DNA Rework Authorisations

* Required

* This form will record your name, please fill your name.

1. Barcode *

2. DNA Priority *

- P1
- P2
- P3

3. Original Result (no mnemonics) *

4. Type of Rework Requested *

- [ ] Reamp
- [ ] Re-CE
- [ ] Other

5. Likely outcome of rework *

6. Risk of undertaking the rework (eg. NCIDD removal) *

7. Date for result release *

Please input date (dd/MM/yyyy)

Notice 132 - Item 5

Information provided by email on 19 September 2022 from

Paula Brisotto
Team Leader – Evidence Recovery & Quality Team

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

a) "As of 30 June, 2019, any rework on a previously reported Major Crime (Priority 2) result is not to be ordered without Managing Scientist or Executive Director authorisation." SOP 17117V21.6 (draft), page 11.
    a. A rework can mean microcon concentration, amplification or capillary electrophoresis.

    "Any process that is likely to exhaust all the DNA extract is required to have written approval from QPS to proceed prior to the process being conducted." SOP 17117V21.6 (draft) page 11.
b) Priority 2 samples require Managing Scientist or Executive Director authorisation to rework on a previously reported result.
    Any priority requires QPS approval to rework if likely to exhaust sample.
c) As for a)
d) 17117 Procedure for Case Management
e) MS Teams for request to Managing Scientist/Executive Director for approval. SOP 17117V21.6 (draft), page 11.
    Forensic Register Request/Task to the QPS for approval to rework if likely to exhaust sample. SOP 17117V21.6 (draft), page 12.

Current published SOP version is 17117V21

Document 17117v21.6 is currently in draft under review in QIS2. This draft version contains the QPS approval required for work if sample may be exhausted, as per DG memo 19/08/2022.

Josie Entwistle

From: Justin Howes
Sent: Wednesday, 30 January 2019 12:00 PM
To: Allan McNevin; Justin Howes; Kerry-Anne Lancaster; Kirsten Scott; Luke Ryan; Paula Brisotto; Adrian Pippia; Alicia Quartermain; Allison Lloyd; Angela Adamson; Angelina Keller; Anne Finch; Cassandra James; Claire Gallagher; Deborah Nicoletti; Emma Caunt; Hannah Pattison; Ingrid Moeller; Jacqui Wilson; Josie Entwistle; Kylie Rika; Matthew Hunt; Penelope Taylor; Rhys Parry; Sharon Johnstone; Thomas Nurthen
Subject: new process - reworking Major Crime

Hi all
Last week the QPS were in contact with GM Michel Lok, ED John Doherty and Cathie Allen regarding retraction of results.

Effective immediately, ED John Doherty has directed that any reported Major Crime sample is not to be reworked without Cathie Allen's authorisation.

Cathie will be seeking clarification through John on the finer points of Major vs Volume Crime samples.

I will add a note to the relevant SOPs.

Regards
Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

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

[redacted]

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

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Report for QIS OQI as of 28/06/2022 3:34:28 PM

Report for QIS OQI -

50753 Non compliance with reworking procedure for a validated result

OQI Details

Status	Closed Approved
Subject	A rework of a sample with a validated result was ordered without authorisation. As per directive from the Executive Director communicated via email dated 30 January 2019, 'any reported Major Crime sample is not to be reworked without [the Managing Scientist's] authorisation'. This process was not followed. A sample was originally reported as a 3 person mixture with an intel upload to NCIDD (UKM1). A link was obtained and a ref sample sent in generating a likelihood ratio of greater than 100 billion support for contribution. At statement stage, the reported results for this sample was viewed. Due to sub-threshold information and a low level profile, doubt was cast over the initial assessment and so a rework was ordered. The reporter initially believed that the result was un-validated because it was not green in FR. In fact, it was the updated results for the reference comparison that was not validated. The result linking UKM1 to the profile had been validated and, therefore, sent to QPS. This meant that the rework was ordered on a sample that had a validated initial result. Once the reporter realised the mistake, the HP6 was notified who advised to let the rework progress at it was on an amp batch. The rework came back and appeared to be from 4 contributors. The statement reviewer noticed that D18 looked odd with the proportions and so it was further reworked resulting in information to suggest the profile was comprised of at least 5 contributors.
Source of OQI	Internal Problem
Date Identified	26/03/2019

OQI Creator Contact Details

Creator	Hannah PATTISON
Organisational Unit/s	Reporting 2
Service/s	Forensic and Scientific Service
Site Location/s	Coopers Plains

Investigator/Actioner Contact Details

Actioner	Justin HOWES
Organisational Unit/s	Forensic Reporting and Intelligence
Service/s	Forensic and Scientific Service
Site Location/s	Coopers Plains

Investigation Details

Investigation Completed 05/04/2019 **Root Cause Type** Unintended Human Error

Investigation Details [redacted] was viewed in the FR to be incomplete. This was due to the presence of an orange symbol in the Exhibit Register. Consequently the Reporting Scientist requested a rework.

While monitoring progress of the rework, it was found that the final result had actually been reported and the orange indicator related to the update required after comparison of a reference sample.

The rework was at or beyond amplification stage when the Team Leader was notified. Advice was provided to the case manager that the rework will proceed through to profile. This advice was consistent with the 'No Further Testing' protocol.

A further rework was conducted after observing the first rework's DNA profile.

Unintended human error occurred in the following places: requesting a rework (x2) without authorisation from the Managing Scientist as per direction from the FSS Executive Director, and in the Team Leader forgetting to notify the Managing Scientist that a rework had been processed accidentally without Managing Scientist authorisation.

The Managing Scientist was notified of the unintended human error and strategies for further work were devised.

Preformed By Justin HOWES

Action Details

Action Complete 05/04/2019 **Action Fix Type** OtherNon-compliance with reworking process for Major Crime

Title

Action Description

Spin basket relating to the extraction of [redacted] was ordered for processing.

A second sample in the case [redacted] was reworked in an attempt to improve the previous result obtained and reported. NB. The previous result was reported as too complex for interpretation.

Reiteration of the Executive Director directive sent to case managers to ensure that all rework requests for Major Crime cases, after results have been reported, have had authorisation from the Managing Scientist. Reminder email sent by Supervising Scientist on 20 March, 2019.

A DNA profile loaded to NCIDD for [redacted] was removed. The same DNA profile was obtained from the rework of [redacted] and was marked for loading to NCIDD as of 02 April, 2019.

An Intelligence Report was written and issued on 02 April, 2019 detailing the DNA profile results for [redacted]. NB. The spin basket result also related to [redacted].

The Managing Scientist was notified that the Intelligence Report was issued on 02 April, 2019.

Task Details

No Tasks found

Follow-up And Approval

Follow-up Status Accepted

Follow-up Status Comment 8/04/2019 11:48:29 AM Hannah PATTISON:

	Follow-up accepted.
Approver	Cathie ALLEN
Approval/Rejection Date	03/06/2019
Approval/Rejection Comment	3/06/2019 3:16:43 PM Cathie ALLEN: This unintended human error has been a learning opportunity for all staff and allowed staff to be reminded of the processes in place.

Associations

Module	Audit		
QIS Record	Result Reporting including NCIDD Upload		
QIS Record Number	28406	**Associated Version**	OQI
Status	Closed	**Current Version**	
Association Description			

Records

No Records found

50753 Non compliance with reworking procedure for a validated result

Josie Entwistle

From: Kylie Rika
Sent: Wednesday, 20 March 2019 4:59 PM
To: Thomas Nurthen; Jacqui Wilson; Claire Gallagher; Allison Lloyd; Alicia Quartermain; Matthew Hunt; Sharon Johnstone; Emma Caunt; Deborah Nicoletti; Ingrid Moeller; Cassandra James; Penelope Taylor; Anne Finch; Angelina Keller; Rhys Parry; Josie Entwistle; Angela Adamson; Hannah Pattison; Adrian Pippia; Luke Ryan; Allan McNevin
Cc: Justin Howes; Paula Brisotto; Cathie Allen
Subject: Reminder: no rework on reported result until authorisation from Managing Scientist

Importance: High

Hi all

Please remember to not order a rework on an already reported result until authorisation has been granted from the Managing Scientist. This process was put in place by John Doherty, Executive Director.

Thanks
Kylie

Kylie Rika
Senior Scientist - Forensic Reporting and Intelligence Team

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

[redacted]

Josie Entwistle

From: Kylie Rika
Sent: Wednesday, 3 April 2019 3:43 PM
To: Alicia Quartermain; Claire Gallagher; Emma Caunt; Ingrid Moeller; Deborah Nicoletti; Penelope Taylor; Angelina Keller; Josie Entwistle; Hannah Pattison
Cc: Sharon Johnstone; Allison Lloyd; Justin Howes
Subject: Reworking

Hi

Just a reminder/clarification:

For P3 samples, at statement stage, you do not need authorisation from Managing Scientist to rework even if the result was already reported.

You DO need authorisation from Managing Scientist to rework a P2 sample that has already been reported.

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

[redacted]

Angelina Keller

From: Justin Howes
Sent: Friday, 21 January 2022 3:53 PM
To: Adrian Pippia; Alicia Quartermain; Allan McNevin; Angela Adamson; Angelina Keller; Anne Finch; Cassandra James; Claire Gallagher; Deborah Nicoletti; Emma Caunt; Ingrid Moeller; Jacqui Wilson; Josie Entwistle; Justin Howes; Kerry-Anne Lancaster; Kylie Rika; Matthew Hunt; Penelope Taylor; Rhys Parry; Sharon Johnstone; Tegan Dwyer; Thomas Nurthen; Justin Howes; Kirsten Scott; Luke Ryan; Megan Mathieson; Paula Brisotto
Subject: A reminder on reworks

Hi all
I just wanted to mention a couple of reminders on process:

- Please note that P3 samples are not to be requested for MIC or NUC reworks. The process is that they can be reworked in exceptional circumstances, and certainly can be reworked to resolve a CE issue (eg. p/up, BB). P3 samples can also be reworked via a reamp if not amped to max and you think there may be an upload as a result of that rework. I am not sure how often you might come across this, given the first amp (if not at max), would be amped at optimum template anyway.

- When requesting a rework, please ensure you 'click the head' and allocate the sample to yourself. This helps TAT as the sample will populate the list at the top as you view it allowing you to send for STRmix/review as soon as it practicable after list repopulation.

It was another busy PDA week – great work everyone!

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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Paula Brisotto

From: Cathie Allen
Sent: Tuesday, 8 February 2022 9:11 AM
To: Luke Ryan; Sharon Johnstone; Paula Brisotto; Kirsten Scott; Allison Lloyd; Justin Howes; Kylie Rika
Subject: RE: Testing restarted process improvement

Hi Everyone

I would encourage this process to be undertaken for a specific process – ie if forensic officers review the DNA results from samples they've taken, and they wish for samples that are DNA insuff to be further processed – then they would request the 'resume work as per advice from QPS'. However other requests for rework (ie incomplete DNA profile) should be requested via a different process.

I'll put this on the agenda for the meeting.

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]

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*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: Luke Ryan <[redacted]
Sent: Monday, 7 February 2022 3:00 PM
To: Sharon Johnstone <[redacted] Paula Brisotto <[redacted] Kirsten Scott <[redacted] Allison Lloyd <[redacted] Justin Howes <[redacted] Kylie Rika <[redacted]
Cc: Cathie Allen <[redacted]
Subject: RE: Testing restarted process improvement

Hi All
Yes lets discuss at Ops meeting, great idea.

Just a bit more context on what I was trying to say. I have had a number of restart after No DNA/DNA Insuff which I have sent to regular Mcon – and subsequently received enquiries from reporters (often for allocated cases) saying they would have preferred me not ordering the regular Mcon, as they would have considered pooling or Mcon to full. I don't mind ordering restarts but I am only ordering regular Mcons. Just wanted everyone to have this info when making the decision.

Thanks
Luke

From: Sharon Johnstone <[redacted]
Sent: Monday, 7 February 2022 1:11 PM
To: Luke Ryan <[redacted] Paula Brisotto <[redacted] Kirsten Scott <[redacted] Allison Lloyd <[redacted] Justin Howes <[redacted] Kylie Rika <[redacted]
Cc: Cathie Allen <[redacted]
Subject: RE: Testing restarted process improvement

Hi there,
I could see how this could work. It would be nice to have it as automated as possible though.
I don't think it necessarily needs to have involvement with reporters though. The re-activation would be determined by what stage it is at i.e what is the next step. If that is PDA or review then they could be inserted onto the PDA worklist and wait there for a reporter to pick it up as part of due course. I'm not sure why there would be any need to be aware of other results in the case as these items have been specifically selected to be restarted.

Happy to discuss though. Could it be a topic at the operational meeting this week?

Cheers,
Sharon

Sharon Johnstone
Senior Scientist – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream
Prevention Division, 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.

[redacted]

From: Luke Ryan <[redacted]
Sent: Monday, 7 February 2022 12:59 PM
To: Paula Brisotto <[redacted] Kirsten Scott <[redacted] Allison Lloyd <[redacted] Justin Howes <[redacted] Kylie Rika <[redacted] Sharon Johnstone <[redacted]
Cc: Cathie Allen <[redacted]
Subject: RE: Testing restarted process improvement

Hi All
Yes agree this would work. I think it would be worth having a chat about who does the reactivation and insertion to appropriate WL. I would prefer Analytical not to do this, as it can involve an element of case management and consideration of other results from the case.

Thanks
Luke

From: Paula Brisotto <[redacted]
Sent: Monday, 7 February 2022 12:37 PM
To: Luke Ryan <[redacted] Kirsten Scott <[redacted] Allison Lloyd <[redacted] Justin Howes <[redacted] Kylie Rika <[redacted] Sharon Johnstone <[redacted]
Cc: Cathie Allen <[redacted]
Subject: Testing restarted process improvement

Hi all,

I received a call from bdna last week morning regarding an enhancement they were looking at for restart testing, to enable automation of this process similar to the No further work process.

Current process for us:

<u>NTR by QPS</u>

NTR selected by QPS. Result line added “No testing required as per QPS” and validated. Removes from outstanding lists.

SSLU receive notice from SMU that testing is now required, and they enter an FR note, scan the email and send the email to Allison/Janine.

This requires manual reallocation onto an appropriate worklist (dependant on where the sample was at when testing was stopped). Samples progresses as per standard operating procedures.

<u>NDNAD/DIFP</u>

Quant values fall within NDNAD and DIFP range, Analytical staff enter result line and review.

QPS request further processing – FR task is sent to HP5 Analytical to restart testing.

This requires manual reallocation onto the appropriate worklist for additional processing.

Proposed enhancement:

The discussion I had was about using the similar process where we get notified of the NTR through FR, add a result line and validate – but in reverse.

Using a similar process to the No Further Work process, we would receive a generic result line to request testing to recommence, which FDNA would acknowledge through validation of the result line. My understanding is that the result line would populate a worklist for us to be able to validate and manually re-allocate to the correct process. I believe this could work for both NTR and NDNAD/DIFP and would remove the need to it to be directed to one person or for the process to be via emails.

The result line would be generic so it could be used for both, with the proposed as below:

"EXRMnemonic": "RWQPS",
"Result": "Resume work as per advice from QPS",
"Explanation": "QPS have provided advice that work is to resume for this item/sample. Testing has resumed, results pending.",

Please let me know what you think.

Thanks,
Paula

Paula Brisotto
Team Leader – Evidence Recovery & Quality Team

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

[redacted]

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RE: CTS sample 1096638267

From: Josie Entwistle <[redacted]
To: Lara Keller <[redacted]
Date: Tue, 12 Apr 2022 14:41:20 +1000

Hi Lara,

Thanks very much for that, and for hearing me out this morning. I appreciate your time and input.

Regards

Josie

From: Lara Keller <[redacted]
Sent: Tuesday, 12 A
To: Josie Entwistle [redacted]
Subject: RE: CTS sample [redacted]

Hello Josie

My thoughts or suggestions below for inclusion in your response…. Of course you are under no obligation to include anything I suggest.

I thought that as I'm the reviewer for this CTS, I would be safe to offer my interpretive opinion and have my suggestions considered in good faith.

I have not challenged your ability to undertake proficiency testing or handle samples with due diligence. I am surprised that our difference of scientific opinion has led to my line manager being included in your response.

In terms of this case, at this time I'm unable to concur. On that basis, if you wish, I can step away so you can seek an alternate reviewer.

Josie, feel free to blind copy me into your response if you wish.

Best wishes,
Lara

From: Josie Entwistle <[redacted]
Sent: Tuesday, 12 April
To: Lara Keller <[redacted]
Subject: FW: CTS sample [redacted]

From: Justin Howes <[redacted]
Sent: Monday, 11 Apr
To: Josie Entwistle <Jos
Cc: Sharon Johnstone <[redacted]ov.au>
Subject: RE: CTS sample [redacted]

Hi Josie
Thanks for the clarification on locus.

I am aware that stutter is one aspect that could indicate another contributor. It is observed in SS and mixtures, and can also be observed in mixtures to be higher that the values we use.

I will treat this sample with the same due diligence that I would treat any sample and consider the need for reworks. In this situation I don't see any need for a rework given the profile obtained and data within. This would not be any

different to any casework sample.

From your email, I do have some points for you to clarify with me please. I am curious how having an impending NATA audit should affect the case manager's decision making on reworks? Please also clarify where the number of contributors forms part of our external CTS assessment? I have been doing proficiency tests for over 20 years in three labs and for nearly 10 years, I have advocated for this sort of assessment in CTS.

On NATA, while the standards explain that the tech review must not be performed such that it shifts the perceived responsibility of the findings from the examiner to the reviewer, I have still taken on board your view that you would consider 3mx for this profile. I have run as a 3p and have obtained the same data for the profile record and imported the new pdf. We have the same LR order of magnitude and I have attached the new LR pdf in the sample notation. The only difference is that this signal is used as a peak – I will have to add this as an allele to the table of alleles in the CTS. Please redirect the CTS back to me for the edit.

Thanks
Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team
Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
[redacted]
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: Josie Entwistle <[redacted]
Sent: Monday, 11
To: Justin Howes
[redacted] CTS[redacted]

Hi Justin,

I listed D3 in error, my feedback was in relation to D1.
I understand that the profile is well amped, however the high stutter in itself is an indication of an additional contributor.
The reference to the single source guidelines was to illustrate that we have guided leniency regarding stutters above threshold for single source, but this guided/supported leniency has not been extended to mixtures.
We have been instructed to treat CTS as per casework samples. In a casework scenario I would consider this profile either as a 3mx, or I would rework to check if the stutter changed in a subsequent run and re-assess.
It is certainly possible that a change in the number of contributors may not affect the LRs, however the assessment of the number of contributors is one of the first steps in our interpretation process, is reported, and forms part of our external CTS assessment. In the interests of giving this sample due diligence and with an awareness of upcoming laboratory reviews (eg NATA), it is my preference to rework this profile as the next step.

Regards

Josie

From: Justin Howes <[redacted]
Sent: Friday, 8 Apri
To: Josie Entwistle
Subject: RE: CTS[redacted]

Hi Josie

At D3, I didn't make a note for this locus as I considered the possibility of n-1 and n-2rpt stutters contributing to the pk ht of the 14 [redacted] For this sample at PDA, I didn't consider a rework necessary as it was amped at optimum and was a good quality profile; I didn't see any analytical considerations that would lead me to think it needed a rework. I think from a risk point of view, whether 3p or 2p, there will be no effect on LRs, NCIDD is not relevant, and the final outcome would be unchanged. I think it can be reasonably explained as a min number of 2p which is where my opinion went here.

The SS high stutter work was a guideline only as it may not fit with all profiles and the weight scientists put to different aspects observed in the profile eg additional s/t peaks, no. stutters, location of stutters etc. This is what I considered for D1 in this sample which was viewed in context with the rest of the evidence in the profile ie. in combination with observations (…or lack of observations really…) elsewhere in the profile.

Please let me know if this makes sense here.

Thanks for checking in with me on it.

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: Josie Entwistle <[redacted]
Sent: Friday, 8 Ap
To: Justin Howes [redacted]>
Subject: CTS sample [redacted]

Hi Justin,

I'm wondering if you'd consider reworking this one? If I was considering this as a casework sample, I would be considering this as a possible 3mx given the high stutter @D3 as we currently don't have an allowance for high stutter in mixtures as we do for single source. Let me know.

Thanks

Josie

Josie Entwistle
Reporting Scientist - Forensic Reporting & Intelligence Team
Forensic DNA Analysis, Forensic & Scientific Services
Prevention Division, Queensland Health
[redacted]

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Kylie Rika 8.4.22

- Kylie said she is putting all ducks in a row
- She gave me a large collection of documents, with tab's

DIFP

- Went back to our quant validation
- there are holes in the validation

- Big problems in the lab
  - No true science leaders
  - No proper review of experiments
  - Rank & power model

QUANT = estimate how much DNA is in the sample
BUT used to set up limit ; Very specific threshold is worrying — should not drive process change

- Summary is attached to the report provided.
  - Emma helped Kylie prepare this

Other issues :

- Not allowed to reach out to other labs for advice
- Staff need to be empowered to rework, not "think twice, go through me"
- Can't data mine FR
- Feedback asked for but met ; hostility
  ↳ justify / brush under carpet
- Huge pressure to sign off
- mgt team arrogant & egos
- Previously asked for scientific advisory board — no action

When I challenged the DIFP, my team was broken up

- Now set up a spreadsheet to capture variances Nov 21
  ↳ email
- SOP 17117 V21 states ED to authorise rework ???
- Business not science
- Cathie not competent anymore
- Luke just validates w/o taking other considerations
- Kylie went back over a recent case to see if there were any DIFF
  - examples provided

Luke Ryan

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

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

[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 <Lai-[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]