Feedback due 20/12/2017	
Staff member	**Feedback date**
LBR	1/12/2017
KDS	1/12/2017

ARM	5/12/2017
KAL	7/12/2017

PMB	19/12/2017
KDR	3/01/2018
AJR	5/01/2018

Feedback

Hi Justin
Looks good to me. Just a few minor formatting comments:

Figure 2 – maybe reduce to 4 decimal places?, also add X and Y axis labels
Figure 6 – add X and Y axis labels
Figure 7 – reduce decimals in labels
Figure 10 – re-format legend so that graph has more room
Thoughout – sometimes the ® is superscript and sometimes not (sorry that's very picky)

Thanks
Luke

Justin

Feedback as follows:

Abstract: A little disjointed to read – can the sentences/ideas be linked.

Section 4:2 (and throughout)– I don't really like the use of the work "Fail" it indicates we did something wrong, or that there is a quality issue - which is not the case. We have processed them correctly, but the outcome from the biological submission is not informative. Can we use another term "Nil result" or "Nil Intel" or similar?

Section 7: Could we/should we suggest case managers review cases on finalisation? If they think there is not much useful information in the case, and where they believe that the available profiles maybe useful (using their discretion) that they may consider manual Microcon reworks? While success rates are low, there are still potential successes.

Kirsten

G day,

Just a few things:

Abstract
Suggest reword
"Given this, further workflow streamlining processes could be implemented that would provide significant processing efficiencies, and cost and time savings such that these efforts could be better placed in processing higher DNA-yielding samples"
to
"Given this, further streamlining of workflow processes could be implemented that would provide significant efficiencies such that these efforts could be better placed in processing higher DNA-yielding samples"
or
"Given this, further workflow process streamlining could be implemented that would provide significant processing efficiencies in order for resources to be better utilised processing higher DNA-yielding samples"

5.2
"A total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection."

I'm trying to work out why there are so many samples without quant as the whole point of m'con to 35 was so that they were quanted after microcon and they should have a pre-microcon quant as well – is there are a problem with the data export?

Figure 1

Figure 2

Recommendations

Recommendation 2 – I'd support up to 0.02ng/uL (template of 300ng) as this is the "cross-over" point and I'd also support implementing for both P2 and P3 samples, as recommendation 3 and 5 still give the QPS an option to ask for more work on the sample, it's easy for them to do & it's an extension of the triaging process

Hi Justin

I've had a look through the report (just in case it isn't signed off by the time Kirsten goes on holiday)..

And with the recommendations – we will need to change the quant results upload programming in the FR to fit in line with the new values. I'm not sure how much work that would be for Troy etc. We would also then need to test the functionality works….

This would include:
- P1 and Coronial samples only to go to auto-microcon
- P2 samples at the auto-micorcon value range to go to "DNA Insufficient" (we would have to make sure this works for samples, currently it only works for QPS envm samples)
- P3 samples – would we keep the undetermined ones as "No DNA", then those up to 0.0133ng/uL make "DNA Inusufficient"?
- I think that's all…

Just some things to keep in mind.

Thanks
Kerry-Anne

Hi Justin, I've reviewed and happy with the theory and recommendations. I asked Lisa to have a look in the FR training site to see how the process for P3 samples would work once they move to PP21. I will forward you the email summarising this. Once a decision is reached on the range for quant values, we will need to submit enhancements to VSTS and create/write manual procedures for P3 samples both through Analytical and reporting. These manual processes will be in place until the enhancements are in FR. Thanks,
via track changes on doc in parent folder.
via track changes on doc in parent folder.

Response
Fig 2 - the pivot table uses the raw data from the Quant file. Unable to change here. Fig 6 and Fig 2 - changes the image type in the doc so now have the labels. Fig 10 fixed. Fixed superscript.
Abstract being re-written.

Abstract being re-written, and suggested wording used. Note support for higher Q value, but will go with auto-mic range for implementation and check post-implementation.

Feedback due 9/01/2018

Staff	Date
LBR	9/01/2018
KAL	9/01/2018
PMB	9/01/2018
KDR and AJR	9/01/2018
SMJ	9/01/2018
ARM	10/01/2018

Feedback
Hi Justin Looks great, I assume the recommendations apply to P3 samples amped in PP21? I'm ready to sign. Thanks Luke
Ok excellent. Might be worth specifying. I would either add a Scope section at the start (and say that recommendations apply to all P2 and P3 samples processed with PP21, or just specify in the Conclusion and Recommendations section – perhaps at start of recommendation 2? i.e. "For all Priority 2 and 3 samples processed with PP21, automatically….."
Hi Justin Looks good – apart from the typo in my name that you already know about. Thanks Kerry-Anne
Doesn't apply to P3 with PP21. Best to be option paper as QPS should make the decision on this.
via track changes on doc in parent folder.
via notes on doc in parent folder.
Hi, I am happy with the report (pie chart excluded …) – however, I would actually be in favour of rolling out DNA insufficient to 0.02 ng/uL, and consider an extension of the DNA triaging process Cheers Al

Response
Hey, yes all samples. Do you think I should just expand this a bit? jah
Hey, added to R1: 1. Cease ‘auto-microcon’ (Quant range: 0.001ng/uL to 0.0088ng/uL) processing for all samples of Priority 2 and 3 requested to be amplified with PowerPlex 21, with the following exceptions: jah
Adjusted
Agree