or called complex unsuitable.

Allan if you decide to not rework then you will have to get a third expert to give their opinion on this sample. If it turns out that the third person agrees with your interpretation, then my opinion as original reviewer will need to be documented including the grounds for the dismissal of my viewpoint. This could be included in the FR as a notation against the sample.

As a side discussion, I note that none of our SOPs actually list LOD as being 16rfu except for 33538 which is an information document, not a SOP. If the definition of LOD is mean + 3 SD, then that is 8 rfu.

I also note the following from the number of contributors guidelines:

The aim of these guidelines is to assist in the assessment of the number of contributors for mixed DNA profiles obtained using the PowerPlex 21 system. These guidelines should be used in conjunction with the training and experience of the scientist. There may be features within the DNA profile other than those detailed in this document that may inform the number of contributors. If the scientist observes information/behaviours within the DNA profile that override these guidelines, it is acceptable for these observations to be used in the determination of the number of contributors. There are also certain reworks that are required, for example for quality reasons, before a reasonable assessment of the number of contributors can be made and these should be performed separately to the guidelines provided. Background information has also been presented in this document as this has been considered

in the development of the recommendations provided. References to stochastic effects relate to peaks which may drop out or be imbalanced.

Further, I would like to take this opportunity to formally challenge our SOPs and information documents in QIS as needing to be updated to better reflect what the validation data shows, what is suggested in current literature and what we have learned and experienced with DNA profiles over the last few years, in the interest of continuous quality improvement. Could you please advise on the most appropriate channel for me to request a review of the LOD and how we use it?

Thanks
Kylie

From: Justin Howes
Sent: Friday, 1 May 2020 4:07 PM
To: Kylie Rika [redacted]; Allan McNevin [redacted]
Subject: RE: [redacted]

Hi Kylie
I have considered the information you have provided further here.

To follow my email where I described where we are supported and non-supported, I direct you to use our Standard Operating Procedures and associated guidelines to complete the review interpretation of [redacted]

Thankyou
Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream
Forensic & Scientific Services, Health Support Queensland, Queensland Health

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From: Kylie Rika [redacted]
Sent: Monday, 27 April 2020 10:48 AM
To: Justin Howes [redacted] Allan McNevin [redacted]
Subject: RE: [redacted]

Thanks Justin

The LOD of 16 rfu which was calculated in 2012 was valid at the time with the data that was obtained. The number of contributors guidelines and intuitive exclusions guidelines were written based on this LOD and this data. The baseline was recalculated in 2017, after the creation of these guidelines. In this recalculation it was shown that the LOD was only 8 rfu. In order to maintain a smooth workflow (to avoid changing plate reading rules, STRmix settings etc) it was decided that since the LOR/LOD had not increased it would be ok to leave them as they are. This seemed to be the appropriate decision at the time and this is why the SOPs and training material reflect this value.

However, it has been noted over time that the baseline of the 3130 is significantly lower than 16 rfu and therefore peaks are regularly distinct from baseline but below the implemented LOD of 16 rfu. This means that, as scientists we are regularly in the position as outlined in Talyor et al, where we have peaks below the threshold that we feel we cannot ignore. Maybe, if we had had this journal article when we agreed to keeping the thresholds the same, we would not have made this decision.

We are now in the position where some scientists are using their scientific knowledge and experience and looking below LOD and some scientists that don't want to go against the SOP and won't look below LOD even though this is against their scientific judgement. This is leading to samples being incorrected at statement stage. In fact, it is my opinion that if this sample is reported as it currently stands, it will be incorrected at a later date.

The scientific data and published journal articles support the use of peaks below 16 rfu (down to 8rfu in fact), and therefore I don't think I can ethically use the 16 rfu threshold and ignore these peaks.

Maybe it is time for all reporting scientists to discuss this topic and come to an agreement on the way forward – after all, it is the reporters that need to defend the interpretations in court.

Agree that it is good that we can have healthy scientific debate.

Thanks
Kylie

From: Justin Howes [redacted]
Sent: Friday, 24 April 2020 4:33 PM
To: Kylie Rika [redacted]; Allan McNevin [redacted]
Subject: RE: [redacted]

Hi both
Healthy discussion is great! Firstly, yes this is not a world of fully continuous interpretations yet so we need to use what we have developed and supported as a Management Team.

We have supported LOD=16RFU since the PP21 validation in 2012, and continually supported this value through a number of reassessments since then. Our PP21 training presentations support above LOD of 16 and our case mgt SOPs support this as well, including the intuitive exclusion workflow and no. contributor guidelines.

We don't have any SOPs or guidelines supporting below this value. We are supported in below LOR within our documentation for assistance in determining possible number of contributors.

We use, and have used for years the same value for assessment of controls; we are not supported in our quality system below this value.

We'll keep moving with the values we have supported and we can look forward to the assessments of these values with VFP in conjunction with the latest versions of GMIDx and STRmix.

Independently I have assessed this profile and am satisfied with the interpretation as entered. I don't think a rework will work here; the only option would be a microcon. I think this is suitable to review as it is.

Regards
Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream
Forensic & Scientific Services, Health Support Queensland, Queensland Health

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From: Kylie Rika [redacted]
Sent: Friday, 24 April 2020 10:41 AM
To: Allan McNevin [redacted]
Cc: Justin Howes [redacted]
Subject: RE: [redacted]

Thanks Allan

In a world where we are not yet fully continuous, we have no choice but to assign thresholds. However, we must also take into consideration the experience and subjectivity of the analyst. We have DNA profile interpretation guidelines to assist in helping to group staff's interpretation approaches as closely together as possible, but the fact still remains, these are guidelines and interpretation is subjective.

I would be more confident explaining why I had considered the 21 peak at D2 (when it is only a few rfu less than the 25 and is clear from bassline and has good morph) than explaining why I ignored it because we have an arbitrary LOD of 16rfu (which isn't even the true LOD). 16rfu was decided on out of convenience after the laser change in 2017. I note that the # of contrib. guidelines talks about not using S/T peaks under LOD, but those guidelines were developed before the laser change. I guess what I am saying is that in the interests of continuous improvements in the way we interpret, we are probably overdue for a re-think on some things.

I also note the following from Taylor, Buckleton and Bright:

Does the use of probabilistic genotyping change the way we should view sub-threshold data?

Duncan Taylor, John Buckleton & Jo-Anne Bright

3. Conclusion
Continuous systems (at least STRmix as trialled here) can overcome the issues of missing low-level data with minimal effects on the outcome of the analysis. The effects of overestimation of the number of contributors may not be too severe as long as the system has been reliably validated for this policy. This situation should not be used to

enable a reduction of valid quality practices such as replication and careful expert inspection of profiles and cannot be assumed to be conservative. However, any system, even one possessing the soundest theoretical basis, that cannot withstand the rigours of practical use, is destined to remain nothing more than a nice idea. We have discussed strategies to mitigate the effect of uncertainty in the number of trace contributors present when sub-threshold information is present in a DNA profile. We support replication and lowering the AT whenever practical. The use of sub-threshold data without lowering the AT may be useful in some cases. The effects of mis-assignment of N in either direction are relatively mild and restricted to LRs less than one when comparing known contributors and low LRs greater than one when comparing known non-contributors.
We believe that treating the number of contributors as an unknown nuisance variable is the best long-term solution. An even better solution would be to combine the treatment of number of contributors as a nuisance variable with an expert system that utilises fluorescent signal directly and has models for different known artefacts. In such a system all data would be treated probabilistically and the tyranny of thresholds would be completely abolished. We are not aware of any system that can perform at this level and so can provide no examples of how it would perform.
Last, we suggest that some profiles are simply too complex and should not be interpreted. Ultimately it is the role of the scientist to assess each profile on its own merits and the case context in order to determine if and how analysis will proceed.

New baseline work with VFP will be a good opportunity to re-consider the way we consider LOD and LOR (or just one AT). It doesn't matter where you put a threshold you will always have peaks under it that you need to decide what to do with.

Thanks
Kylie

From: Allan McNevin [redacted]
Sent: Thursday, 23 April 2020 2:43 PM
To: Kylie Rika [redacted]
Subject: RE: [redacted]

Hi Kylie,
Apologies for the delayed response. I have consulted with Justin, and his advice was that the inclusion of any possible peaks below the agreed upon 16RFU LOD limit is not a supported approach. There was a previous discussion and subsequent voting e-mail where the management team agreed to maintaining this LOD. Please discuss this with Justin if you would like more information or would like to discuss further the inclusion of sub LOD peaks.
Cheers
Al

Allan McNevin
Senior Scientist – Evidence Recovery

Evidence Recovery Team, Forensic DNA Analysis
Forensic & Scientific Services, Health Support Queensland, Queensland Health

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From: Kylie Rika [redacted]
Sent: Wednesday, 11 March 2020 11:38 AM
To: Allan McNevin [redacted]
Subject: RE: [redacted]

Hi Allan

In my opinion this profile is 4p or complex and for me I would say complex.

I can't justify calling the 25 peak at D2 sub thresh and then just ignoring the 21 peak just because it is below LOD when they both look very similar. In addition our actual calculated LOD is 8 not 16 as per:

I:\Change Management\Verification of Equipment (post part replacement)\Review Baseline 3130xl B post laser change January 2017/Summary Report 3130xl B laser change January 2017 vfinal

Feel free to ask another scientist for their opinion.

Thanks
Kylie

From: Allan McNevin [redacted]
Sent: Thursday, 6 February 2020 3:01 PM
To: Kylie Rika [redacted]
Subject: RE: [redacted]

Hi,

I've uploaded a further zoom from GMIDX on the D2 locus, there is a 16,19 "major" 18,20 above threshold in the minor, 22 & 25 subthreshold, everything else is below LOD

Cheers
Al

Allan McNevin
Senior Scientist – Evidence Recovery

Evidence Recovery Team, Forensic DNA Analysis
Forensic & Scientific Services, Health Support Queensland, Queensland Health

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From: Kylie Rika [redacted]
Sent: Thursday, 6 February 2020 2:54 PM
To: Allan McNevin [redacted]
Subject: RE: [redacted]

D2

From: Allan McNevin [redacted]
Sent: Thursday, 6 February 2020 12:12 PM
To: Kylie Rika [redacted]
Subject: RE: [redacted]

HI,
I had another look. I'm still not seeing greater than 3P, can you point me in the direction of what you are seeing?
Thanks
Al

Allan McNevin
Senior Scientist – Evidence Recovery

Evidence Recovery Team, Forensic DNA Analysis
Forensic & Scientific Services, Health Support Queensland, Queensland Health

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From: Kylie Rika [redacted]
Sent: Thursday, 6 February 2020 11:37 AM
To: Allan McNevin [redacted]
Subject: [redacted]

Hi Allan

It is my opinion that this is >3p

Can you please have another look

Thanks
Kylie

Kylie Rika
Senior Scientist - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream
Forensic & Scientific Services, Health Support Queensland, Queensland Health

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